STIC Search Report

Biotech-Chem Library

Scientific & Technical Information Center
USPTO

STIC Database Tracking Number: 114881

To: Terra Gibbs
Location: rem/2d10/2c18
Art Unit: 1635
Wednesday, March 03, 2004

Case Serial Number: 10/029115

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

SEARCH REQUEST FORM

Requestor's Name: ______________________ Serial Number: ______________________

Date: ______________ Phone: ______________ Art Unit: ______________

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

Date completed: 03-03-04
Searcher: Beverly c 2528
Terminal time: 20
Elapsed time: ______
CPU time: ______
Total time: 25
Number of Searches: ______
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ Other CGN

114881

STIC-Biotech/ChemLib

From: Gibbs, Terra
Sent: Sunday, February 22, 2004 1:51 PM
To: STIC-Biotech/ChemLib
Subject: Seqeunce search request

Please do a regular search of SEQ ID NO:1 of USSN 10/029,115.

Also, include an oligomer search of SEQ ID NO:1 as I am looking for a nucleic acid capable of hybridizing to SEQ ID NO:1.

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
571-272-0758

Searcher:____________
Phone:____________
Location:____________
Date Picked Up:____________
Date Completed:____________
Searcher Prep/Review:____________
Clerical:____________
Online time:____________

TYPE OF SEARCH:
NA Sequences:____________
AA Sequences:____________
Structures:____________
Bibliographic:____________
Litigation:____________
Full text:____________
Patent Family:____________
Other:____________

VENDOR/COST (where applic.)
STN:____________
DIALOG:____________
Questel/Orbit:____________
DRLink:____________
Lexis/Nexis:____________
Sequence Sys.:____________
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Other (specify):____________

Gibbs, T.
10/029115
Seq. ID 1 w/ Inters

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          March  2, 2004, 09:55:00 ; Search time 8004 Seconds
                                            (without alignments)
                                            17368.860 Million cell updates/sec

Title:           US-10-029-115-1
Perfect score:   3951
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters:      75154660

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3892	98.5	3951	1	PCT-US02-33845-2	Sequence 2, Appli
3	3870.2	98.0	5014	1	PCT-US03-37730-22	Sequence 22, Appl
4	3867	97.9	4989	1	PCT-US03-37730-26	Sequence 26, Appl
5	3838.6	97.2	5191	89	US-60-324-185-5555	Sequence 5555, Ap
6	3792.8	96.0	4033	43	US-10-029-115-5	Sequence 5, Appli
7	3772.8	95.5	4032	1	PCT-US02-33845-6	Sequence 6, Appli
8	3637.4	92.1	4631	107	US-60-500-337-1177	Sequence 1177, Ap
9	3637.4	92.1	4881	107	US-60-500-337-1176	Sequence 1176, Ap
10	3637.4	92.1	4982	107	US-60-500-337-1175	Sequence 1175, Ap
11	3635	92.0	4133	54	US-10-725-121-11	Sequence 11, Appl
12	3635	92.0	4133	54	US-10-725-329-11	Sequence 11, Appl
13	3635	92.0	4133	54	US-10-725-330-11	Sequence 11, Appl
14	3635	92.0	4133	64	US-60-081-784-11	Sequence 11, Appl
15	3635	92.0	4436	46	US-10-170-235-34328	Sequence 34328, A
16	3635	92.0	4553	25	US-09-607-200-6297	Sequence 6297, Ap
17	3635	92.0	4557	32	US-09-770-174-3346	Sequence 3346, Ap
18	3635	92.0	4557	32	US-09-770-175-7824	Sequence 7824, Ap
19	3635	92.0	4878	1	PCT-US03-37730-25	Sequence 25, Appl
20	3632.2	91.9	3888	1	PCT-US02-01048-37	Sequence 37, Appl
21	3632.2	91.9	3888	1	PCT-US03-37730-21	Sequence 21, Appl
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42	3358.2	85.0	3735	32	US-09-789-390-12	Sequence 12, Appl
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45	3036.4	76.9	4849	45	US-10-144-771-21878	Sequence 21878, A

ALIGNMENTS

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RESULT 1
US-10-029-115-1
; Sequence 1, Application US/10029115
; GENERAL INFORMATION:
;  APPLICANT: Luo, Ying
;  APPLICANT:  Fu, Alan C
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION: Novel Germinal Center Kinase Cell Cycle Protiens, Compositions an
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: A-70229/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/10/029,115
;  CURRENT FILING DATE:  2001-10-19
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 3951
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-1
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  Matches 3951;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     1081 CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAG 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAG 1140

Qy     1141 CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA 1200

Qy     1201 GAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 GAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG 1260

Qy     1261 CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG 1320

Qy     1321 GAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 GAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG 1380

Qy     1381 CAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCC 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 CAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCC 1440

Qy     1441 CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCT 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCT 1500

Qy     1501 GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC 1560

Qy     1561 TGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 TGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC 1620

Qy     1621 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCC 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCC 1680

Qy     1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG 1740

Qy     1741 CACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 CACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC 1800

Qy     1801 CCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGC 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 CCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGC 1860

Qy     1861 CAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 CAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC 1920

Qy     1921 CGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCC 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 CGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCC 1980

Qy     1981 CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGC 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGC 2040

Qy     2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100

Qy     2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160

Qy     2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220

Qy     2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280

Qy     2281 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGG 2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2281 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGG 2340

Qy     2341 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAG 2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2341 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAG 2400

Qy     2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460

Qy     2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520

Qy     2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580

Qy     2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640

Qy     2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700

Qy     2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760

Qy     2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820

Qy     2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880

Qy     2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940

Qy     2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000

Qy     3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060

Qy     3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120

Qy     3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180

Qy     3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240
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Db       3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240

Qy       3241 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC 3300
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Db       3241 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC 3300

Qy       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360

Qy       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420

Qy       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480

Qy       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540

Qy       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600

Qy       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660

Qy       3661 ACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTG 3720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 ACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTG 3720

Qy       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780

Qy       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840

Qy       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA 3900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA 3900

Qy       3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
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RESULT 2
PCT-US02-33845-2
; Sequence 2, Application PC/TUS0233845
; GENERAL INFORMATION:
; APPLICANT: Rigel Pharmaceuticals, Inc.
; APPLICANT: Leo, Cindy
; APPLICANT: Luo, Ying
; APPLICANT: Xu, Xiang
; APPLICANT: Yu, Simon
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE PROTEINS, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: 021044-005600PC
; CURRENT APPLICATION NUMBER: PCT/US02/33845
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 10/029,115
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 3951
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: misshapen/NIK-related kinase isoform 3a
PCT-US02-33845-2

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  Query Match             98.5%;  Score 3892;  DB 1;  Length 3951;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 3948;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    5;

Qy          1 GCCCTTATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCCTTATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTG 60

Qy         61 CGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAG 120

Qy        121 GTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC 180

Qy        181 ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC 240

Qy        241 CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGAT 300

Qy        301 GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG 360

Qy        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420

Qy        421 AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT 480

Qy        481 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG 540

Qy        541 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG 600

Qy        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660

Qy        661 CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 720

Qy        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780

Qy        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840

Qy        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCAT-CCGGGACCAGCCCACGGAGCGGCAGGT 899
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCCGGGACCAGCCCACGGAGCGGCAGGT 900

Qy        900 CCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGA 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGA 960

Qy        960 GACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGA 1019
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 GACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGA 1020

Qy         1020 GCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCT 1079
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 GCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCT 1080

Qy         1080 CCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCA 1139
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 CCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCA 1140

Qy         1140 GCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCAT 1199
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 GCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCAT 1200

Qy         1200 AGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCA 1259
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 AGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCA 1260

Qy         1260 GCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCG 1319
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 GCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCG 1320

Qy         1320 GGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGA 1379
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 GGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGA 1380

Qy         1380 GCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTC 1439
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1381 GCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTC 1440

Qy         1440 CCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCC 1499
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1441 CCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCC 1500

Qy         1500 TGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGC 1559
                |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db         1501 TGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG-ATCCCGCTGACAAACCAGC 1559

Qy         1560 CTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGC 1619
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1560 CTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGC 1619

Qy         1620 CAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCATCCCCAGGCCTCCCCAGGGCC 1679
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1620 CAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCATCCCCAGGCCTCCCCAGGGCC 1679

Qy         1680 CCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACC 1739
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1680 CCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACC 1739

Qy         1740 GCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGA 1799
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1740 GCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGA 1799

Qy         1800 CCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCG 1859
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1800 CCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCG 1859

Qy         1860 CCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGT 1919
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1860 CCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGT 1919

Qy         1920 CCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGC 1979
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1920 CCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGC 1979

Qy         1980 CCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCG 2039
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1980 CCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCG 2039

Qy         2040 CAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCC 2099
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Db         2040 CAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCC 2099

Qy         2100 TCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAG 2159
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db         2100 TCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGA--TCAG 2157

Qy         2160 GAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCT 2219
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2158 GAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCT 2217

Qy         2220 CCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGAGCCTCCTCCAAACTGGACAGCTC 2279
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2218 CCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGAGCCTCCTCCAAACTGGACAGCTC 2277

Qy         2280 CCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCG 2339
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2278 CCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCG 2337

Qy         2340 GCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAA 2399
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2338 GCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAA 2397

Qy         2400 GAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGA 2459
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Db         2398 GAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGA 2457

Qy         2460 GGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGG 2519
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2458 GGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGG 2517

Qy         2520 GGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCA 2579
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2518 GGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCA 2577

Qy         2580 GCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCT 2639
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2578 GCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCT 2637

Qy         2640 GCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTC 2699
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Db         2638 GCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTC 2697

Qy         2700 ACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCA 2759
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Db         2698 ACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCA 2757

Qy         2760 GTCTCGTGGGCTGGTAAAGGCCCCTGGC-AAGAGCTCGTTCACGATGTTTGTGGATCTAG 2818
                |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db         2758 GTCTCGTGGGCTGGTAAAGGCCCCTGGCAAAGAGCTCGTTCACGATGTTTGTGGATCTAG 2817

Qy         2819 GGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAG 2878
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2818 GGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAG 2877

Qy         2879 AGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGA 2938
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2878 AGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGA 2937

Qy         2939 ATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGAT 2998
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2938 ATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGAT 2997

Qy         2999 TCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGA 3058
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2998 TCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGA 3057

Qy         3059 ACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGC 3118
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3058 ACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGC 3117

Qy         3119 GACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGA 3178
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3118 GACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGA 3177
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Qy       3179 AAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATG 3238
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Db       3178 AAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATG 3237

Qy       3239 ACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGACATGGAGGGCTGCGGGC 3298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3238 ACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGACATGGAGGGCTGCGGGC 3297

Qy       3299 ACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCG 3358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3298 ACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCG 3357

Qy       3359 TGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTG 3418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3358 TGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTG 3417

Qy       3419 CCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCA 3478
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Db       3418 CCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCA 3477

Qy       3479 AGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCT 3538
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Db       3478 AGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCT 3537

Qy       3539 ATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCC 3598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3538 ATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCC 3597

Qy       3599 TCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTC- 3657
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3598 TCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCA 3657

Qy       3658 AACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCT 3717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3658 AACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCT 3717

Qy       3718 GTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGC 3777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3718 GTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGC 3777

Qy       3778 TCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAG 3837
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Db       3778 TCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAG 3837

Qy       3838 TTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGC 3897
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Db       3838 TTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGC 3897

Qy       3898 CAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
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RESULT 3

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PCT-US03-37730-22
; Sequence 22, Application PC/TUS0337730
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: MAPKs AS MODIFIERS OF THE RAC, AXIN, AND BETA-CATENIN PATHWAYS
;  TITLE OF INVENTION:  AND METHODS OF USE
;  FILE REFERENCE: EX03-089C-PC
;  CURRENT APPLICATION NUMBER: PCT/US03/37730
;  CURRENT FILING DATE:  2003-11-24
;  PRIOR APPLICATION NUMBER: US 60/429,061
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: US 60/437,163
;  PRIOR FILING DATE: 2002-12-30
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 5014
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-37730-22

  Query Match             98.0%;  Score 3870.2;  DB 1;  Length 5014;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 3942;  Conservative    0;  Mismatches    3;  Indels   60;  Gaps    1;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 256

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
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Db        257 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 316

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
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Db        317 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 376

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 436

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
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Db        437 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 496

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 556

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Db        557 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 616

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
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Db        617 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 676

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Db        677 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 736

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
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Db        737 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 796

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 856

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 916

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Db        917 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 976

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1036

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1096

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
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Db       1097 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1156

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
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Db   1157 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1216

Qy   1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
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Db   1217 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1276

Qy   1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
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Db   1277 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1336

Qy   1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
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Db   1337 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1396

Qy   1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1397 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1456

Qy   1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1457 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1516

Qy   1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   1517 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1576

Qy   1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1577 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1636

Qy   1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
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Db   1637 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1696

Qy   1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
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Db   1697 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1756

Qy   1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1757 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1816

Qy   1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
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Db   1817 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1876

Qy   1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1877 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1936

Qy   1745 ----------------------------------------------------------AG 1746
                                                                    ||
Db   1937 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1996

Qy   1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1997 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2056

Qy   1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
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Db   2057 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2116

Qy   1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
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Db   2117 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2176

Qy   1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
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Db   2177 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2236

Qy   1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2237 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2296

Qy   2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2297 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2356

Qy   2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2357 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2416

Qy   2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2417 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2476

Qy   2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2477 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2536

Qy   2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2537 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2596

Qy   2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2597 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2656

Qy   2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2657 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2716

Qy   2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2717 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2776

Qy   2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2777 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2836

Qy   2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2837 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2896

Qy   2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2897 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2956

Qy   2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2957 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 3016

Qy   2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3017 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 3076

Qy   2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3077 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 3136

Qy   2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3137 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 3196

Qy   2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3197 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3256

Qy   3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3257 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3316

Qy   3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3317 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3376
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Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3377 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3436

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3437 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3496

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3497 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3556

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3557 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3616

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3617 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3676

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3677 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3736

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3737 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3796

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3797 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3856

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3857 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3916

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3917 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3976

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3977 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 4036

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4037 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 4096

Qy       3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4097 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 4156

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              |||||||||||||||||||||||||||||||||||||||  ||||
Db       4157 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 4201
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RESULT 4
PCT-US03-37730-26
; Sequence 26, Application PC/TUS0337730
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MAPKs AS MODIFIERS OF THE RAC, AXIN, AND BETA-CATENIN PATHWAYS
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: EX03-089C-PC
; CURRENT APPLICATION NUMBER: PCT/US03/37730
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 60/429,061
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 60/437,163
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 4989
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-37730-26

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  Query Match             97.9%;  Score 3867;  DB 1;  Length 4989;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 3940;  Conservative    0;  Mismatches    5;  Indels   60;  Gaps    1;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 256

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 316

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 376

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 436

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 496

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 556

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 616

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
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Db        617 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 676

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Db        677 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 736

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
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Db        737 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 796

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 856

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 916

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 976

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1036

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1096

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1156
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Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1157 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1216

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1276

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1277 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1336

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1337 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1396

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1397 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1456

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1457 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1516

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1517 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1576

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1577 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1636

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1637 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1696

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1697 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1756

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1757 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1816

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1817 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1876

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db       1877 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1936

Qy       1745 ----------------------------------------------------------AG 1746
                                                                        ||
Db       1937 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1996

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
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Db       1997 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2056

Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
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Db       2057 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2116

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
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Db       2117 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2176

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2177 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2236

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2237 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2296

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2297 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2356

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2357 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2416

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2417 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2476

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
              ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Db       2477 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTG 2536

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2537 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2596

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2597 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2656

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2657 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2716

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2717 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2776

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2777 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2836

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2837 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2896

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2897 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2956

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2957 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 3016

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3017 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 3076

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3077 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 3136

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3137 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 3196

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3197 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3256

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3257 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3316

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3317 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3376

Qy     3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3377 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3436

Qy     3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3437 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3496

Qy     3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3497 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3556

Qy     3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3557 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3616

Qy     3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3617 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3676

Qy     3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3677 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3736

Qy     3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3737 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3796

Qy     3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3797 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3856

Qy     3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3857 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3916

Qy     3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3917 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3976

Qy     3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3977 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 4036

Qy     3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4037 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 4096

Qy     3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4097 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 4156

Qy     3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
            |||||||||||||||||||||||||||||||||||||||  ||||
Db     4157 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 4201
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RESULT 5
US-60-324-185-5555
; Sequence 5555, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 5555
;   LENGTH: 5191
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 1098431.17
US-60-324-185-5555

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  Query Match             97.2%;  Score 3838.6;  DB 89;  Length 5191;
  Best Local Similarity   98.1%;  Pred. No. 0;
  Matches 3931;  Conservative    0;  Mismatches   14;  Indels   64;  Gaps    2;

Qy        7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      403 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 462

Qy       67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      463 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 522

Qy      127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      523 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 582

Qy      187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      583 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 642

Qy      247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      643 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 702

Qy      307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      703 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 762

Qy      367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      763 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 822

Qy      427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      823 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 882

Qy      487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      883 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 942

Qy      547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      943 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 1002

Qy      607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1003 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 1062

Qy      667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1063 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 1122

Qy      727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1123 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 1182

Qy      787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1183 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1242

Qy      847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1243 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1302

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1362

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1422

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1482

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1542

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1543 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1602

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1662

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1663 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1722

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1723 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1782

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1783 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1842

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAA----CAGCAGCAGCAGCAGCTCCTGCCTGG 1502
              ||||||||||||||||||||||||||||||    ||    |    |||||||||||||||
Db       1843 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACACGCACGCACGCACGCAGCTCCTGCCTGG 1902

Qy       1503 GGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTG 1562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1903 GGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTG 1962

Qy       1563 GGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAA 1622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1963 GGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAA 2022

Qy       1623 GAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCC 1682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2023 GAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCC 2082

Qy       1683 AGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCA 1742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2083 AGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCA 2142

Qy       1743 CA---------------------------------------------------------- 1744
              ||
Db       2143 CAAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATC 2202

Qy       1745 --AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCC 1802
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2203 CCAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCC 2262

Qy       1803 CGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCA 1862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2263 CGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCA 2322

Qy       1863 GAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCG 1922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2323 GAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCG 2382

Qy       1923 CCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCT 1982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2383 CCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCT 2442

Qy       1983 TAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAG 2042
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2443 TAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAG 2502

Qy       2043 CAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCC 2102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2503 CAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCC 2562

Qy       2103 AGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAG 2162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2563 AGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAG 2622

Qy       2163 GAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCC 2222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2623 GAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCC 2682

Qy       2223 CCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCC 2282
              ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Db       2683 CCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCC 2742

Qy       2283 TGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCC 2342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2743 TGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCC 2802

Qy       2343 CGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAA 2402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2803 CGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAA 2862

Qy       2403 GGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGA 2462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2863 GGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGA 2922

Qy       2463 AGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGA 2522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2923 AGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGA 2982

Qy       2523 TACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCC 2582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2983 TACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCC 3042

Qy       2583 CCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCT 2642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3043 CCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCT 3102

Qy       2643 GCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACC 2702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3103 GCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACC 3162

Qy       2703 CACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTC 2762
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       3163 CACCGAGAACAGCAAAGGCCAAAGCCCACCCTCAAAGGATGGGAGTGGTGACTACCAGTC 3222

Qy       2763 TCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGAT 2822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3223 TCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGAT 3282

Qy       2823 CTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGG 2882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3283 CTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGG 3342

Qy       2883 CACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCC 2942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3343 CACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCC 3402

Qy       2943 CACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAA 3002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3403 CACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAA 3462
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Qy       3003 CTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGG 3062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3463 CTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGG 3522

Qy       3063 GCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACG 3122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3523 GCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACG 3582

Qy       3123 CTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAG 3182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3583 CTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAG 3642

Qy       3183 GAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCC 3242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3643 GAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCC 3702

Qy       3243 AGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTA 3302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3703 AGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTA 3762

Qy       3303 CCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGA 3362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3763 CCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGA 3822

Qy       3363 GGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGA 3422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3823 GGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGA 3882

Qy       3423 CCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGT 3482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3883 CCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGT 3942

Qy       3483 CATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGA 3542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3943 CATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGA 4002

Qy       3543 CATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCC 3602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4003 CATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCC 4062

Qy       3603 CAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACAC 3662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4063 CAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACAC 4122

Qy       3663 GTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGC 3722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4123 GTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGC 4182

Qy       3723 CTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGT 3782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4183 CTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGT 4242

Qy       3783 GGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCT 3842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4243 GGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCT 4302

Qy       3843 GTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGT 3902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4303 GTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGT 4362

Qy       3903 TTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              |||||||||||||||||||||||||||||||||||||||||||  ||||
Db       4363 TTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 4411
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RESULT 6
US-10-029-115-5
; Sequence 5, Application US/10029115
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: Novel Germinal Center Kinase Cell Cycle Protiens, Compositions an
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: A-70229/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 4033
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-5

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  Query Match             96.0%;  Score 3792.8;  DB 43;  Length 4033;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 3877;  Conservative    0;  Mismatches    2;  Indels   63;  Gaps    2;

Qy         64 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 154

Qy        124 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 214

Qy        184 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 274

Qy        244 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 334

Qy        304 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 394

Qy        364 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 454

Qy        424 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 514

Qy        484 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 574

Qy        544 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 634

Qy        604 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 694

Qy        664 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 754

Qy        724 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 814

Qy        784 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 874

Qy        844 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 934

Qy        904 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 963
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          935 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 994

Qy          964 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1023
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          995 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1054

Qy         1024 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1083
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1055 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1114

Qy         1084 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAG 1143
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1115 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAG 1174

Qy         1144 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1203
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1175 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1234

Qy         1204 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1263
                |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db         1235 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGGGCGGGAGCAGCGG 1294

Qy         1264 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1323
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1295 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1354

Qy         1324 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1383
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1355 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1414

Qy         1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1415 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1474

Qy         1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1503
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1475 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1534

Qy         1504 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1563
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1535 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1594

Qy         1564 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1623
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1595 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1654

Qy         1624 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1683
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1655 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1714

Qy         1684 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1743
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1715 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1774

Qy         1744 A----------------------------------------------------------- 1744
                |
Db         1775 AAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCC 1834

Qy         1745 -AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1803
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1835 CAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1894

Qy         1804 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1863
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1895 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1954

Qy         1864 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 1923
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1955 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 2014

Qy         1924 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 1983
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2015 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 2074

Qy         1984 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2043
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2075 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2134

Qy         2044 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2103
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2135 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2194

Qy         2104 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2163
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2195 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2254

Qy         2164 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2223
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2255 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2314

Qy         2224 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2283
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2315 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2374

Qy         2284 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2343
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2375 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2434

Qy         2344 GCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAG 2403
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2435 GCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAG 2494

Qy         2404 GCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAA 2463
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2495 GCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAA 2554

Qy         2464 GGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGAT 2523
                ||||||||||||||||||||||||||||||||||||||||||||||   |||||||||||
Db         2555 GGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGAT 2611

Qy         2524 ACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCC 2583
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2612 ACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCC 2671

Qy         2584 CCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTG 2643
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2672 CCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTG 2731

Qy         2644 CATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCC 2703
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2732 CATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCC 2791

Qy         2704 ACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCT 2763
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2792 ACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCT 2851

Qy         2764 CGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATC 2823
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2852 CGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATC 2911

Qy         2824 TACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGC 2883
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2912 TACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGC 2971

Qy         2884 ACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCC 2943
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2972 ACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCC 3031

Qy         2944 ACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAAC 3003
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3032 ACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAAC 3091

Qy         3004 TCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGG 3063
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3092 TCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGG 3151
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Qy       3064 CTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGCGGCGACGC 3123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3152 CTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGCGGCGACGC 3211

Qy       3124 TTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGG 3183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3212 TTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGG 3271

Qy       3184 AACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCA 3243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3272 AACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCA 3331

Qy       3244 GAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTAC 3303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3332 GAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTAC 3391

Qy       3304 CGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAG 3363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3392 CGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAG 3451

Qy       3364 GTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGAC 3423
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Db       3452 GTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGAC 3511

Qy       3424 CTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTC 3483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3512 CTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTC 3571

Qy       3484 ATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGAC 3543
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       3572 ATCTATGGCTCCAGTGCTGGCTTCCATGCTGCGGATGTCGACTCGGGGAACAGCTATGAC 3631

Qy       3544 ATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCC 3603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3632 ATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCC 3691

Qy       3604 AACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACG 3663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3692 AACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACG 3751

Qy       3664 TACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCC 3723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3752 TACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCC 3811

Qy       3724 TACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTG 3783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3812 TACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTG 3871

Qy       3784 GAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTG 3843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3872 GAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTG 3931

Qy       3844 TGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTT 3903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3932 TGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTT 3991

Qy       3904 TACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              ||||||||||||||||||||||||||||||||||||||||||
Db       3992 TACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4033
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RESULT 7
PCT-US02-33845-6
; Sequence 6, Application PC/TUS0233845
; GENERAL INFORMATION:
;  APPLICANT: Rigel Pharmaceuticals, Inc.
;  APPLICANT:  Leo, Cindy
;  APPLICANT:  Luo, Ying
;  APPLICANT:  Xu, Xiang
;  APPLICANT:  Yu, Simon
;  TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE PROTEINS, COMPOSITIONS,
;  TITLE OF INVENTION:  AND METHODS OF THEIR USE
;  FILE REFERENCE: 021044-005600PC
;  CURRENT APPLICATION NUMBER: PCT/US02/33845
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: US 10/029,115
;  PRIOR FILING DATE: 2001-10-19
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 4032
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: misshapen/NIK-related Kinase isoform c
PCT-US02-33845-6

  Query Match             95.5%;  Score 3772.8;  DB 1;  Length 4032;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches 3871;  Conservative    0;  Mismatches    7;  Indels   64;  Gaps    3;

Qy         64 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 123
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Db         95 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 154

Qy        124 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 183
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Db        155 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 214

Qy        184 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 274

Qy        244 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        275 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGAAAACGATGAC 334

Qy        304 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 394

Qy        364 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 454

Qy        424 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 514

Qy        484 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 574

Qy        544 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 634

Qy        604 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 694

Qy        664 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 754

Qy        724 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 814

Qy        784 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 874

Qy        844 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 903
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Db     875 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 934

Qy     904 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 963
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     935 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 994

Qy     964 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1023
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     995 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1054

Qy    1024 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1083
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1055 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1114

Qy    1084 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAG 1143
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1115 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAG 1174

Qy    1144 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1175 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1234

Qy    1204 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1263
           |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    1235 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGGGCGGGAGCAGCGG 1294

Qy    1264 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1323
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1295 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1354

Qy    1324 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1383
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1355 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1414

Qy    1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1415 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1474

Qy    1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1475 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1534

Qy    1504 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1563
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1535 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1594

Qy    1564 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1595 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1654

Qy    1624 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1683
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1655 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1714

Qy    1684 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1743
           |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    1715 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGGCCCAGGAGGGACCGCAC 1774

Qy    1744 A----------------------------------------------------------- 1744
           |
Db    1775 AAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCC 1834

Qy    1745 -AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1803
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1835 CAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1894

Qy    1804 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1863
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1895 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1954

Qy    1864 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 1923
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    1955 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTTCCG 2014

Qy    1924 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 1983
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2015 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 2074

Qy    1984 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2043
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2075 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2134

Qy    2044 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2103
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2135 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2194

Qy    2104 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2195 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2254

Qy    2164 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2255 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2314

Qy    2224 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2315 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2374

Qy    2284 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2375 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2434

Qy    2344 GCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAG 2403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2435 GCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAG 2494

Qy    2404 GCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAA 2463
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2495 GCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAA 2554

Qy    2464 GGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGAT 2523
           ||||||||||||||||||||||||||||||||||||||||||||||   |||||||||||
Db    2555 GGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGAT 2611

Qy    2524 ACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCC 2583
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2612 ACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCC 2671

Qy    2584 CCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTG 2643
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2672 CCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTG 2731

Qy    2644 CATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCC 2703
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Db    2732 CATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCC 2791

Qy    2704 ACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCT 2763
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792 ACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCT 2851

Qy    2764 CGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATC 2823
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2852 CGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATC 2911

Qy    2824 TACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGC 2883
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Db    2912 TACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGC 2971

Qy    2884 ACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCC 2943
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Db    2972 ACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCC 3031

Qy    2944 ACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAAC 3003
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Db    3032 ACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAAC 3091
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Qy       3004 TCCGAGATCCTCTGTGCAGCCCTTTGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGG 3063
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Qy       3064 CTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGC 3123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3152 CTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGC 3211

Qy       3124 TTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGG 3183
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Db       3212 TTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGG 3271

Qy       3184 AACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCA 3243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3272 AACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCA 3331

Qy       3244 GAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGACATGGAGGGCTGCGGGCACTAC 3303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3332 GAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGACATGGAGGGCTGCGGGCACTAC 3391

Qy       3304 CGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAG 3363
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Db       3392 CGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAG 3451

Qy       3364 GTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGAC 3423
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Db       3452 GTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGAC 3511

Qy       3424 CTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTC 3483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3512 CTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTC 3571

Qy       3484 ATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGAC 3543
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       3572 ATCTATGGCTCCAGTGCTGGCTTCCATGCTGCGGATGTCGACTCGGGGAACAGCTATGAC 3631

Qy       3544 ATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCC 3603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3632 ATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCC 3691

Qy       3604 AACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACG 3663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3692 AACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACG 3751

Qy       3664 TACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCC 3723
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Db       3752 TACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCC 3811

Qy       3724 TACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTG 3783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3812 TACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTG 3871

Qy       3784 GAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTG 3843
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Db       3872 GAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTG 3931

Qy       3844 TGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTT 3903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3932 TGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTT 3991

Qy       3904 TACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              || |||||||||||||||||||||||||||||||||||||||
Db       3992 TA-TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4032
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RESULT 8
US-60-500-337-1177
; Sequence 1177, Application US/60500337
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001483
; CURRENT APPLICATION NUMBER: US/60/500,337
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 123188
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1177
; LENGTH: 4631
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-500-337-1177

Query Match 92.1%; Score 3637.4; DB 107; Length 4631;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 3826; Conservative 6; Mismatches 2; Indels 171; Gaps 2;

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Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 255

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 315

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 375

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 435

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 495

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 555

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 615

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 675

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 735

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 795

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 855

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        856 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 915

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 975

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1035

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1036 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1095

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1155

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1215

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1275

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db       1276 GAAAATAAGAGCAACTCRGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1335

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 CGAGACCCCRAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1395

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1455

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1515

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db       1516 GAGCGGCGGCAGGCGGAGCGYGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1575

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1635

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCTCCTGCCTGGGGAC 1695

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1755

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1815

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1875

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1935

Qy       1745 ----------------------------------------------------------AG 1746
                                                                        ||
Db       1936 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1995

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1996 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2055

Qy       1807 CCTGCCATCCCCGCACCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2056 CCTGCCATCCCCGCACCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2115

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2116 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2175

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2176 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2235

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
              |||||||||||||||||||||||||||||||||||||||||||||
Db       2236 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2280

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db       2281 ------------------------------------------------------------ 2280

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                                  ||||||||||||||||||||||||
Db       2281 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2304

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2305 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2364

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
              |||||||||||||||||||||||||||||||:||||||||||:|||||||||||||||||
Db       2365 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGYCTCCTCCAAACYGGACAGCTCCCCTGTG 2424

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2425 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2484

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2485 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2544

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2545 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2604

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2605 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2664

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2665 GACAGCRTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2724

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2725 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2784

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2785 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2844

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2845 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2904

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2905 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2964

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2965 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 3024

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3025 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 3084

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3085 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3144
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Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3145 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3204

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3205 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGCGGCGACGCTTC 3264

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3265 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3324

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3325 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3384

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3385 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3444

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3445 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3504

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3505 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3564

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3565 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3624

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3625 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3684

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3685 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3744

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3745 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3804

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3805 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3864

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3865 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3924

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3925 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3984

Qy       3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3985 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 4044

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              |||||||||||||||||||||||||||||||||||||||  ||||
Db       4045 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 4089
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RESULT 9
US-60-500-337-1176
; Sequence 1176, Application US/60500337
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001483
; CURRENT APPLICATION NUMBER: US/60/500,337
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 123188
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1176
;   LENGTH: 4881
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-500-337-1176

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  Query Match             92.1%;  Score 3637.4;  DB 107;  Length 4881;
  Best Local Similarity   95.5%;  Pred. No. 0;
  Matches 3826;  Conservative    6;  Mismatches    2;  Indels  171;  Gaps    2;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 255

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 315

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 375

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 435

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 495

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 555

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 615

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 675

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 735

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 795

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 855

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        856 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 915

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 975

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1035

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1036 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1095

Qy     907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1096 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1155

Qy     967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1156 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1215

Qy    1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1216 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1275

Qy    1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
           |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db    1276 GAAAATAAGAGCAACTCRGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1335

Qy    1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
           |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1336 CGAGACCCCRAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1395

Qy    1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1396 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1455

Qy    1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1456 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1515

Qy    1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
           ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db    1516 GAGCGGCGGCAGGCGGAGCGYGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1575

Qy    1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1576 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1635

Qy    1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1636 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1695

Qy    1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1696 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1755

Qy    1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1756 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1815

Qy    1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1816 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1875

Qy    1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db    1876 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1935

Qy    1745 ----------------------------------------------------------AG 1746
                                                                     ||
Db    1936 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1995

Qy    1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1996 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2055

Qy    1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2056 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2115

Qy    1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2116 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2175

Qy    1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2176 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2235

Qy    1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
           |||||||||||||||||||||||||||||||||||||||||||||
Db    2236 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2280

Qy    2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db    2281 ------------------------------------------------------------ 2280

Qy    2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                               ||||||||||||||||||||||||
Db    2281 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2304

Qy    2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2305 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2364

Qy    2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
           |||||||||||||||||||||||||||||||:|||||||||||:||||||||||||||||
Db    2365 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGYCTCCTCCAAACYGGACAGCTCCCCTGTG 2424

Qy    2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2425 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2484

Qy    2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2485 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2544

Qy    2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2545 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2604

Qy    2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2605 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2664

Qy    2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
           ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2665 GACAGCRTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2724

Qy    2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2725 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2784

Qy    2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2785 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2844

Qy    2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2845 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2904

Qy    2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2905 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2964

Qy    2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2965 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 3024

Qy    2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3025 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 3084

Qy    2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3085 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3144
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Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3145 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3204

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3205 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3264

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3265 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3324

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3325 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3384

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3385 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3444

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3445 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3504

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3505 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3564

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3565 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3624

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3625 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3684

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3685 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3744

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3745 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3804

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3805 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3864

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3865 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3924

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3925 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3984

Qy       3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3985 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 4044

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              ||||||||||||||||||||||||||||||||||||||  ||||
Db       4045 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 4089
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RESULT 10
US-60-500-337-1175
; Sequence 1175, Application US/60500337
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001483
; CURRENT APPLICATION NUMBER: US/60/500,337
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 123188
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1175
;   LENGTH: 4982
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-500-337-1175

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  Query Match             92.1%;  Score 3637.4;  DB 107;  Length 4982;
  Best Local Similarity   95.5%;  Pred. No. 0;
  Matches 3826;  Conservative    6;  Mismatches    2;  Indels  171;  Gaps    2;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 255

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 315

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 375

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 435

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 495

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 555

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 615

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 675

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 735

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 795

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 855

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        856 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 915

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 975

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1035

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1036 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1095

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1155

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1215

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1275

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db       1276 GAAAATAAGAGCAACTCRGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1335

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 CGAGACCCCRAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1395

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1455

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1515

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db       1516 GAGCGGCGGCAGGCGGAGCGYGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1575

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1635

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1695

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1755

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1815

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1875

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1935

Qy       1745 ----------------------------------------------------------AG 1746
                                                                        ||
Db       1936 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1995

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1996 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2055

Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2056 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2115

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2116 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2175

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2176 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2235

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
              |||||||||||||||||||||||||||||||||||||||||||||
Db       2236 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2280

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db       2281 ------------------------------------------------------------ 2280

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                                  ||||||||||||||||||||||||
Db       2281 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2304

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2305 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2364

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
              |||||||||||||||||||||||||||||||:|||||||||||:||||||||||||||||
Db       2365 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGYCTCCTCCAAACYGGACAGCTCCCCTGTG 2424

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2425 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2484

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2485 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2544

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2545 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2604

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2605 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2664

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2665 GACAGCRTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2724

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2725 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2784

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2785 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2844

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2845 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2904

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2905 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2964

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2965 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 3024

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3025 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 3084

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3085 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3144
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Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3145 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3204

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3205 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3264

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3265 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3324

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3325 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3384

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3385 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3444

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3445 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3504

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3505 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3564

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3565 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3624

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3625 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3684

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3685 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3744

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3745 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3804

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3805 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3864

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3865 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3924

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3925 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3984

Qy       3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3985 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 4044

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              |||||||||||||||||||||||||||||||||||||||  ||||
Db       4045 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 4089
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RESULT 11
US-10-725-121-11
; Sequence 11, Application US/10725121
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/10/725,121
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US/09/688,188B
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-725-121-11

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  Query Match             92.0%;  Score 3635;  DB 54;  Length 4133;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 3824;  Conservative    0;  Mismatches   15;  Indels  150;  Gaps    3;

Qy        110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
              | |  ||  ||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db          2 CATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 61

Qy        170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 121

Qy        230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 181

Qy        290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 241

Qy        350 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 301

Qy        410 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 361

Qy        470 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 421

Qy        530 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 481

Qy        590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 541

Qy        650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 601

Qy        710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 661

Qy        770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 721

Qy        830 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 781
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Qy        890 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 841

Qy        950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 901

Qy       1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 961

Qy       1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1021

Qy       1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1081

Qy       1190 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1141

Qy       1250 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1201

Qy       1310 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCA----------------- 1352
              ||||||||||||||||||||||||||||||||||||| |||||
Db       1202 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACA 1261

Qy       1353 ------------------------------------------------------------ 1352

Db       1262 GGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGG 1321

Qy       1353 ----------GGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1402
                        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 CCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1381

Qy       1403 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1441

Qy       1463 AGCAGCTTCAGAAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1522
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1442 AGCAGCTTCAGAAACAACAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1501

Qy       1523 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1561

Qy       1583 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1621

Qy       1643 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1681

Qy       1703 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA------------------ 1744
              ||||||||||||||||||||||||||||||||||||||||||
Db       1682 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAGAGCCTGGTGGCACACC 1741

Qy       1745 ------------------------------------------AGTCCCTGCAGGACCAGC 1762
                                                        ||||||||||||||||||
Db       1742 GGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAGC 1801

Qy       1763 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1861

Qy       1823 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1921

Qy       1883 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1981

Qy       1943 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2041

Qy       2003 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2101

Qy       2063 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2161

Qy       2123 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2162 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2221

Qy       2183 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2222 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2281

Qy       2243 GGAACCGCGTGGGAGCCTCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2302
              ||||||||||||||| |||||||||| |||||||||||||||||||||||||||||||||
Db       2282 GGAACCGCGTGGGAGTCTCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2341

Qy       2303 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2342 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2401

Qy       2363 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2402 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2461

Qy       2423 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2462 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2521

Qy       2483 AGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCA 2542
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db       2522 AGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATACAGACAGCGTCAGCACCA 2578

Qy       2543 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2579 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2638

Qy       2603 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2639 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2698

Qy       2663 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2699 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2758

Qy       2723 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2759 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2818

Qy       2783 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2819 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2878

Qy       2843 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2879 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2938

Qy       2903 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2962
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Db       2939 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2998

Qy       2963 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3022
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2999 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3058

Qy       3023 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3082
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3059 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3118

Qy       3083 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3119 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3178

Qy       3143 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3179 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3238

Qy       3203 ACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3262
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3239 ACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3298

Qy       3263 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3299 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3358

Qy       3323 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3359 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3418

Qy       3383 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3419 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3478

Qy       3443 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3479 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3538

Qy       3503 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3539 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3598

Qy       3563 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3599 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3658

Qy       3623 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3659 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3718

Qy       3683 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3719 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3778

Qy       3743 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3779 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3838

Qy       3803 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3839 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3898

Qy       3863 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3899 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3958

Qy       3923 GTAACTGCATCATGAACTGGTGAAAGGGC 3951
              ||||| |||||||||||||||||  ||||
Db       3959 GTAACCGCATCATGAACTGGTGACGGGGC 3987
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RESULT 12
US-10-725-329-11

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; Sequence 11, Application US/10725329
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0328
;  CURRENT APPLICATION NUMBER: US/10/725,329
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: US/09/688,188B
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 09/291,417
;  PRIOR FILING DATE: 1999-04-14
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-725-329-11

  Query Match             92.0%;  Score 3635;  DB 54;  Length 4133;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 3824;  Conservative    0;  Mismatches   15;  Indels  150;  Gaps    3;

Qy        110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
              | |  ||  |||||||  ||||||||||||||||||||||||||||||||||||||||||
Db          2 CATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 61

Qy        170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 121

Qy        230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 181

Qy        290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 241

Qy        350 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 301

Qy        410 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 361

Qy        470 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 421

Qy        530 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 481

Qy        590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 541

Qy        650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 601

Qy        710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 661

Qy        770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
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Db      662 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 721

Qy      830 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 889
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      722 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 781

Qy      890 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 949
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      782 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 841

Qy      950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      842 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 901

Qy     1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      902 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 961

Qy     1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      962 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1021

Qy     1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1022 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1081

Qy     1190 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1082 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1141

Qy     1250 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1309
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1142 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1201

Qy     1310 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCA----------------- 1352
            ||||||||||||||||||||||||||||||||||||| |||||
Db     1202 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACA 1261

Qy     1353 ------------------------------------------------------------ 1352

Db     1262 GGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGG 1321

Qy     1353 ----------GGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1402
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1322 CCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1381

Qy     1403 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1462
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1382 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1441

Qy     1463 AGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1522
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db     1442 AGCAGCTTCAGAAACAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1501

Qy     1523 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1582
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1502 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1561

Qy     1583 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1642
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1562 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1621

Qy     1643 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1702
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1622 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1681

Qy     1703 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA------------------ 1744
            ||||||||||||||||||||||||||||||||||||||||||
Db     1682 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAGAGCCTGGTGGCACACC 1741

Qy     1745 ------------------------------------------AGTCCCTGCAGGACCAGC 1762
                                                      ||||||||||||||||||
Db     1742 GGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAGC 1801

Qy     1763 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1822
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1802 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1861

Qy     1823 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1882
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1862 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1921

Qy     1883 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1942
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1922 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1981

Qy     1943 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2002
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1982 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2041

Qy     2003 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2062
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2042 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2101

Qy     2063 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2102 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2161

Qy     2123 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2182
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Db     2162 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2221

Qy     2183 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2222 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2281

Qy     2243 GGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2302
            ||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||
Db     2282 GGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2341

Qy     2303 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2342 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2401

Qy     2363 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2422
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2402 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2461

Qy     2423 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2482
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2462 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2521

Qy     2483 AGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCA 2542
            |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db     2522 AGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATACAGACAGCGTCAGCACCA 2578

Qy     2543 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2602
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2579 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2638

Qy     2603 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2662
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2639 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2698

Qy     2663 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2722
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2699 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2758

Qy     2723 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2782
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2759 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2818

Qy     2783 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2842
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2819 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2878
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Qy       2843 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2879 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2938

Qy       2903 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2939 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2998

Qy       2963 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3022
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2999 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3058

Qy       3023 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3082
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3059 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3118

Qy       3083 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3119 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3178

Qy       3143 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3179 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3238

Qy       3203 ACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3262
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3239 ACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3298

Qy       3263 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3299 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3358

Qy       3323 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3359 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3418

Qy       3383 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3419 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3478

Qy       3443 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3479 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3538

Qy       3503 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3539 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3598

Qy       3563 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3599 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3658

Qy       3623 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3659 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3718

Qy       3683 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3719 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3778

Qy       3743 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3779 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3838

Qy       3803 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3839 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3898

Qy       3863 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3899 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3958

Qy       3923 GTAACTGCATCATGAACTGGTGAAAGGGC 3951
              ||||| |||||||||||||||||  ||||
Db       3959 GTAACCGCATCATGAACTGGTGACGGGGC 3987
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RESULT 13
US-10-725-330-11
; Sequence 11, Application US/10725330
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0328
;  CURRENT APPLICATION NUMBER: US/10/725,330
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: US/09/688,188B
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 09/291,417
;  PRIOR FILING DATE: 1999-04-14
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-725-330-11

  Query Match             92.0%;  Score 3635;  DB 54;  Length 4133;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 3824;  Conservative    0;  Mismatches   15;  Indels  150;  Gaps    3;

Qy        110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
              | |  ||  |||||||  ||||||||||||||||||||||||||||||||||||||||||
Db          2 CATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 61

Qy        170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 121

Qy        230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 181

Qy        290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 241

Qy        350 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 301

Qy        410 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 361

Qy        470 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 421

Qy        530 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 481

Qy        590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 541

Qy        650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 601
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Qy        710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 661

Qy        770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 721

Qy        830 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 781

Qy        890 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 841

Qy        950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 901

Qy       1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 961

Qy       1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1021

Qy       1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1081

Qy       1190 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1141

Qy       1250 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1201

Qy       1310 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCA----------------- 1352
              ||||||||||||||||||||||||||||||||||||| |||||
Db       1202 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACA 1261

Qy       1353 ------------------------------------------------------------ 1352

Db       1262 GGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGG 1321

Qy       1353 ----------GGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1402
                        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 CCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1381

Qy       1403 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1441

Qy       1463 AGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1522
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1442 AGCAGCTTCAGAAACAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1501

Qy       1523 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1561

Qy       1583 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1621

Qy       1643 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1681

Qy       1703 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGACCGCACA------------------- 1744
              |||||||||||||||||||||||||||||||||||||||||
Db       1682 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGACCGCACAAGAGCCTGGTGGCACACC 1741

Qy       1745 ------------------------------------------AGTCCCTGCAGGACCAGC 1762
                                                        ||||||||||||||||||
Db       1742 GGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAGC 1801

Qy       1763 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1861

Qy       1823 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1921

Qy       1883 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1981

Qy       1943 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2041

Qy       2003 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2101

Qy       2063 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2161

Qy       2123 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2162 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2221

Qy       2183 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2222 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2281

Qy       2243 GGAACCGCGTGGGAGCCTCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2302
              ||||||||||||||| ||||||||||| |||||||||||||||||||||||||||||||
Db       2282 GGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2341

Qy       2303 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2342 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2401

Qy       2363 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2402 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2461

Qy       2423 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2462 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2521

Qy       2483 AGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCA 2542
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db       2522 AGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATACAGACAGCGTCAGCACCA 2578

Qy       2543 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2579 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2638

Qy       2603 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2639 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2698

Qy       2663 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2699 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2758

Qy       2723 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2782
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Db       2759 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2818

Qy       2783 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2819 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2878

Qy       2843 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2879 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2938

Qy       2903 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2939 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2998

Qy       2963 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3022
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2999 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3058

Qy       3023 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3082
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3059 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3118

Qy       3083 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3119 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3178

Qy       3143 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3179 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3238

Qy       3203 ACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3262
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3239 ACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3298

Qy       3263 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3299 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3358

Qy       3323 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3359 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3418

Qy       3383 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3419 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3478

Qy       3443 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3479 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3538

Qy       3503 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3539 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3598

Qy       3563 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3599 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3658

Qy       3623 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3659 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3718

Qy       3683 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3719 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3778

Qy       3743 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3779 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3838

Qy       3803 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3839 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3898

Qy       3863 TGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3899 TGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3958

Qy       3923 GTAACTGCATCATGAACTGGTGAAAGGGC 3951
              ||||| |||||||||||||||||  ||||
Db       3959 GTAACCGCATCATGAACTGGTGACGGGGC 3987
```

RESULT 14
US-60-081-784-11
; Sequence 11, Application US/60081784
; GENERAL INFORMATION:
; APPLICANT: GREGORY PLOWMAN and
; APPLICANT: RICARDO MARTINEZ
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/081,784
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 232/279
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4133 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Mammalian (Human) ZC3
US-60-081-784-11

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  Query Match             92.0%;  Score 3635;  DB 64;  Length 4133;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 3824;  Conservative    0;  Mismatches   15;  Indels  150;  Gaps    3;

Qy        110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
              | |  ||  |||||||  ||||||||||||||||||||||||||||||||||||||||||
Db          2 CATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 61

Qy        170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 121

Qy        230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 181
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Qy     290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 241

Qy     350 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 301

Qy     410 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 361

Qy     470 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 421

Qy     530 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     422 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 481

Qy     590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     482 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 541

Qy     650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     542 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 601

Qy     710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     602 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 661

Qy     770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     662 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 721

Qy     830 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     722 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 781

Qy     890 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     782 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 841

Qy     950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     842 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 901

Qy    1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     902 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 961

Qy    1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     962 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1021

Qy    1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1022 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1081

Qy    1190 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1082 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1141

Qy    1250 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1309
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1142 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1201

Qy    1310 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCA----------------- 1352
           |||||||||||||||||||||||||||||||||||| ||||||
Db    1202 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACA 1261

Qy    1353 ------------------------------------------------------------ 1352

Db    1262 GGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGG 1321

Qy    1353 ----------GGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1402
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1322 CCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1381

Qy    1403 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1462
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1382 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1441

Qy    1463 AGCAGCTTCAGAAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1522
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1442 AGCAGCTTCAGAAACAACAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1501

Qy    1523 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGCCCGAGAGGTAGAAGAGA 1582
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1502 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGCCCGAGAGGTAGAAGAGA 1561

Qy    1583 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1642
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1562 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1621

Qy    1643 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1702
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1622 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1681

Qy    1703 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA------------------ 1744
           ||||||||||||||||||||||||||||||||||||||||||
Db    1682 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAGAGCCTGGTGGCACACC 1741

Qy    1745 ------------------------------------------AGTCCCTGCAGGACCAGC 1762
                                                     ||||||||||||||||||
Db    1742 GGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAGC 1801

Qy    1763 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1822
           ||||||||||||||||||||||||||||||||||||.|||||||||||||||||||||||
Db    1802 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1861

Qy    1823 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1882
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1862 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1921

Qy    1883 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1942
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1922 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1981

Qy    1943 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2002
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1982 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2041

Qy    2003 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2062
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2042 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2101

Qy    2063 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2102 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2161

Qy    2123 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2162 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2221

Qy    2183 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2222 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2281

Qy    2243 GGAACCGCGTGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2302
           |||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||||
Db    2282 GGAACCGCGTGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2341

Qy    2303 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      2342 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2401

Qy      2363 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2402 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2461

Qy      2423 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2462 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2521

Qy      2483 AGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCA 2542
             ||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db      2522 AGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATACAGACAGCGTCAGCACCA 2578

Qy      2543 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2579 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2638

Qy      2603 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2639 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2698

Qy      2663 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2699 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2758

Qy      2723 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2759 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2818

Qy      2783 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2819 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2878

Qy      2843 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2879 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2938

Qy      2903 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2939 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2998

Qy      2963 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2999 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3058

Qy      3023 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3059 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3118

Qy      3083 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3119 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3178

Qy      3143 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3179 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3238

Qy      3203 ACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3262
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3239 ACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3298

Qy      3263 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3299 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3358

Qy      3323 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3359 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3418

Qy      3383 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3442
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3419 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3478

Qy      3443 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3502
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3479 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3538

Qy      3503 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3562
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3539 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3598

Qy      3563 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3622
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3599 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3658

Qy      3623 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3659 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3718

Qy      3683 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3719 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3778

Qy      3743 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3802
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3779 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3838

Qy      3803 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3839 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3898

Qy      3863 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3899 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3958

Qy      3923 GTAACTGCATCATGAACTGGTGAAAGGGC 3951
             ||||| ||||||||||||||||  ||||
Db      3959 GTAACCGCATCATGAACTGGTGACGGGGC 3987
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RESULT 15
US-10-170-235-34328
; Sequence 34328, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 34328
;   LENGTH: 4436
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-170-235-34328

```
  Query Match             92.0%;  Score 3635;  DB 46;  Length 4436;
  Best Local Similarity   95.6%;  Pred. No. 0;
  Matches 3829;  Conservative    0;  Mismatches    5;  Indels  171;  Gaps    2;

Qy         7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 60

Qy        67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 120

Qy       127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 180

Qy       187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy     247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 300

Qy     307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 360

Qy     367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 420

Qy     427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 480

Qy     487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 540

Qy     547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

Qy     607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 660

Qy     667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 720

Qy     727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 780

Qy     787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 840

Qy     847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy     907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 960

Qy     967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

Qy    1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1080

Qy    1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1140

Qy    1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1200

Qy    1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1260

Qy    1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1320

Qy    1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    1321 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1380

Qy    1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1440

Qy    1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1500

Qy    1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1560

Qy    1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1620

Qy    1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1680

Qy    1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1740

Qy    1745 ----------------------------------------------------------AG 1746
                                                                     ||
Db    1741 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1800

Qy    1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1860

Qy    1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1920

Qy    1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1980

Qy    1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2040

Qy    1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
           |||||||||||||||||||||||||||||||||||||||||||||
Db    2041 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2085

Qy    2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db    2086 ------------------------------------------------------------ 2085

Qy    2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                                       ||||||||||||||||||||||||
Db    2086 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2109

Qy    2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2110 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2169

Qy    2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
           ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Db    2170 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTG 2229

Qy    2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2230 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2289
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Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2290 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2349

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2409

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGCCGCAGCGATGGGGATACA 2469

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2529

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2589

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2649

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2709

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2769

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2770 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2829

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2830 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2889

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2890 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 2949

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3009

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3069

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3129

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3189

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3249

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3309

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3369

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3370 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3429

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3430 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3489

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3490 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3549

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3550 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3609

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3669

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3729

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
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Qy       3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
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Search completed: March 2, 2004, 17:00:49
Job time : 8056 secs

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OM nucleic - nucleic search, using sw model

Run on:         March  2, 2004, 09:47:59 ; Search time 9931 Seconds
                                           (without alignments)
                                           17243.815 Million cell updates/sec

Title:          US-10-029-115-1
Perfect score:  3951
Sequence:       1 gcccttatgggcgacccagc..........tcatgaactggtgaaagggc 3951

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3870.2	98.0	5014	9	BC034673	BC034673 Homo sapi
2	3635	92.0	4133	6	BD243845	BD243845 STE20-rel
3	3635	92.0	4133	6	AR435598	AR435598 Sequence
4	3632.2	91.9	3888	9	AB035698	AB035698 Homo sapi
5	3601	91.1	4863	9	AB041926	AB041926 Homo sapi
6	3583.8	90.7	3912	6	AX235361	AX235361 Sequence
7	3501.2	88.6	3999	6	AX235359	AX235359 Sequence
8	3358.2	85.0	3735	6	AX235365	AX235365 Sequence
9	3275.6	82.9	3822	6	AX235363	AX235363 Sequence
10	3230.8	81.8	4842	10	BC052474	BC052474 Mus muscu
11	3026.8	76.6	4848	10	AB035697	AB035697 Mus muscu
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13	2884	73.0	4590	9	HSM802420	AL157418 Homo sapi
14	2824.2	71.5	4381	10	BC011346	BC011346 Mus muscu
15	2531.6	64.1	3824	6	BD183377	BD183377 Novel gen
16	1551	39.3	1717	6	AX235422	AX235422 Sequence
17	1468.4	37.2	1787	6	AX235419	AX235419 Sequence
18	1466	37.1	1482	6	AX235417	AX235417 Sequence
19	1463.4	37.0	1649	6	AX235415	AX235415 Sequence
20	1440.8	36.5	4483	5	BC055134	BC055134 Danio rer
21	1407.2	35.6	3996	6	AR316824	AR316824 Sequence
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24	1407.2	35.6	3996	6	AX127187	AX127187 Sequence
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26	1391.2	35.2	3972	6	AR316828	AR316828 Sequence
27	1391.2	35.2	3972	6	AR316853	AR316853 Sequence
28	1391.2	35.2	3972	6	AR338487	AR338487 Sequence
29	1391.2	35.2	3972	6	AX127191	AX127191 Sequence
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34	1358.6	34.4	4083	6	AR316848	AR316848 Sequence
35	1358.6	34.4	4083	6	AR338482	AR338482 Sequence
36	1358.6	34.4	4083	6	AX127186	AX127186 Sequence
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39	1345.6	34.1	4055	6	BD243844	BD243844 STE20-rel
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45	1342.6	34.0	4059	9	AF172267	AF172267 Homo sapi

ALIGNMENTS

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LOCUS       BC034673                5014 bp    mRNA    linear   PRI 12-NOV-2003
DEFINITION  Homo sapiens misshapen/NIK-related kinase, transcript variant 3,
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ACCESSION   BC034673
VERSION     BC034673.1  GI:21961594
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5014)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
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  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 26 Row: n Column: 8
            This clone was selected for full length sequencing because it
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Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1997 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2056

Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
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Db       2057 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2116

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
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Db       2117 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2176

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
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Db       2177 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2236

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2237 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2296

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106
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Db       2297 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2356

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2357 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2416

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
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Db       2417 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2476

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
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Db       2477 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2536

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
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Db       2537 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2596

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2597 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2656

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2657 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2716

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
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Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
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Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
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Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
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Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
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Db       2957 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 3016

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
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Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
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Db       3077 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 3136

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
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Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
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Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
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Db       3257 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3316

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
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Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
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Db       3377 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3436

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
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Db       3437 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3496

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
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Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
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Db       3557 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3616

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
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Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
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Db       3677 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3736

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
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Db       3737 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3796

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
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Db       3797 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3856

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Db       3857 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3916

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
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Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
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Db       3977 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 4036

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
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Db       4037 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 4096

Qy       3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTTAC 3906
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Db       4097 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTTAC 4156

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
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RESULT 2
BD243845
LOCUS       BD243845                4133 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  STE20-related protein kinases.
ACCESSION   BD243845
VERSION     BD243845.1  GI:33053615
KEYWORDS    JP 2002522009-A/7.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4133)
  AUTHORS   Plowman,G., Martinez,R. and Whyte,D.
  TITLE     STE20-related protein kinases
  JOURNAL   Patent: JP 2002522009-A 7 23-JUL-2002;
            SUGEN INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002522009-A/7
            PD   23-JUL-2002
            PF   13-APR-1999 JP 2000543584
            PR   14-APR-1998 US    60/081784
            PI   GREGORY PLOWMAN,RICARDO MARTINEZ,DAVID WHYTE
            PC   C12N15/09,A61K38/55,A61P9/00,A61P9/10,A61P13/12,A61P25/00, PC
             A61P35/00,
            PC   A61P37/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   12,C12Q1/68,
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            CC   Mammalian ZC3
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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             92.0%;  Score 3635;  DB 6;  Length 4133;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 3824;  Conservative    0;  Mismatches   15;  Indels  150;  Gaps    3;

Qy        110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
              | |  ||  |||||||  ||||||||||||||||||||||||||||||||||||||||||
Db          2 CATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 61

Qy        170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 121

Qy        230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 181

Qy        290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 241
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Qy        350 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 409
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Db        242 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 301

Qy        410 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 469
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Db        302 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 361

Qy        470 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 529
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Db        362 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 421

Qy        530 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 589
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Qy        590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
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Db        482 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 541

Qy        650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
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Db        542 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 601

Qy        710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 661

Qy        770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
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Db        662 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 721

Qy        830 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 889
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Db        722 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 781

Qy        890 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 841

Qy        950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 901

Qy       1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 961

Qy       1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
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Db        962 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1021

Qy       1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
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Qy       1190 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1249
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Qy       1250 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1309
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Db       1142 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1201

Qy       1310 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCA----------------- 1352
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Db       1202 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACA 1261

Qy       1353 ------------------------------------------------------------ 1352

Db       1262 GGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGG 1321

Qy       1353 ----------GGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1402
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Db       1322 CCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1381

Qy       1403 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1462
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Qy       1463 AGCAGCTTCAGAAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1522
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Db       1442 AGCAGCTTCAGAAACAACAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1501

Qy       1523 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1582
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Db       1502 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1561

Qy       1583 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1642
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Qy       1703 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA------------------ 1744
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Qy       1745 ------------------------------------------AGTCCCTGCAGGACCAGC 1762
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Qy       1763 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1822
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Db       1802 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1861

Qy       1823 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1882
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Db       1862 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1921

Qy       1883 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1942
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Db       1922 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1981

Qy       1943 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2002
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Db       1982 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2041

Qy       2003 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2062
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Qy       2063 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2122
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Db       2102 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2161

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Db       2222 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2281

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Qy       2363 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2422
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Qy         2663 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2722
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Qy         3923 GTAACTGCATCATGAACTGGTGAAAGGGC 3951
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DEFINITION  Sequence 11 from patent US 6656716.
ACCESSION   AR435598
VERSION     AR435598.1  GI:40198579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4133)
  AUTHORS   Plowman,G., Martinez,R. and Whyte,D.
  TITLE     Polypeptide fragments of human PAK5 protein kinase
  JOURNAL   Patent: US 6656716-A 11 02-DEC-2003;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             92.0%;  Score 3635;  DB 6;  Length 4133;
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  Matches 3824;  Conservative    0;  Mismatches   15;  Indels  150;  Gaps    3;

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Db            2 CATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 61

Qy          170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           62 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 121

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Qy          290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
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RESULT 4
AB035698
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DEFINITION  Homo sapiens mRNA for Misshapen/NIK-related kinase MINK-1, complete
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ACCESSION   AB035698
VERSION     AB035698.1  GI:6970477
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
            Fukagaya,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
            Matsumoto,K., Ninomiya-Tsuji,J. and Kusumi,A.
  TITLE     Molecular cloning of MINK, a novel member of mammalian GCK family
            kinases, which is up-regulated during postnatal mouse cerebral
            development
  JOURNAL   FEBS Lett. 469 (1), 19-23 (2000)
  MEDLINE   20175403
   PUBMED   10708748
REFERENCE   2  (bases 1 to 3888)
  AUTHORS   Dan,I., Watanabe,N.M. and Kusumi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-1999) Ippeita Dan, ERATO, Kusumi Membrane
            Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi
            460-0012, Japan (E-mail:dang@bio.nagoya-u.ac.jp,
            Tel:81-52-789-2497, Fax:81-52-789-2968)
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ORIGIN

  Query Match             91.9%;  Score 3632.2;  DB 9;  Length 3888;
  Best Local Similarity   95.6%;  Pred. No. 0;
  Matches 3825;  Conservative    0;  Mismatches    3;  Indels  171;  Gaps    2;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
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Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
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Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
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Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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RESULT 5
AB041926
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ACCESSION   AB041926
VERSION     AB041926.1  GI:7637420
KEYWORDS    MINK-2.
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
            Fukagaya,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
            Matsumoto,K., Ninomiya-Tsuji,J. and Kusumi,A.
  TITLE     Molecular cloning of MINK, a novel member of mammalian GCK family
            kinases, which is up-regulated during postnatal mouse cerebral
            development
  JOURNAL   FEBS Lett. 469 (1), 19-23 (2000)
  MEDLINE   20175403
   PUBMED   10708748
REFERENCE   2  (bases 1 to 4863)
  AUTHORS   Watanabe,N.M., Dan,I. and Kusumi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2000) Ippeita Dan, Nagoya University, Dept. of
            Biological Science; Chikusa-ku, Furo-cho, Nagoya, Aichi 464-8602,
            Japan (E-mail:dang@bio.nagoya-u.ac.jp,
            URL:http://www.supra.bio.nagoya-u.ac.jp/DNA/, Tel:81-52-789-2497,
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ORIGIN

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AX235361
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DEFINITION  Sequence 8 from Patent WO0162928.
ACCESSION   AX235361
VERSION     AX235361.1  GI:15593893
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
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ORIGIN

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RESULT 7
AX235359
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DEFINITION  Sequence 6 from Patent WO0162928.
ACCESSION   AX235359
VERSION     AX235359.1  GI:15593891
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
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ORIGIN

  Query Match             88.6%;  Score 3501.2;  DB 6;  Length 3999;
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RESULT 8
AX235365
LOCUS       AX235365                3735 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 12 from Patent WO0162928.
ACCESSION   AX235365
VERSION     AX235365.1  GI:15593897
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 12 30-AUG-2001;
            Curagen Corporation (US)
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ORIGIN

  Query Match             85.0%;  Score 3358.2;  DB 6;  Length 3735;
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Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
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Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
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Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
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Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
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Db        841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
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Db        961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

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Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
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Db       1081 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1140

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Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
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Qy       2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
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Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
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Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
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Db        3013 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGAC 3072

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Qy        3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
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Db        3673 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3732

Qy        3943 TGA 3945
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RESULT 9
AX235363
LOCUS       AX235363                3822 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 10 from Patent WO0162928.
ACCESSION   AX235363
VERSION     AX235363.1  GI:15593895
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 10 30-AUG-2001;
            Curagen Corporation (US)
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ORIGIN

  Query Match            82.9%;  Score 3275.6;  DB 6;  Length 3822;
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Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
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Db        121 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
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Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
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Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
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Db    541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

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Qy    667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
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Qy    727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Qy    787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
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Db    781 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 840

Qy    847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
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Db    841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy    907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
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Db    961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

Qy   1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
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Qy   1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
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Qy   1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
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Qy   1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
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Qy   1327 GAGCGGCGGCAGGCGGAGCGTGAGCA---------------------------------- 1352
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Qy   1480 CAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG 1539
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Db   1621 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAG----------------------- 1657

Qy   1600 CAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCATC 1659
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Qy   1660 CCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCG 1719
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Qy   1720 GTGGAGCCCCAGGAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCT 1779
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Qy   2140 TCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTT 2199
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Qy   2536 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2595
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Db   2473 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2532
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Qy        2656 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2715
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Qy        3496 AGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCT 3555
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RESULT 10
BC052474
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DEFINITION  Mus musculus mitogen-activated protein kinase kinase kinase kinase
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ACCESSION   BC052474
VERSION     BC052474.1  GI:30851420
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
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REFERENCE   1  (bases 1 to 4842)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 4842)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2003) National Institutes of Health, Mammalian
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            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library Preparation: M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
            Thomas L. Casavant.
            Web site: http://genome.uiowa.edu
            Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
            Bonaldo,M.F., Akabogu,I.,  Bair,T., Bair,J., Crouch,K., Davis,A.,
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ORIGIN

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DEFINITION  Mus musculus mRNA for Misshapen/NIKs-related kinase MINK-1,
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ACCESSION   AB035697
VERSION     AB035697.1  GI:6970475
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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REFERENCE   1  (sites)
  AUTHORS   Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
            Fukagaya,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
            Matsumoto,K., Ninomiya-Tsuji,J. and Kusumi,A.
  TITLE     Molecular cloning of MINK, a novel member of mammalian GCK family
            kinases, which is up-regulated during postnatal mouse cerebral
            development
  JOURNAL   FEBS Lett. 469 (1), 19-23 (2000)
  MEDLINE   20175403
   PUBMED   10708748
REFERENCE   2  (bases 1 to 4848)
  AUTHORS   Dan,I., Watanabe,N.M. and Kusumi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-DEC-1999) Ippeita Dan, ERATO, Kusumi Membrane
            Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi
            460-0012, Japan (E-mail:dang@bio.nagoya-u.ac.jp,
            Tel:81-52-789-2497, Fax:81-52-789-2968)
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ORIGIN

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Qy    667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
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VERSION     AB041925.1  GI:7637418
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REFERENCE   1  (sites)
  AUTHORS   Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
            Fukagaya,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
            Matsumoto,K., Ninomiya-Tsuji,J. and Kusumi,A.
  TITLE     Molecular cloning of MINK, a novel member of mammalian GCK family
            kinases, which is up-regulated during postnatal mouse cerebral
            development
  JOURNAL   FEBS Lett. 469 (1), 19-23 (2000)
  MEDLINE   20175403
   PUBMED   10708748
REFERENCE   2  (bases 1 to 4873)
  AUTHORS   Watanabe,N.M., Dan,I. and Kusumi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2000) Ippeita Dan, Nagoya University, Dept. of
            Biological Science; Chikusa-ku, Furo-cho, Nagoya, Aichi 464-8602,
            Japan (E-mail:dang@bio.nagoya-u.ac.jp,
            URL:http://www.supra.bio.nagoya-u.ac.jp/DNA/, Tel:81-52-789-2497,
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ORIGIN

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Qy      247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
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Qy      307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db      476 CTCTGGCTGGTGATGGAGTTCTGCGGTGCTGGTTCAGTGACCGACCTGGTAAAGAACACA 535

Qy      367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db      536 AAAGGGAACGCACTGAAGGAGGATTGCATTGCTTACATCTGCAGGGAGATTCTCAGGGGT 595

Qy      427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db      596 CTTGCCCATCTCCATGCCCACAAGGTGATCCACAGAGATATCAAGGGACAAAATGTGCTG 655

Qy      487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db      656 CTGACAGAGAATGCTGAAGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 715

Qy      547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db      716 ACTGTGGGCAGGCGGAACACTTTCATTGGAACCCCATACTGGATGGCTCCAGAAGTCATT 775

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Db      776 GCCTGTGACGAGAACCCCGATGCCACCTATGACTACAGGAGTGACATTTGGTCTCTAGGA 835

Qy      667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
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Qy     1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
Db     1496 GAGAGGCGGCAAGCAGAGCGGGAACAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1555

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Qy     1621 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCC 1680
Db     1796 AAGCGAAGCCAAGCAGGTGCGGGGCCAGAGCCCCCCATCTCCCAGGCCTCTCCTAGCCCC 1855

Qy     1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG 1740
Db     1856 CCAGGACCTCTTTCCCAGACTCCTCCTATGCAGAGGCCTGTGGAGCCCCAGGAAGGACCG 1915

Qy     1741 CACA-------------------------------------------------------- 1744
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Db   1916 CACAAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGA 1975

Qy   1745 ----AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC 1800
Db   1976 TCCCAGTCCCTGCAGGACCAGCCGACTCGAAACCTGGCTGCCTTCCCAGCCTCCCACGAC 2035

Qy   1801 CCCGACC---CTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATC 1857
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Qy   2038 CGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAG 2097
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Db   2645 AGCAGAGACACTCCCGGGGGCCGCAGTGATGGTGATACAGACAGCGTCACGACCATGGTG 2704

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Qy   2608 GTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACA 2667
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Qy   3148 GGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTG 3207
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Qy   3208 TCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGG 3267
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Qy   3808 TTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTT 3867
Db   3965 TTCATGCACAAACGAGCCCAGAGGCTCAAGTTCCTGTGTGAGCGCAATGACAAGGTGTTT 4024
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RESULT 13
HSM802420
LOCUS       HSM802420               4590 bp    mRNA    linear   PRI 18-FEB-2000
DEFINITION  Homo sapiens mRNA; cDNA DKFZp761K18121 (from clone DKFZp761K18121).
ACCESSION   AL157418
VERSION     AL157418.1  GI:7018439
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4590)
  AUTHORS   Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2000) MIPS, Am Klopferspitz 18a, D-82152
            Martinsried, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp761K18121) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://www.mips.biochem.mpg.de/proj/cDNA/.
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                     /clone_lib="761 (synonym: hamy2). Vector pSport1; host
                     DH10B; sites NotI + SalI"
                     /dev_stage="adult"
     polyA_signal    4544..4549
     polyA_site      4568
ORIGIN

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        479 ATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGC 538
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Db        841 AGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGC 900

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Qy       1351 ------------------------------------------------------------ 1350

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Qy   1744 A----------------------------------------------------------- 1744
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Qy   1984 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2043
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Qy   2044 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2103

Db   1971 ------------------------------------------------------------ 1970

Qy   2104 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2163
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Qy   2224 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2283
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Qy   2284 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2343
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Db   2110 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2169

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Qy   2920 GGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATC 2979
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Db   2770 GGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATC 2829

Qy   2980 CGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAAC 3039
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RESULT 14
BC011346
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DEFINITION  Mus musculus mitogen-activated protein kinase kinase kinase kinase
            6, mRNA (cDNA clone IMAGE:3710317), partial cds.
ACCESSION   BC011346
VERSION     BC011346.1  GI:15030180
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4381)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 4381)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUL-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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ORIGIN

  Query Match             71.5%;  Score 2824.2;  DB 10;  Length 4381;
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Qy       3887 GGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAA 3946
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VERSION     BD183377.1  GI:31875577
KEYWORDS    JP 2002345492-A/90.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 3824)
  AUTHORS   Ohara,O., Nagase,T. and Nakajima,D.
  TITLE     Novel genes and proteins encoded by the genes
  JOURNAL   Patent: JP 2002345492-A 90 03-DEC-2002;
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ORIGIN

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  Best Local Similarity   90.7%;  Pred. No. 0;
  Matches 2885;  Conservative    0;  Mismatches    4;  Indels  291;  Gaps    6;

Qy        943 CGGGGTGAGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGC 1002
Db          1 CTGGATGAGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGC 60

Qy       1003 CATGGAGAGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGC 1062
Db         61 CATGGAGAGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGC 120

Qy       1063 CGGGAGTTTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAG 1122
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Qy       3592 ATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTC 3651
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Db       2701 ATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTC 2760

Qy       3652 TACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCT 3711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCT 2820

Qy       3712 ACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAG 3771
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Db       2821 ACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAG 2880

Qy       3772 ATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGG 3831
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Db       2881 ATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGG 2940

Qy       3832 CTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGC 3891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGC 3000

Qy       3892 AGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db       3001 AGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 3060
```

Search completed: March 2, 2004, 12:58:38
Job time : 10015 secs

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OM nucleic - nucleic search, using sw model

Run on:         March 2, 2004, 09:47:24 ; Search time 975 Seconds
                                          (without alignments)
                                          17215.006 Million cell updates/sec

Title:          US-10-029-115-1
Perfect score:  3951
Sequence:       1 gcccttatgggcgacccagc..........tcatgaactggtgaaagggc 3951

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:      6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_29Jan04:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002s:*
                7:  geneseqn2003as:*
                8:  geneseqn2003bs:*
                9:  geneseqn2003cs:*
                10:  geneseqn2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3951	100.0	3951	9	ADE34151	Ade34151 Human DNA
2	3792.8	96.0	4033	9	ADE34155	Ade34155 Human DNA
3	3632.2	91.9	3888	6	AAL48627	Aal48627 Human ins
4	3622.2	91.7	4133	2	AAZ40485	Aaz40485 Human ZC3
5	3601	91.1	4863	4	AAK52286	Aak52286 Human pol
6	3601	91.1	4863	6	AAL48626	Aal48626 Human ins
7	3601	91.1	4863	8	AAL61132	Aal61132 Human MIN
8	3583.8	90.7	3912	5	AAD17760	Aad17760 Human nov
9	3501.2	88.6	3999	5	AAD17759	Aad17759 Human nov
10	3437.2	87.0	4414	9	ADE34153	Ade34153 Human DNA
11	3392.8	85.9	7132	5	AAS88207	Aas88207 DNA encod
12	3358.2	85.0	3735	5	AAD17762	Aad17762 Human nov
13	3275.6	82.9	3822	5	AAD17761	Aad17761 Human nov
14	1502.6	38.0	2345	3	AAC98909	Aac98909 Human pan
15	1407.2	35.6	3996	4	AAF84940	Aaf84940 Nucleotid
16	1391.2	35.2	3972	4	AAF84944	Aaf84944 Nucleotid
17	1360	34.4	5727	9	ADD14765	Add14765 Human src
18	1358.6	34.4	4083	4	AAC90436	Aac90436 Large NIK
19	1358.6	34.4	4083	4	AAF84939	Aaf84939 Nucleotid
20	1358.6	34.4	4083	6	AAL48625	Aal48625 Human ins
21	1356.8	34.3	5716	4	AAK52538	Aak52538 Human pol
22	1348.2	34.1	4180	3	AAA10669	Aaa10669 Human pro
23	1345.6	34.1	4055	2	AAZ40484	Aaz40484 Human ZC2
24	1342.6	34.0	4059	4	AAF84942	Aaf84942 Nucleotid
25	1324.2	33.5	5123	4	AAK51554	Aak51554 Human pol
26	1288	32.6	3918	4	AAF84941	Aaf84941 Nucleotid
27	1273.4	32.2	3831	4	AAF84943	Aaf84943 Nucleotid
28	1272	32.2	3894	4	AAF84945	Aaf84945 Nucleotid
29	1257.4	31.8	3807	4	AAF84946	Aaf84946 Nucleotid
30	1257.4	31.8	3807	9	ADE31764	Ade31764 Human 154
31	1240.2	31.4	1964	6	ABL39593	Abl39593 Human can
32	1145.4	29.0	3798	2	AAZ40483	Aaz40483 Human ZC1
33	1094	27.7	3775	5	AAS81656	Aas81656 DNA encod
34	1065	27.0	3925	5	AAD08642	Aad08642 Human kin
35	1065	27.0	3925	9	ADE25654	Ade25654 Human cDN
36	995.2	25.2	3866	3	AAC77225	Aac77225 Human ORF
37	994	25.2	4266	5	AAS81655	Aas81655 DNA encod
38	994	25.2	4266	6	ABK11027	Abk11027 DNA encod
39	891	22.6	3864	5	AAS81657	Aas81657 DNA encod
40	891	22.6	3864	6	AAL48628	Aal48628 Human ins
41	891	22.6	3864	7	ABX08783	Abx08783 Angiogene
42	871.8	22.1	1131	4	ABA08794	Aba08794 Human MIN
43	871.8	22.1	1131	4	AAK53270	Aak53270 Human pol
44	818.6	20.7	3786	3	AAZ46153	Aaz46153 cDNA sequ
45	790.6	20.0	4969	5	AAS81653	Aas81653 DNA encod

ALIGNMENTS

```
RESULT 1
ADE34151
ID   ADE34151 standard; DNA; 3951 BP.
XX
AC   ADE34151;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human DNA encoding misshapen/NIKs-related kinase, Mink3a.
XX
KW   Human; misshapen/NIKs-related kinase; Mink3a; ds; antiinflammatory;
KW   immunosuppressive; cytostatic; germinal centre kinase;
KW   c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;
KW   growth factor induced-ERK activation; proliferation;
KW   cell proliferation disorder; cell survival;
KW   intracellular signal transduction; apoptosis; morphological change;
KW   cell migration; gene therapy; inflammatory disease; autoimmune disease;
KW   immunodeficiency; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .3945
FT                   /*tag=  a
FT                   /product= "Mink3a"
XX
PN   US2003077597-A1.
XX
PD   24-APR-2003.
XX
PF   19-OCT-2001; 2001US-00029115.
XX
PR   19-OCT-2001; 2001US-00029115.
XX
PA   (LUOY/) LUO Y.
PA   (FUCA/) FU C A.
PA   (SHEN/) SHEN M.
XX
PI   Luo Y,  Fu CA,  Shen M;
XX
DR   WPI; 2003-635076/60.
DR   P-PSDB; ADE34150.
XX
PT   New misshapen/NIKs-related kinase nucleic acids and proteins useful in
PT   gene therapy and for treating disorders, e.g. acute and chronic
PT   inflammatory diseases.
```

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XX
PS   Claim 3; SEQ ID NO 1; 53pp; English.
XX
CC   The invention relates to a recombinant nucleic acid capable of
CC   hybridising to a Human DNA encoding misshapen/NIKs-related kinase
CC   (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as
CC   ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or
CC   their complements. Also included are a recombinant polypeptide at least
CC   95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,
CC   ADE34152 and ADE34154), screening for a candidate bioactive agent capable
CC   of modulating c-JUN N-terminal kinase (JNK) or extracellular signal
CC   response kinase (ERK) phosphorylation or activity, screening for a
CC   candidate bioactive agent capable of modulating growth factor induced-ERK
CC   activation in a mammalian cell, screening for a candidate bioactive agent
CC   capable of modulating proliferation in a mammalian cell, diagnosing a
CC   mammalian cell proliferation disorder, a medicament for treating a
CC   mammalian cell proliferation disorder and screening for a candidate agent
CC   capable of modulating cell survival. The MINK3 (misshapen/NIKs-related
CC   kinase) nucleic acids are useful in the modulation of intracellular
CC   signal transduction, cell proliferation, apoptosis, morphological change
CC   and migration of mammalian cells. MINK3 nucleic acids and proteins are
CC   specifically useful in gene therapy, and for treating, preventing or
CC   diagnosing acute and chronic inflammatory diseases, autoimmune diseases
CC   and diseases characterised by immunodeficiency. The compositions may also
CC   be used to treat MINK3 dysfunction related disorders, e.g. cancer. The
CC   nucleotide sequences may also be used as hybridisation probes, in
CC   chromosome and gene mapping, and in generating antisense RNA and DNA. The
CC   present sequence encodes Mink3a.
XX
SQ   Sequence 3951 BP; 928 A; 1196 C; 1199 G; 628 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 3951;  DB 9;  Length 3951;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3951;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCCTTATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCCTTATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTG 60

Qy         61 CGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAG 120

Qy        121 GTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC 180

Qy        181 ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC 240

Qy        241 CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGAT 300

Qy        301 GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG 360

Qy        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420

Qy        421 AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT 480

Qy        481 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG 540

Qy        541 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG 600

Qy        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660

Qy        661 CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 720

Qy        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780

Qy        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840

Qy        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC 900

Qy        901 CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG 960

Qy        961 ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG 1020

Qy       1021 CCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTC 1080

Qy       1081 CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAG 1140
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Db       1081 CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAG 1140

Qy       1141 CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA 1200
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Db       1141 CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA 1200

Qy       1201 GAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG 1260
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Db       1201 GAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG 1260

Qy       1261 CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG 1320
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Db       1261 CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG 1320

Qy       1321 GAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG 1380
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Db       1321 GAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG 1380

Qy       1381 CAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCC 1440
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Qy       1441 CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCT 1500
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Qy       1501 GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC 1560
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Db       1501 GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC 1560

Qy       1561 TGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC 1620

Qy       1621 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCC 1680
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Qy       1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG 1740

Qy       1741 CACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC 1800

Qy       1801 CCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1861 CAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC 1920
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Db       1861 CAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC 1920

Qy       1921 CGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCC 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCC 1980

Qy       1981 CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGC 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGC 2040

Qy       2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100

Qy       2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160
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Db       2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160

Qy       2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220
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Db       2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220

Qy       2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280

Qy       2281 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGG 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2341 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAG 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460

Qy       2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520

Qy       2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580

Qy       2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640

Qy       2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700

Qy       2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760

Qy       2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820

Qy       2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880

Qy       2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940

Qy       2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000

Qy       3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060

Qy       3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120

Qy       3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180

Qy       3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240

Qy       3241 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC 3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC 3300

Qy       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360

Qy       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420

Qy       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480

Qy       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540

Qy       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600

Qy       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660

Qy       3661 ACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTG 3720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 ACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTG 3720

Qy       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780

Qy       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840

Qy       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAA 3900
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAA 3900

Qy         3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
                 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951


RESULT 2
ADE34155
ID   ADE34155 standard; DNA; 4033 BP.
XX
AC   ADE34155;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human DNA encoding misshapen/NIKs-related kinase, Mink3c.
XX
KW   Human; misshapen/NIKs-related kinase; Mink3c; ds; antiinflammatory;
KW   immunosuppressive; cytostatic; germinal centre kinase;
KW   c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;
KW   growth factor induced-ERK activation; proliferation;
KW   cell proliferation disorder; cell survival;
KW   intracellular signal transduction; apoptosis; morphological change;
KW   cell migration; gene therapy; inflammatory disease; autoimmune disease;
KW   immunodeficiency; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             203. .4033
FT                   /*tag=  a
FT                   /product= "Mink3c"
XX
PN   US2003077597-A1.
XX
PD   24-APR-2003.
XX
PF   19-OCT-2001; 2001US-00029115.
XX
PR   19-OCT-2001; 2001US-00029115.
XX
PA   (LUOY/) LUO Y.
PA   (FUCA/) FU C A.
PA   (SHEN/) SHEN M.
XX
PI   Luo Y,  Fu CA,  Shen M;
XX
DR   WPI; 2003-635076/60.
DR   P-PSDB; ADE34154.
XX
PT   New misshapen/NIKs-related kinase nucleic acids and proteins useful in
PT   gene therapy and for treating disorders, e.g. acute and chronic
PT   inflammatory diseases.
XX
PS   Claim 3; SEQ ID NO 5; 53pp; English.
XX
CC   The invention relates to a recombinant nucleic acid capable of
CC   hybridising to a Human DNA encoding misshapen/NIKs-related kinase
CC   (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as
CC   ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or
CC   their complements. Also included are a recombinant polypeptide at least
CC   95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,
CC   ADE34152 and ADE34154), screening for a candidate bioactive agent capable
CC   of modulating c-JUN N-terminal kinase (JNK) or extracellular signal
CC   response kinase (ERK) phosphorylation or activity, screening for a
CC   candidate bioactive agent capable of modulating growth factor induced-ERK
CC   activation in a mammalian cell, screening for a candidate bioactive agent
CC   capable of modulating proliferation in a mammalian cell, diagnosing a
CC   mammalian cell proliferation disorder, a medicament for treating a
CC   mammalian cell proliferation disorder and screening for a candidate agent
CC   capable of modulating cell survival. The MINK3 (misshapen/NIKs-related
CC   kinase) nucleic acids are useful in the modulation of intracellular
CC   signal transduction, cell proliferation, apoptosis, morphological change
CC   and migration of mammalian cells. MINK3 nucleic acids and proteins are
CC   specifically useful in gene therapy, and for treating, preventing or
CC   diagnosing acute and chronic inflammatory diseases, autoimmune diseases
CC   and diseases characterised by immunodeficiency. The compositions may also
CC   be used to treat MINK3 dysfunction related disorders, e.g. cancer. The
CC   nucleotide sequences may also be used as hybridisation probes, in
CC   chromosome and gene mapping, and in generating antisense RNA and DNA. The
CC   present sequence encodes Mink3c.
XX
SQ   Sequence 4033 BP; 959 A; 1213 C; 1210 G; 651 T; 0 U; 0 Other;

  Query Match             96.0%;  Score 3792.8;  DB 9;  Length 4033;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 3877;  Conservative    0;  Mismatches    2;  Indels   63;  Gaps    2;

Qy           64 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 123
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           95 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 154

Qy          124 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 183
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          155 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 214

Qy          184 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 243
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          215 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 274

Qy          244 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 303
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          275 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 334

Qy          304 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 363
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          335 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 394

Qy          364 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 423
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          395 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 454

Qy          424 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 483
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          455 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 514

Qy          484 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 543
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          515 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 574

Qy          544 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 603
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          575 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 634

Qy          604 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 663
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          635 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 694

Qy          664 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 723
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          695 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 754

Qy          724 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 783
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          755 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 814

Qy          784 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 843
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          815 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 874

Qy          844 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 903
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          875 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 934

Qy          904 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 963
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       935 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 994

Qy       964 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1023
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       995 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1054

Qy      1024 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1083
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1055 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1114

Qy      1084 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAG 1143
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1115 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAG 1174

Qy      1144 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1203
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1175 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1234

Qy      1204 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1263
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      1235 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGGGCGGGAGCAGCGG 1294

Qy      1264 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1323
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1295 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1354

Qy      1324 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1383
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1355 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1414

Qy      1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1415 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1474

Qy      1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCTCCTGCCTGGG 1503
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1475 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCTCCTGCCTGGG 1534

Qy      1504 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1563
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1535 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1594

Qy      1564 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1623
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1595 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1654

Qy      1624 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1683
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1655 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1714

Qy      1684 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1743
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1715 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1774

Qy      1744 A----------------------------------------------------------- 1744
             |
Db      1775 AAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCC 1834

Qy      1745 -AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1803
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1835 CAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1894

Qy      1804 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1863
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1895 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1954

Qy      1864 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 1923
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1955 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 2014

Qy      1924 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 1983
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2015 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 2074

Qy      1984 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2043
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2075 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2134

Qy      2044 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2103
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2135 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2194

Qy      2104 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2163
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2195 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2254

Qy      2164 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2223
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2255 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2314

Qy      2224 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2283
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2315 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2374

Qy      2284 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2375 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2434

Qy      2344 GCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAG 2403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2435 GCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAG 2494

Qy      2404 GCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAA 2463
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2495 GCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAA 2554

Qy      2464 GGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGAT 2523
             ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db      2555 GGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGAT 2611

Qy      2524 ACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCC 2583
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2612 ACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCC 2671

Qy      2584 CCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTG 2643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2672 CCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTG 2731

Qy      2644 CATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCC 2703
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2732 CATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCC 2791

Qy      2704 ACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCT 2763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2792 ACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCT 2851

Qy      2764 CGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATC 2823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2852 CGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATC 2911

Qy      2824 TACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGC 2883
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2912 TACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGC 2971

Qy      2884 ACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCC 2943
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2972 ACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCC 3031

Qy      2944 ACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAAC 3003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3032 ACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAAC 3091

Qy      3004 TCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGG 3063
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3092 TCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGG 3151
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Qy       3064 CTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGC 3123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3152 CTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGC 3211

Qy       3124 TTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGG 3183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3212 TTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGG 3271

Qy       3184 AACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCA 3243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3272 AACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCA 3331

Qy       3244 GAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGACATGGAGGGCTGCGGGCACTAC 3303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3332 GAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGACATGGAGGGCTGCGGGCACTAC 3391

Qy       3304 CGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAG 3363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3392 CGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAG 3451

Qy       3364 GTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGAC 3423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3452 GTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGAC 3511

Qy       3424 CTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTC 3483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3512 CTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTC 3571

Qy       3484 ATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGAC 3543
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       3572 ATCTATGGCTCCAGTGCTGGCTTCCATGCTGCGGATGTCGACTCGGGGAACAGCTATGAC 3631

Qy       3544 ATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCC 3603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3632 ATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCC 3691

Qy       3604 AACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACG 3663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3692 AACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACG 3751

Qy       3664 TACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCC 3723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3752 TACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCC 3811

Qy       3724 TACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTG 3783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3812 TACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTG 3871

Qy       3784 GAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTG 3843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3872 GAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTG 3931

Qy       3844 TGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTT 3903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3932 TGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTT 3991

Qy       3904 TACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              ||||||||||||||||||||||||||||||||||||||||||
Db       3992 TACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4033

RESULT 3
AAL48627
ID   AAL48627 standard; cDNA; 3888 BP.
XX
AC   AAL48627;
XX
DT   11-OCT-2002  (first entry)
XX
DE   Human insulin receptor signaling modifier cDNA SEQ ID NO: 37.
XX
KW   Human; insulin receptor signaling; insulin receptor signaling modifier;
KW   ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200255664-A2.
XX
PD   18-JUL-2002.
XX
PF   11-JAN-2002; 2002WO-US001048.
XX
PR   12-JAN-2001; 2001US-0261226P.
PR   12-JAN-2001; 2001US-0261303P.
PR   12-JAN-2001; 2001US-0261304P.
PR   12-JAN-2001; 2001US-0261335P.
PR   12-JAN-2001; 2001US-0261336P.
PR   12-JAN-2001; 2001US-0261361P.
PR   12-JAN-2001; 2001US-0261456P.
PR   12-JAN-2001; 2001US-0261457P.
PR   12-JAN-2001; 2001US-0261458P.
PR   12-JAN-2001; 2001US-0261459P.
PR   12-JAN-2001; 2001US-0261461P.
PR   12-JAN-2001; 2001US-0261518P.
PR   12-JAN-2001; 2001US-0261531P.
PR   12-JAN-2001; 2001US-0261532P.
PR   12-JAN-2001; 2001US-0261589P.
PR   12-JAN-2001; 2001US-0261590P.
PR   12-JAN-2001; 2001US-0261694P.
PR   12-JAN-2001; 2001US-0261695P.
PR   12-JAN-2001; 2001US-0261697P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Seidel-Dugan C,  Ferguson KC,  Kidd T;
XX
DR   WPI; 2002-599664/64.
DR   P-PSDB; AAO18508.
XX
PT   Identifying an insulin receptor signaling modulator, useful as drug
PT   targets for treating diabetes or metabolic disorders, comprises
PT   contacting an assay system comprising insulin receptor signaling
PT   modifiers with a test agent.
XX
PS   Disclosure; Page 118-120; 232pp; English.
XX
CC   The present invention relates to a method of identifying a candidate
CC   insulin receptor (INR) signaling modulating agent, involving contacting
CC   an assay system comprising an insulin receptor signaling modifier (ISM)
CC   polypeptide or nucleic acid with a test agent, and detecting a test agent
CC   -biased activity of the assay system. The method is useful for
CC   identifying candidate INR signaling modulating agents. ISM genes may be
CC   used as drug targets for treatment of disorders related to INR signaling
CC   such as diabetes or metabolic syndrome. ISM nucleic acids and
CC   polypeptides are useful for identifying and testing agents that modulate
CC   ISM function and for other applications related to the involvement of ISM
CC   in INR signaling, and for identifying subjects having a predisposition to
CC   such diseases associated with INR signaling. The present sequence is an
CC   ISM coding sequence described in the exemplification of the invention
XX
SQ   Sequence 3888 BP; 917 A; 1168 C; 1182 G; 621 T; 0 U; 0 Other;

  Query Match             91.9%;  Score 3632.2;  DB 6;  Length 3888;
  Best Local Similarity   95.6%;  Pred. No. 0;
  Matches 3825;  Conservative    0;  Mismatches    3;  Indels  171;  Gaps    2;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 60

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 300

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 480

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 540

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 660

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 720

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 780

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 840

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 960

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1080

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1140

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1200

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1260

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1320

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1321 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1380

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1440

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1500

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1560

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1620

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1680

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1740

Qy       1745 ----------------------------------------------------------AG 1746
                                                                        ||
Db       1741 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1800

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1860

Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1920

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1980

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2040

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
              |||||||||||||||||||||||||||||||||||||||||||||
Db       2041 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2085

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db       2086 ------------------------------------------------------------ 2085

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                                  ||||||||||||||||||||||||
Db       2086 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2109

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2110 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2169

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
              ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Db       2170 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTG 2229
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Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2289

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2290 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2349

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2409

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2469

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2529

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2589

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2649

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2709

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2769

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2770 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2829

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2830 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2889

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2890 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 2949

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3009

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3069

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3129

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3189

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3249

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3309

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3369

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3370 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3429

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3430 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3489

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3490 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3549

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3550 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3609

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3669

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3729

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3730 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3789

Qy       3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3790 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3849

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||
Db       3850 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3888
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RESULT 4
AAZ40485
ID   AAZ40485 standard; DNA; 4133 BP.
XX
AC   AAZ40485;
XX
DT   18-FEB-2000  (first entry)
XX
DE   Human ZC3 DNA.
XX
KW   Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
KW   antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
KW   neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW   vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7;
KW   ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist;
KW   antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW   inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW   rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW   myocardial infarction; cardiovascular disease; stroke; renal failure;
KW   oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW   amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW   ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW   mesangial disorder; growth regulation; wound healing; T cell activation;
KW   immunosuppressant; ss.
XX
OS   Homo sapiens.
XX
PN   WO9953036-A2.
XX
PD   21-OCT-1999.
XX
PF   13-APR-1999;    99WO-US008150.
```

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XX
PR   14-APR-1998;   98US-0081784P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman G,  Martinez R,  Whyte D;
XX
DR   WPI; 1999-611301/52.
DR   P-PSDB; AAY55933.
XX
PT   Novel kinase-related polypeptides used for the diagnosis and treatment of
PT   kinase-related diseases and disorders.
XX
PS   Disclosure; Page 267-269; 387pp; English.
XX
CC   This sequence represents the coding sequence for a novel STE20-related
CC   protein kinase. The invention relates to nucleic acid molecule encoding a
CC   kinase polypeptide selected from STLK2, STLK3, STLK4, STLK5, STLK6,
CC   STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The
CC   proteins are used to identify agonists and antagonists, and to raise
CC   antibodies. The polynucleotides are useful in gene therapy protocols. The
CC   polynucleotides, polypeptides, antibodies, antagonists and agonists may
CC   be used to treat diseases such as immune-related disorders and diseases
CC   (e.g. rheumatoid arthritis, artherosclerosis, chronic inflammatory bowel
CC   disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis,
CC   atherosclerosis, rhinitis, autoimmunity, and organ transplantation,
CC   chronic inflammatory pelvic disease, multiple sclerosis, organ
CC   transplantation, myocardial infarction, cardiovascular disease, stroke,
CC   renal failure, oxidative stress-related neurodegenerative disorders (e.g.
CC   amylotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome),
CC   cancer, cardiomyopathies, ischemic disorders, inflammatory disorders,
CC   diabetes mellitus, fibrotic and mesangial disorders. The proteins may
CC   also be useful for cell growth regulation (e.g. in wound healing), T cell
CC   activation, mitosis control, and as immunosuppressants
XX
SQ   Sequence 4133 BP; 960 A; 1258 C; 1246 G; 669 T; 0 U; 0 Other;

  Query Match             91.7%;  Score 3622.2;  DB 2;  Length 4133;
  Best Local Similarity   95.7%;  Pred. No. 0;
  Matches 3816;  Conservative    0;  Mismatches   23;  Indels  150;  Gaps    3;

Qy        110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
              | |  ||  |||||||  ||||||||||||||||||||||||||||||||||||||||||
Db          2 CATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 61

Qy        170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 121

Qy        230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 181

Qy        290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 241

Qy        350 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 301

Qy        410 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 361

Qy        470 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 421

Qy        530 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 481

Qy        590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 541

Qy        650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 601

Qy        710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 661

Qy        770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 721

Qy        830 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 781

Qy        890 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 841

Qy        950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 901

Qy       1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 961

Qy       1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1021

Qy       1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1081

Qy       1190 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1141

Qy       1250 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1201

Qy       1310 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCA----------------- 1352
              ||||||||||||||||||||||||||||||||||||| |||||
Db       1202 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACA 1261

Qy       1353 ------------------------------------------------------------ 1352

Db       1262 GGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGG 1321

Qy       1353 ----------GGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1402
                        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 CCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1381

Qy       1403 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1441

Qy       1463 AGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1522
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1442 AGCAGCTTCAGAAACAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1501

Qy       1523 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1561

Qy       1583 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1642
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1562 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1621

Qy          1643 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1702
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1622 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1681

Qy          1703 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA------------------ 1744
                 ||||||||||||||||||||||||||||||||||||||||||
Db          1682 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAGAGCCTGGTGGCACACC 1741

Qy          1745 ------------------------------------------AGTCCCTGCAGGACCAGC 1762
                                                           ||||||||||||||||||
Db          1742 GGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCAGTCCCTGCAGGACCAGC 1801

Qy          1763 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1822
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1802 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1861

Qy          1823 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1882
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1862 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1921

Qy          1883 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1942
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1922 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1981

Qy          1943 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2002
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1982 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2041

Qy          2003 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2062
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2042 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2101

Qy          2063 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2122
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2102 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2161

Qy          2123 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2182
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2162 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2221

Qy          2183 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2242
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2222 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2281

Qy          2243 GGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2302
                 ||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||
Db          2282 GGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2341

Qy          2303 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2362
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2342 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2401

Qy          2363 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2422
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2402 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2461

Qy          2423 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2482
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2462 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2521

Qy          2483 AGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCA 2542
                 |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db          2522 AGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATACAGACAGCGTCAGCACCA 2578

Qy          2543 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2602
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2579 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2638

Qy          2603 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2662
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2639 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2698

Qy          2663 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2722
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2699 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2758

Qy          2723 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2782
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2759 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2818

Qy          2783 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2842
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2819 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2878

Qy          2843 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2902
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2879 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2938

Qy          2903 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2962
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2939 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2998

Qy          2963 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3022
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2999 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3058

Qy          3023 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3082
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3059 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3118

Qy          3083 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3142
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3119 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3178

Qy          3143 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3202
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3179 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3238

Qy          3203 ACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3262
                 || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3239 ACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3298

Qy          3263 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3322
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3299 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3358

Qy          3323 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3382
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3359 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3418

Qy          3383 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3442
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3419 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3478

Qy          3443 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3502
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3479 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3538

Qy          3503 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3562
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3539 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3598

Qy          3563 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3622
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3599 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3658

Qy          3623 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3682
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3659 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3718

Qy          3683 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3742
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3719 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3778
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Qy       3743 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3779 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3838

Qy       3803 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3862
              |||||||||||||||||||||||||||||||   |  |     |||||||||||||||||
Db       3839 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCGTGAGCGGAAGTGAGCGGAATGACAAGG 3898

Qy       3863 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3899 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3958

Qy       3923 GTAACTGCATCATGAACTGGTGAAAGGGC 3951
              ||||| ||||||||||||||||   ||||
Db       3959 GTAACCGCATCATGAACTGGTGACGGGGC 3987


RESULT 5
AAK52286
ID   AAK52286 standard; cDNA; 4863 BP.
XX
AC   AAK52286;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 831.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM79153.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 1; Page 2771-2777; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 4863 BP; 1072 A; 1509 C; 1447 G; 835 T; 0 U; 0 Other;

  Query Match             91.1%;  Score 3601;  DB 4;  Length 4863;
  Best Local Similarity   95.0%;  Pred. No. 0;
  Matches 3829;  Conservative    0;  Mismatches    5;  Indels  195;  Gaps    3;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 244

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 304

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 364

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 424

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 484

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 544

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 604

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 664

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 724

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 784

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1085 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1144

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1384

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1685 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1744

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924

Qy       1745 ----------------------------------------------------------AG 1746
                                                                        ||
Db       1925 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1984

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1985 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2044

Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2045 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2104

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2105 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2164

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2165 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2224

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
              |||||||||||||||||||||||||||||||||||||||||||||
Db       2225 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2269

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db       2270 ------------------------------------------------------------ 2269

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                                  ||||||||||||||||||||||||
Db       2270 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2293

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2294 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2353

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGAGCCTCTCCAAACTGGACAGCTCCCCTGTG 2286
              |||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||
Db       2354 GCTGGCTCACTGGAGCGGAACCGCGTGGAGTCTCTCCAAACCGGACAGCTCCCCTGTG 2413

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2414 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2473

Qy       2347 ------------------------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
                                      ||||||||||||||||||||||||||||||||||||
Db       2474 AGCTATAAGCGAGCAATTGGTGAGGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2533

Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2534 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2593

Qy       2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2594 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2653

Qy       2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2654 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2713

Qy       2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2714 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2773

Qy       2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2774 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2833

Qy       2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2834 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2893

Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2894 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2953

Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2954 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 3013

Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3014 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 3073

Qy       2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3074 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 3133

Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3134 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3193
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Qy       3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGCAGGGCAAGGTGTAT 3102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3194 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGCAGGGCAAGGTGTAT 3253

Qy       3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3254 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3313

Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3314 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3373

Qy       3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3374 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3433

Qy       3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3434 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3493

Qy       3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3494 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3553

Qy       3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3554 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3613

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3614 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3673

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3674 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3733

Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3734 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3793

Qy       3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3794 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3853

Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGCTGGGGTGAGAAA 3762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3854 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGCTGGGGTGAGAAA 3913

Qy       3763 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3914 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3973

Qy       3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGC 3882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3974 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGC 4033

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4034 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 4093

Qy       3943 TGAAAGGGC 3951
              |||  ||||
Db       4094 TGACGGGGC 4102
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RESULT 6
AAL48626
ID   AAL48626 standard; cDNA; 4863 BP.
XX
AC   AAL48626;
XX
DT   11-OCT-2002  (first entry)
XX
DE   Human insulin receptor signaling modifier cDNA SEQ ID NO: 35.
XX
KW   Human; insulin receptor signaling; insulin receptor signaling modifier;
KW   ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200255664-A2.
XX
PD   18-JUL-2002.
XX
PF   11-JAN-2002; 2002WO-US001048.
XX
PR   12-JAN-2001; 2001US-0261226P.
PR   12-JAN-2001; 2001US-0261303P.
PR   12-JAN-2001; 2001US-0261304P.
PR   12-JAN-2001; 2001US-0261335P.
PR   12-JAN-2001; 2001US-0261336P.
PR   12-JAN-2001; 2001US-0261361P.
PR   12-JAN-2001; 2001US-0261456P.
PR   12-JAN-2001; 2001US-0261457P.
PR   12-JAN-2001; 2001US-0261458P.
PR   12-JAN-2001; 2001US-0261459P.
PR   12-JAN-2001; 2001US-0261461P.
PR   12-JAN-2001; 2001US-0261518P.
PR   12-JAN-2001; 2001US-0261531P.
PR   12-JAN-2001; 2001US-0261532P.
PR   12-JAN-2001; 2001US-0261589P.
PR   12-JAN-2001; 2001US-0261590P.
PR   12-JAN-2001; 2001US-0261694P.
PR   12-JAN-2001; 2001US-0261695P.
PR   12-JAN-2001; 2001US-0261697P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Seidel-Dugan C,  Ferguson KC,  Kidd T;
XX
DR   WPI; 2002-599664/64.
DR   P-PSDB; AAO18507.
XX
PT   Identifying an insulin receptor signaling modulator, useful as drug
PT   targets for treating diabetes or metabolic disorders, comprises
PT   contacting an assay system comprising insulin receptor signaling
PT   modifiers with a test agent.
XX
PS   Disclosure; Page 110-112; 232pp; English.
XX
CC   The present invention relates to a method of identifying a candidate
CC   insulin receptor (INR) signaling modulating agent, involving contacting
CC   an assay system comprising an insulin receptor signaling modifier (ISM)
CC   polypeptide or nucleic acid with a test agent, and detecting a test agent
CC   -biased activity of the assay system. The method is useful for
CC   identifying candidate INR signaling modulating agents. ISM genes may be
CC   used as drug targets for treatment of disorders related to INR signaling
CC   such as diabetes or metabolic syndrome. ISM nucleic acids and
CC   polypeptides are useful for identifying and testing agents that modulate
CC   ISM function and for other applications related to the involvement of ISM
CC   in INR signaling, and for identifying subjects having a predisposition to
CC   such diseases associated with INR signaling. The present sequence is an
CC   ISM coding sequence described in the exemplification of the invention
XX
SQ   Sequence 4863 BP; 1072 A; 1509 C; 1447 G; 835 T; 0 U; 0 Other;

  Query Match             91.1%;  Score 3601;  DB 6;  Length 4863;
  Best Local Similarity   95.0%;  Pred. No. 0;
  Matches 3829;  Conservative    0;  Mismatches    5;  Indels  195;  Gaps    3;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 244

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 304

Qy     127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 364

Qy     187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     365 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 424

Qy     247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 484

Qy     307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     485 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 544

Qy     367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     545 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 604

Qy     427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     605 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 664

Qy     487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     665 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 724

Qy     547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     725 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 784

Qy     607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy     667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy     727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy     787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy     847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy     907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1085 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1144

Qy     967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy    1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy    1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy    1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1325 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1384

Qy    1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy    1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy    1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy    1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy    1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

Qy    1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1685 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1744

Qy    1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy    1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy    1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924

Qy    1745 ----------------------------------------------------------AG 1746
                                                                     ||
Db    1925 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1984

Qy    1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1985 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2044

Qy    1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2045 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2104

Qy    1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2105 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2164

Qy    1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2165 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2224

Qy    1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
           |||||||||||||||||||||||||||||||||||||||||||||
Db    2225 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2269

Qy    2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db    2270 ------------------------------------------------------------ 2269

Qy    2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                               ||||||||||||||||||||||||
Db    2270 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2293

Qy    2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2294 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2353
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Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCAAACTGGACAGCTCCCCTGTG 2286
              ||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||
Db       2354 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCAAACCGGACAGCTCCCCTGTG 2413

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2414 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2473

Qy       2347 ------------------------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
                                      ||||||||||||||||||||||||||||||||||||
Db       2474 AGCTATAAGCGAGCAATTGGTGAGGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2533

Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2534 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2593

Qy       2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2594 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2653

Qy       2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2654 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2713

Qy       2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2714 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2773

Qy       2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2774 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2833

Qy       2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2834 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2893

Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2894 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2953

Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2954 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 3013

Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3014 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 3073

Qy       2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3074 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 3133

Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3134 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3193

Qy       3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3194 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3253

Qy       3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3254 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3313

Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3314 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3373

Qy       3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3374 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3433

Qy       3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3434 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3493

Qy       3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3494 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3553

Qy       3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3554 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3613

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3614 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3673

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3674 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3733

Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3734 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3793

Qy       3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3794 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3853

Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3854 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3913

Qy       3763 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3914 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3973

Qy       3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3974 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 4033

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4034 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 4093

Qy       3943 TGAAAGGGC 3951
              |||  ||||
Db       4094 TGACGGGGC 4102
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RESULT 7
AAL61132
ID   AAL61132 standard; DNA; 4863 BP.
XX
AC   AAL61132;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Human MINK2 antisense transcript DNA.
XX
KW   Transcript; therapy; systemic lupus erythematosus; inflammatory disease;
KW   cardiovascular; gastrointestinal disease; atherosclerosis; skin disease;
KW   rheumatoid disorder; autoimmune disease; diabetes; multiple sclerosis;
KW   cancer; neuroprotective; human; MINK2; antisense; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003046220-A1.
XX
PD   05-JUN-2003.
XX
PF   11-NOV-2002; 2002WO-IL000904.
XX
PR   26-NOV-2001; 2001US-00993398.
PR   24-JUL-2002; 2002US-00201605.
```

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XX
PA   (COMP-) COMPUGEN LTD.
XX
PI   Levanon E,  Pollock S,  Nemzer S,  Shoshan A,  Khosravi R,  Walach S;
PI   Levine Z,  Bernstein J,  Dahari D,  Wasserman A,  Rotman G;
XX
DR   WPI; 2003-505211/47.
XX
PT   Identifying putative naturally occurring antisense transcripts, useful
PT   for quantifying gene expression levels, and detecting and/or treating
PT   inflammatory, autoimmune or cardiovascular diseases, diabetes, arthritis
PT   and cancer.
XX
PS   Example; Page 214-216; 230pp; English.
XX
CC   The invention relates to methods and systems for identifying naturally
CC   occurring antisense transcripts. The method is useful for quantifying
CC   gene expression levels and for detecting, quantifying or specifically
CC   regulating antisense and respective sense transcripts thereby enabling
CC   detection and treatment of a wide range or disorders, such as systemic
CC   lupus erythematosus, inflammatory diseases, rheumatoid disorders,
CC   autoimmune diseases, diabetes, multiple sclerosis, cardiovascular and
CC   gastrointestinal diseases, atherosclerosis, skin diseases and cancer. The
CC   present sequence is human MINK2 transcript DNA used to illustrate the
CC   method of the invention
XX
SQ   Sequence 4863 BP; 1072 A; 1509 C; 1447 G; 835 T; 0 U; 0 Other;

  Query Match             91.1%;  Score 3601;  DB 8;  Length 4863;
  Best Local Similarity   95.0%;  Pred. No. 0;
  Matches 3829;  Conservative    0;  Mismatches    5;  Indels  195;  Gaps    3;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 244

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 304

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 364

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 424

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 484

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 544

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 604

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 664

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 724

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 784

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1085 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1144

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1384

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1685 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1744

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924

Qy        1745 ----------------------------------------------------------AG 1746
                                                                         ||
Db        1925 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1984

Qy        1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1985 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2044

Qy        1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2045 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2104

Qy        1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2105 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2164

Qy        1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2165 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2224

Qy        1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
               |||||||||||||||||||||||||||||||||||||||||||||
Db        2225 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2269

Qy        2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db        2270 ------------------------------------------------------------ 2269

Qy        2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                                    ||||||||||||||||||||||||
Db        2270 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2293

Qy        2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2294 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2353

Qy        2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
               ||||||||||||||||||||||||||||||| |||||||||| |||||||||||||||||
Db        2354 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTG 2413

Qy        2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2414 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2473

Qy        2347 ------------------------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
                                       ||||||||||||||||||||||||||||||||||||
Db        2474 AGCTATAAGCGAGCAATTGGTGAGGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2533

Qy        2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2534 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2593

Qy        2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2594 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2653

Qy        2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2654 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2713

Qy        2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2714 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2773

Qy        2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2774 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2833

Qy        2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2834 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2893

Qy        2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2894 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2953

Qy        2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2954 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 3013

Qy        2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3014 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 3073

Qy        2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3074 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 3133

Qy        2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3134 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3193

Qy        3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3194 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3253

Qy        3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3254 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3313

Qy        3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3314 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3373

Qy        3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3374 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3433

Qy        3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3434 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3493

Qy        3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3402
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3494 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3553

Qy        3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3554 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3613

Qy        3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3614 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3673

Qy        3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3674 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3733

Qy        3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3734 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3793

Qy        3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3794 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3853

Qy        3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3762
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3854 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3913

Qy        3763 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3822
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3914 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3973
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Qy       3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGC 3882
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Db       3974 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGC 4033

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4034 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 4093

Qy       3943 TGAAAGGGC 3951
              |||  ||||
Db       4094 TGACGGGGC 4102


RESULT 8
AAD17760
ID   AAD17760 standard; DNA; 3912 BP.
XX
AC   AAD17760;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human novel STE20-like protein, NOV-3b encoding DNA.
XX
KW   Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;
KW   trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;
KW   immunological disorder; neurodegenerative disorder; Alzheimer's disease;
KW   Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;
KW   human immunodeficiency virus; HIV; fertility disorder; neuroprotective;
KW   cytostatic; nootropic; anti-infertility; cancer; chromosome 17;
KW   NOV-3b protein; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3912
FT                   /*tag=  a
FT                   /product= "Human novel STE20-like protein, NOV-3b"
XX
PN   WO200162928-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US006151.
XX
PR   25-FEB-2000; 2000US-0184951P.
PR   28-FEB-2000; 2000US-0185548P.
PR   01-MAR-2000; 2000US-0185967P.
PR   18-APR-2000; 2000US-0197723P.
PR   27-APR-2000; 2000US-0199957P.
PR   23-FEB-2001; 2001US-00789390.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Vernet CAM,  Fernandes E,  Shimkets RA,  Macdougall J,  Spaderna SK;
XX
DR   WPI; 2001-582051/65.
DR   P-PSDB; AAE10612.
XX
PT   New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like
PT   polypeptide for diagnosing and treating pathological disorders, such as
PT   Parkinson's disease and for use in pharmocogenomics.
XX
PS   Claim 9; Page 51-52; 189pp; English.
XX
CC   The invention relates to novel human polypeptides referred as NOV-X and
CC   their corresponding nucleic acid sequences. NOV-X collectively include
CC   NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-
CC   3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and
CC   NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin
CC   inhibitor-like polypeptides. NOV-X is used to identify a potential
CC   therapeutic agent that can modulate its activity and can be used for
CC   treating a pathology related to aberrant expression or aberrant
CC   physiological interactions of NOV-X. NOV-X or its DNA is used to
CC   determine the presence or predisposition to a disease associated with
CC   altered levels of NOV-X. NOV-X, its DNA and its antibody are used to
CC   treat or prevent a pathology associated with NOV-X. The pathological
CC   states that can be treated or prevented are haematopoietic, cancer,
CC   immunological, tumour, neurodegenerative (e.g. Alzheimer's and
CC   Parkinson's disease), human immunodeficiency virus (HIV) illness and
CC   fertility disorders. NOV-X and its DNA are used in pharmacogenomics for
CC   predictive medicine. NOV-X DNA is used in gene therapy. The present
CC   sequence is a DNA encoding human novel STE20-like protein, NOV-3b. NOV-3b
CC   gene is located at chromosome 17
XX
SQ   Sequence 3912 BP; 924 A; 1171 C; 1187 G; 630 T; 0 U; 0 Other;

  Query Match             90.7%;  Score 3583.8;  DB 5;  Length 3912;
  Best Local Similarity   94.9%;  Pred. No. 0;
  Matches 3816;  Conservative    0;  Mismatches   12;  Indels  195;  Gaps    3;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 60

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
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Db        121 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 300

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
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Db        301 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Db        361 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 480

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 540

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 660

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 720

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Db        721 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 780

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 840
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Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 960

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
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Db       1021 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1080

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1140

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1200

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1260

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
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Db       1261 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1320

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||||| ||||||||||| |  ||  |   ||| ||||||||||||
Db       1321 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGCAGCGG 1380

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
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Db       1381 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1440

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
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Db       1441 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1500

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1560

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1620

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1680

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1740

Qy       1745 ----------------------------------------------------------AG 1746
                                                                        ||
Db       1741 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1800

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1860

Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1920

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1980

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2040

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
              |||||||||||||||||||||||||||||||||||||||||||||
Db       2041 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2085

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db       2086 ------------------------------------------------------------ 2085

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                                  ||||||||||||||||||||||||
Db       2086 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2109

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
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Db       2110 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2169

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
              ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Db       2170 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTG 2229

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2289

Qy       2347 ------------------------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
                                      ||||||||||||||||||||||||||||||||||||
Db       2290 AGCTATAAGCGAGCAATTGGTGAGGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2349

Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2409

Qy       2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2469

Qy       2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2529

Qy       2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2589

Qy       2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2649

Qy       2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2709

Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2769

Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2770 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2829

Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2830 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2889

Qy       2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2890 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2949

Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
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Db       2950 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3009

Qy       3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3069

Qy       3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3129

Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3189

Qy       3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3249

Qy       3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3309

Qy       3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGCCCCCAAACCCTACCACAAATTCATG 3402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGCCCCCAAACCCTACCACAAATTCATG 3369

Qy       3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3370 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3429

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3430 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3489

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3490 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3549

Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3550 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3609

Qy       3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3669

Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGCTGGGGTGAGAAA 3762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGCTGGGGTGAGAAA 3729

Qy       3763 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3730 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3789

Qy       3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3790 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3849

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3850 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3909

Qy       3943 TGA 3945
              |||
Db       3910 TGA 3912
```

RESULT 9
AAD17759

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ID   AAD17759 standard; DNA; 3999 BP.
XX
AC   AAD17759;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human novel STE20-like protein, NOV-3a encoding DNA.
XX
KW   Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;
KW   trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;
KW   immunological disorder; neurodegenerative disorder; Alzheimer's disease;
KW   Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;
KW   human immunodeficiency virus; HIV; fertility disorder; neuroprotective;
KW   cytostatic; nootropic; anti-infertility; cancer; chromosome 17;
KW   NOV-3a protein; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3999
FT                   /*tag=  a
FT                   /product= "Human novel STE20-like protein, NOV-3a"
XX
PN   WO200162928-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US006151.
XX
PR   25-FEB-2000; 2000US-0184951P.
PR   28-FEB-2000; 2000US-0185548P.
PR   01-MAR-2000; 2000US-0185967P.
PR   18-APR-2000; 2000US-0197723P.
PR   27-APR-2000; 2000US-0199957P.
PR   23-FEB-2001; 2001US-00789390.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Vernet CAM,  Fernandes E,  Shimkets RA,  Macdougall J,  Spaderna SK;
XX
DR   WPI; 2001-582051/65.
DR   P-PSDB; AAE10611.
XX
PT   New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like
PT   polypeptide for diagnosing and treating pathological disorders, such as
PT   Parkinson's disease and for use in pharmocogenomics.
XX
PS   Claim 9; Page 44-45; 189pp; English.
XX
CC   The invention relates to novel human polypeptides referred as NOV-X and
CC   their corresponding nucleic acid sequences. NOV-X collectively include
CC   NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-
CC   3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and
CC   NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin
CC   inhibitor-like polypeptides. NOV-X is used to identify a potential
CC   therapeutic agent that can modulate its activity and can be used for
CC   treating a pathology related to aberrant expression or aberrant
CC   physiological interactions of NOV-X. NOV-X or its DNA is used to
CC   determine the presence or predisposition to a disease associated with
CC   altered levels of NOV-X. NOV-X, its DNA and its antibody are used to
CC   treat or prevent a pathology associated with NOV-X. The pathological
CC   states that can be treated or prevented are haematopoietic, cancer,
CC   immunological, tumour, neurodegenerative (e.g. Alzheimer's and
CC   Parkinson's disease), human immunodeficiency virus (HIV) illness and
CC   fertility disorders. NOV-X and its DNA are used in pharmacogenomics for
CC   predictive medicine. NOV-X DNA is used in gene therapy. The present
CC   sequence is a DNA encoding human novel STE20-like protein, NOV-3a. NOV-3a
CC   gene is located at chromosome 17
XX
SQ   Sequence 3999 BP; 948 A; 1195 C; 1215 G; 641 T; 0 U; 0 Other;

  Query Match             88.6%;  Score 3501.2;  DB 5;  Length 3999;
  Best Local Similarity   93.1%;  Pred. No. 0;
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Matches 3825; Conservative    0; Mismatches    3; Indels  282; Gaps    4;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 60

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 300

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 480

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 540

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 660

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 720

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Db        721 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 780

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
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Db        781 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 840

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
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Db        841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 960

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
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Db       1021 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1080

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1140

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1200

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1260

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1320

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCA---------------------------------- 1352
              |||||||||||||||||||| |||||
Db       1321 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGGAGCAG 1380

Qy       1353 -----------------------------------------------------GGAATAC 1359
                                                                   |||||||
Db       1381 CGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGGCCCTGCTGCTGGAATAC 1440

Qy       1360 AAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAG 1419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAG 1500

Qy       1420 GAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAG 1479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAG 1560

Qy       1480 CAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG 1539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG 1620

Qy       1540 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAG 1599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAG 1680

Qy       1600 CAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATC 1659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATC 1740

Qy       1660 CCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCG 1719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCG 1800

Qy       1720 GTGGAGCCCCAGGAGGGACCGCACA----------------------------------- 1744
              |||||||||||||||||||||||||
Db       1801 GTGGAGCCCCAGGAGGGACCGCACAAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCA 1860

Qy       1745 -------------------------AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCT 1779
                                       |||||||||||||||||||||||||||||||||||
Db       1861 TATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCT 1920

Qy       1780 GCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGT 1839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGT 1980

Qy       1840 GCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGC 1899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGC 2040

Qy       1900 CCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGG 1959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGG 2100

Qy       1960 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 2019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 2160
```

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Qy       2020 GCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCA 2079
              ||||||||||||
Db       2161 GCAGTCCGTGCC------------------------------------------------ 2172

Qy       2080 GAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCC 2139

Db       2173 ------------------------------------------------------------ 2172

Qy       2140 TCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTT 2199
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2173 ---AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTT 2229

Qy       2200 CCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCC 2259
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       2230 CCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTC 2289

Qy       2260 TCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGAC 2319
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       2290 TCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGAC 2349

Qy       2320 CACCGCTCACGGCCAGGCCGGCCCGCA------------------------GACTTTGTG 2355
              |||||||||||||||||||||||||||                        |||||||||
Db       2350 CACCGCTCACGGCCAGGCCGGCCCGCAAGCTATAAGCGAGCAATTGGTGAGGACTTTGTG 2409

Qy       2356 TTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTAC 2415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 TTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTAC 2469

Qy       2416 TCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGG 2475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 TCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGG 2529

Qy       2476 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2589

Qy       2536 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2649

Qy       2596 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2709

Qy       2656 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2769

Qy       2716 AAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTA 2775
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2770 AAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTA 2829

Qy       2776 AAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGA 2835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2830 AAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGA 2889

Qy       2836 GGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGAC 2895
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2890 GGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGAC 2949

Qy       2896 CAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGG 2955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 CAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGG 3009

Qy       2956 GCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTC 3015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 GCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTC 3069

Qy       3016 TGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTG 3075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 TGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTG 3129

Qy       3076 GACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATG 3135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 GACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATG 3189

Qy       3136 GATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGG 3195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 GATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGG 3249

Qy       3196 GTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAG 3255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 GTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAG 3309

Qy       3256 AAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAA 3315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 AAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAA 3369

Qy       3316 TACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGG 3375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3370 TACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGG 3429

Qy       3376 GCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGC 3435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3430 GCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGC 3489

Qy       3436 CCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCC 3495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3490 CCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCC 3549

Qy       3496 AGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCT 3555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3550 AGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCT 3609

Qy       3556 GTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGC 3615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 GTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGC 3669

Qy       3616 ATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATC 3675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 ATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATC 3729

Qy       3676 ATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCC 3735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3730 ATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCC 3789

Qy       3736 AACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCAC 3795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3790 AACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCAC 3849

Qy       3796 CTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAAT 3855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3850 CTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAAT 3909

Qy       3856 GACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACT 3915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3910 GACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACT 3969

Qy       3916 CTGAACCGTAACTGCATCATGAACTGGTGA 3945
              ||||||||||||||||||||||||||||||
Db       3970 CTGAACCGTAACTGCATCATGAACTGGTGA 3999
```

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RESULT 10
ADE34153
ID   ADE34153 standard; DNA; 4414 BP.
XX
AC   ADE34153;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human DNA encoding misshapen/NIKs-related kinase, Mink3b.
XX
KW   Human; misshapen/NIKs-related kinase; Mink3b; ds; antiinflammatory;
KW   immunosuppressive; cytostatic; germinal centre kinase;
KW   c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;
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KW   growth factor induced-ERK activation; proliferation;
KW   cell proliferation disorder; cell survival;
KW   intracellular signal transduction; apoptosis; morphological change;
KW   cell migration; gene therapy; inflammatory disease; autoimmune disease;
KW   immunodeficiency; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             209. .2587
FT                   /*tag=  a
FT                   /product= "Mink3b"
XX
PN   US2003077597-A1.
XX
PD   24-APR-2003.
XX
PF   19-OCT-2001; 2001US-00029115.
XX
PR   19-OCT-2001; 2001US-00029115.
XX
PA   (LUOY/) LUO Y.
PA   (FUCA/) FU C A.
PA   (SHEN/) SHEN M.
XX
PI   Luo Y,  Fu CA,  Shen M;
XX
DR   WPI; 2003-635076/60.
DR   P-PSDB; ADE34152.
XX
PT   New misshapen/NIKs-related kinase nucleic acids and proteins useful in
PT   gene therapy and for treating disorders, e.g. acute and chronic
PT   inflammatory diseases.
XX
PS   Claim 3; SEQ ID NO 3; 53pp; English.
XX
CC   The invention relates to a recombinant nucleic acid capable of
CC   hybridising to a Human DNA encoding misshapen/NIKs-related kinase
CC   (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as
CC   ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or
CC   their complements. Also included are a recombinant polypeptide at least
CC   95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,
CC   ADE34152 and ADE34154), screening for a candidate bioactive agent capable
CC   of modulating c-JUN N-terminal kinase (JNK) or extracellular signal
CC   response kinase (ERK) phosphorylation or activity, screening for a
CC   candidate bioactive agent capable of modulating growth factor induced-ERK
CC   activation in a mammalian cell, screening for a candidate bioactive agent
CC   capable of modulating proliferation in a mammalian cell, diagnosing a
CC   mammalian cell proliferation disorder, a medicament for treating a
CC   mammalian cell proliferation disorder and screening for a candidate agent
CC   capable of modulating cell survival. The MINK3 (misshapen/NIKs-related
CC   kinase) nucleic acids are useful in the modulation of intracellular
CC   signal transduction, cell proliferation, apoptosis, morphological change
CC   and migration of mammalian cells. MINK3 nucleic acids and proteins are
CC   specifically useful in gene therapy, and for treating, preventing or
CC   diagnosing acute and chronic inflammatory diseases, autoimmune diseases
CC   and diseases characterised by immunodeficiency. The compositions may also
CC   be used to treat MINK3 dysfunction related disorders, e.g. cancer. The
CC   nucleotide sequences may also be used as hybridisation probes, in
CC   chromosome and gene mapping, and in generating antisense RNA and DNA. The
CC   present sequence encodes Mink3b.
XX
SQ   Sequence 4414 BP; 1010 A; 1339 C; 1317 G; 748 T; 0 U; 0 Other;

  Query Match             87.0%;  Score 3437.2;  DB 9;  Length 4414;
  Best Local Similarity   90.1%;  Pred. No. 0;
  Matches 3885;  Conservative    0;  Mismatches    3;  Indels  426;  Gaps    2;

Qy         64 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 160

Qy        124 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 220

Qy        184 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 280

Qy        244 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 340

Qy        304 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 400

Qy        364 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 460

Qy        424 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 520

Qy        484 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 580

Qy        544 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 640

Qy        604 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 700

Qy        664 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 760

Qy        724 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 820

Qy        784 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 880

Qy        844 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 940

Qy        904 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 963
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 1000

Qy        964 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1001 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1060

Qy       1024 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1083
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1120

Qy       1084 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1180

Qy       1144 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1240

Qy       1204 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1241 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1300

Qy       1264 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1360

Qy       1324 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1420

Qy       1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1421 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1480

Qy       1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1481 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1540

Qy       1504 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1541 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1600

Qy       1564 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1601 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1660

Qy       1624 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1661 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1720

Qy       1684 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1721 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1780

Qy       1744 A----------------------------------------------------------- 1744
              |
Db       1781 AAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCC 1840

Qy       1745 -AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1803
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1841 CAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1900

Qy       1804 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1901 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1960

Qy       1864 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 1923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1961 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 2020

Qy       1924 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 1983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2021 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 2080

Qy       1984 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2081 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2140

Qy       2044 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2141 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2200

Qy       2104 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2201 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2260

Qy       2164 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2261 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2320

Qy       2224 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2321 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2380

Qy       2284 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2381 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2440

Qy       2344 GCA--------------------------------------------------------- 2346
              |||
Db       2441 GCAGTGAGTCACCTGGTGGCAGGCATGGCCTGCCTCATCCTGGTTTGGGGCTTAGCCTCA 2500

Qy       2347 ------------------------------------------------------------ 2346

Db       2501 GGGTGCTGGGTGTCAGGGGTGGGGTCTCCGCTGATCTACCGAGAAGGGCTGTGGGGATGG 2560

Qy       2347 ------------------------------------------------------------ 2346

Db       2561 AGGGACTGGTGCTTCTCATGGTGCTAACCTTTCCTAACCTCTCTCCTAACCTCTCTCCTA 2620

Qy       2347 ------------------------------------------------------------ 2346

Db       2621 ACCTCTCTTCTGGCTCTTTCTTCCCCTGCGGCCCCTCCCAGAGCTATAAGCGAGCAATTG 2680

Qy       2347 ------------------------------------------------------------ 2346

Db       2681 GTGAGGTTAGTGAGATGGGCCTGCTTGTGGGAGCCCCTCCTGTCGCCCTGCTGGGGCGTC 2740

Qy       2347 ------------------------------------------------------------ 2346

Db       2741 CCGGCACCCTTTGTCTACCTCCACCCAGGCCCAGCTTCTCCCTGCCCCTCACGTGGCTCC 2800

Qy       2347 ---------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCC 2397
                       |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2801 TCCCTGCAGGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCC 2860

Qy       2398 AAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAG 2457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2861 AAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAG 2920

Qy       2458 GAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGAT 2517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2921 GAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGAT 2980

Qy       2518 GGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACC 2577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2981 GGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACC 3040

Qy       2578 CAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAAC 2637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3041 CAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAAC 3100

Qy       2638 CTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCAC 2697
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3101 CCGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCAC 3160

Qy       2698 TCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTAC 2757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3161 TCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTAC 3220

Qy       2758 CAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTA 2817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3221 CAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTA 3280

Qy       2818 GGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGA 2877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3281 GGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGA 3340

Qy       2878 GAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTG 2937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3341 GAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTG 3400

Qy       2938 AATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGA 2997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3401 AATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGA 3460
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Qy     2998 TTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAG 3057
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3461 TTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAG 3520

Qy     3058 AACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGG 3117
            |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     3521 AACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGACAAGGTGTATGGACTCATTGGGCGA 3580

Qy     3118 CGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGG 3177
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3581 CGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGG 3640

Qy     3178 AAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAAT 3237
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3641 AAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAAT 3700

Qy     3238 GACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGG 3297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3701 GACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGG 3760

Qy     3298 CACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCC 3357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3761 CACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCC 3820

Qy     3358 GTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTT 3417
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3821 GTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTT 3880

Qy     3418 GCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTC 3477
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3881 GCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTC 3940

Qy     3478 AAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGC 3537
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3941 AAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGC 4000

Qy     3538 TATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTC 3597
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4001 TATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTC 4060

Qy     3598 CTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTC 3657
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4061 CTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTC 4120

Qy     3658 AACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCT 3717
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4121 AACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCT 4180

Qy     3718 GTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGC 3777
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4181 GTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGC 4240

Qy     3778 TCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAG 3837
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4241 TCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAG 4300

Qy     3838 TTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGC 3897
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4301 TTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGC 4360

Qy     3898 CAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4361 CAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 4414
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RESULT 11
AAS88207
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ID   AAS88207 standard; cDNA; 7132 BP.
XX
AC   AAS88207;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #24011.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG24020.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
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PS   Claim 1; SEQ ID NO 24011; 103pp; English.
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CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC   coding sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 7132 BP; 1569 A; 2123 C; 2159 G; 1280 T; 0 U; 1 Other;

  Query Match             85.9%;  Score 3392.8;  DB 5;  Length 7132;
  Best Local Similarity   92.6%;  Pred. No. 0;
  Matches 3822;  Conservative    0;  Mismatches   12;  Indels  292;  Gaps   13;

Qy        7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      158 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 217

Qy       67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      218 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 277

Qy      127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      278 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 337

Qy      187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      338 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 397
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Qy      247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      398 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 457

Qy      307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      458 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 517

Qy      367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      518 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 577

Qy      427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      578 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 637

Qy      487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      638 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 697

Qy      547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      698 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 757

Qy      607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      758 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 817

Qy      667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      818 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 877

Qy      727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      878 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 937

Qy      787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      938 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 997

Qy      847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      998 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1057

Qy      907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1058 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1117

Qy      967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1118 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1177

Qy     1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1178 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1237

Qy     1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1238 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1297

Qy     1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1298 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1357

Qy     1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1358 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1417

Qy     1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1418 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1477

Qy     1327 GAGCGGCGGCAGGCGGAGCGTGAGCA---------------------------------- 1352
            |||||||||||||||||||| |||||
Db     1478 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGGAGCAG 1537

Qy     1353 -----------------------------------------------------GGAATAC 1359
                                                                 |||||||
Db     1538 CGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGGCCCTGCTGCTGGAATAC 1597

Qy     1360 AAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAG 1419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1598 AAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAG 1657

Qy     1420 GAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAG 1479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1658 GAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAG 1717

Qy     1480 CAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG 1539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1718 CAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG 1777

Qy     1540 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAG 1599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1778 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAG 1837

Qy     1600 CAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATC 1659
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1838 CAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATC 1897

Qy     1660 CCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCG 1719
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1898 CCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCG 1957

Qy     1720 GTGGAGCCCCAGGAGGGACCGCACA----------------------------------- 1744
            |||||||||||||||||||||||||
Db     1958 GTGGAGCCCCAGGAGGGACCGCACAAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCA 2017

Qy     1745 -------------------------AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCT 1779
                                     |||||||||||||||||||||||||||||||||||
Db     2018 TATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCT 2077

Qy     1780 GCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGT 1839
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2078 GCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGT 2137

Qy     1840 GCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGC 1899
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2138 GCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGC 2197

Qy     1900 CCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGG 1959
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2198 CCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGG 2257

Qy     1960 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 2019
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2258 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 2317

Qy     2020 GCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCA 2079
            ||||||||||||
Db     2318 GCAGTCCGTGCC------------------------------------------------ 2329

Qy     2080 GAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCC 2139

Db     2330 ------------------------------------------------------------ 2329

Qy     2140 TCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTT 2199
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2330 ---AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTT 2386

Qy     2200 CCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCC 2259
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     2387 CCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTC 2446

Qy     2260 TCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGAC 2319
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           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2447 TCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGAC 2506

Qy    2320 CACCGCTCACGGCCAGGCCGGCCCGCA------------------------GACTTTGTG 2355
           |||||||||||||||||||||||||||                        |||||||||
Db    2507 CACCGCTCACGGCCAGGCCGGCCCGCAAGCTATAAGCGAGCAATTGGTGAGGACTTTGTG 2566

Qy    2356 TTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTAC 2415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2567 TTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTAC 2626

Qy    2416 TCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGG 2475
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2627 TCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGG 2686

Qy    2476 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2687 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2746

Qy    2536 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2747 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2806

Qy    2596 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2655
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2807 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2866

Qy    2656 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2715
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2867 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2926

Qy    2716 AAAGGCCAAAGCCCACCCTCGAAGGATGGAGTGGTGACTACCAGTCTCGTGGGCTGGTA 2775
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2927 AAAGGCCAAAGCCCACCCTCGAAGGATGGAGTGGTGACTACCAGTCTCGTGGGCTGGTA 2986

Qy    2776 AAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGA 2835
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2987 AAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGA 3046

Qy    2836 GGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGAC 2895
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3047 GGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGAC 3106

Qy    2896 CAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGG 2955
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3107 CAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGG 3166

Qy    2956 GCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTC 3015
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3167 GCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTC 3226

Qy    3016 TGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGA-GAACGGGCTGATGTTGCT 3074
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    3227 TGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGGAACGGGCTGATGTTGCT 3286

Qy    3075 GGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGAT 3134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3287 GGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGAT 3346

Qy    3135 GGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCG 3194
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3347 GGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCG 3406

Qy    3195 GGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAA 3254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3407 GGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAA 3466

Qy    3255 GAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAA 3314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3467 GAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAA 3526

Qy    3315 ATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTG 3374
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Db    3527 ATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTG 3586

Qy    3375 GGCCCCCAAACCCTACCACAAATTCAT-GGCCTTCAAGTCCTTTGCCGACCTCCCCCACC 3433
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Db    3587 GGCCCCCAAACCCTACCACAAATTCATGGGCCTTCAAGTCCTTTGCCGACCTCCCCCACC 3646

Qy    3434 GCCCTCTGCT-GGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGC 3492
           |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    3647 GCCCTCTGCTGGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGC 3706

Qy    3493 TCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATC 3552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3707 TCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATC 3766

Qy    3553 CCTGTGCACATCCAGAGCCAGATCACG-CCCCATGCCATCATCTTCCTCCCCAACACCGA 3611
           ||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||
Db    3767 CCTGTGCACATCCAGAGCCAGATTACGCCCCCATGCCATCATCTTCCTCCCCAACACCGA 3826

Qy    3612 C-GGCATGGAGATGCTGCTGTGCTACG--AGGACGAGGGTGTCTACGTCAACACGTACGG 3668
           | |||||||||||||||||||||||||   |    ||| ||||||||||||||||||||| 
Db    3827 CGGGCATGGAGATGCTGCTGTGCTACGGAGGACGAAGGTTGTCTACGTCAACACGTACGG 3886

Qy    3669 GCGCATCATTAA-GGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACA 3727
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    3887 GCGCATCATTAAGGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACA 3946

Qy    3728 TCTGCTCCAACCAGA-TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    3947 TCTGCTCCAACCAGATTAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 4006

Qy    3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4007 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 4066

Qy    3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCC-AAGTTTA 3905
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    4067 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCTAAGTTTA 4126

Qy    3906 CTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
           ||||||||||||||||||||||||||||||||||||||||  ||||
Db    4127 CTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 4172
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RESULT 12
AAD17762
ID   AAD17762 standard; DNA; 3735 BP.
XX
AC   AAD17762;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human novel STE20-like protein, NOV-3d encoding DNA.
XX
KW   Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;
KW   trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;
KW   immunological disorder; neurodegenerative disorder; Alzheimer's disease;
KW   Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;
KW   human immunodeficiency virus; HIV; fertility disorder; neuroprotective;
KW   cytostatic; nootropic; anti-infertility; cancer; chromosome 17;
KW   NOV-3d protein; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3735
FT                   /*tag=  a
FT                   /product= "Human novel STE20-like protein, NOV-3d"
XX
PN   WO200162928-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US006151.
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XX
PR   25-FEB-2000; 2000US-0184951P.
PR   28-FEB-2000; 2000US-0185548P.
PR   01-MAR-2000; 2000US-0185967P.
PR   18-APR-2000; 2000US-0197723P.
PR   27-APR-2000; 2000US-0199957P.
PR   23-FEB-2001; 2001US-00789390.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Vernet CAM,  Fernandes E,  Shimkets RA,  Macdougall J,  Spaderna SK;
XX
DR   WPI; 2001-582051/65.
DR   P-PSDB; AAE10614.
XX
PT   New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like
PT   polypeptide for diagnosing and treating pathological disorders, such as
PT   Parkinson's disease and for use in pharmocogenomics.
XX
PS   Claim 9; Page 67-68; 189pp; English.
XX
CC   The invention relates to novel human polypeptides referred as NOV-X and
CC   their corresponding nucleic acid sequences. NOV-X collectively include
CC   NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-
CC   3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and
CC   NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin
CC   inhibitor-like polypeptides. NOV-X is used to identify a potential
CC   therapeutic agent that can modulate its activity and can be used for
CC   treating a pathology related to aberrant expression or aberrant
CC   physiological interactions of NOV-X. NOV-X or its DNA is used to
CC   determine the presence or predisposition to a disease associated with
CC   altered levels of NOV-X. NOV-X, its DNA and its antibody are used to
CC   treat or prevent a pathology associated with NOV-X. The pathological
CC   states that can be treated or prevented are haematopoietic, cancer,
CC   immunological, tumour, neurodegenerative (e.g. Alzheimer's and
CC   Parkinson's disease), human immunodeficiency virus (HIV) illness and
CC   fertility disorders. NOV-X and its DNA are used in pharmacogenomics for
CC   predictive medicine. NOV-X DNA is used in gene therapy. The present
CC   sequence is a DNA encoding human novel STE20-like protein, NOV-3d. NOV-3d
CC   gene is located at chromosome 17
XX
SQ   Sequence 3735 BP; 880 A; 1105 C; 1137 G; 613 T; 0 U; 0 Other;

  Query Match             85.0%;  Score 3358.2;  DB 5;  Length 3735;
  Best Local Similarity   92.7%;  Pred. No. 0;
  Matches 3673;  Conservative    0;  Mismatches   38;  Indels  252;  Gaps    4;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
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Db          1 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 60

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
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Db         61 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 300

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
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Db        301 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Db        361 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
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Db        421 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 480

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Db        481 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 540

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
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Db        541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
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Db        601 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 660

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 720

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 780

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 840

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
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Db        901 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 960

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
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Db        961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
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Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
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Db       1081 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1140

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
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Db       1141 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1200

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
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Db       1201 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1260

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1320

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              ||||||||||||||||||| |||||||||||  |   ||   |    ||| |||||||||||
Db       1321 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGCAGCGG 1380

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
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Db       1381 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1440

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1500
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Qy   1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
Db   1501 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1560

Qy   1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
Db   1561 CGAGAGGTAG-------------------------------------------------- 1570

Qy   1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
Db   1571 ------------------TGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTA 1611

Qy   1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
Db   1612 CCCCGATCCC------------------------------------------------AG 1623

Qy   1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
Db   1624 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1683

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Db   1684 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1743

Qy   1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
Db   1744 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1803

Qy   1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
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Db   1864 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 1908

Qy   2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106
Db   1909 ------------------------------------------------------------ 1908

Qy   2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
Db   1909 -------------------------------------AGTAACCCCGACCTCAGGAGGAGC 1932

Qy   2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
Db   1933 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 1992

Qy   2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
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Qy   2347 ------------------------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
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Qy   2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
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Qy   2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
Db   2233 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2292

Qy   2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
Db   2293 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2352

Qy   2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
Db   2353 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2412

Qy   2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
Db   2413 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2472

Qy   2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
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Qy   2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
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Qy   2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
Db   2593 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2652

Qy   2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
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Db   2713 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2772

Qy   2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
Db   2773 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 2832

Qy   3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
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Qy   3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
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Qy   3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
Db   3193 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3252

Qy   3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
Db   3253 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3312

Qy   3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
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Db   3373 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3432

Qy   3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
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Db       3553 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3612

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Db       3673 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3732

Qy       3943 TGA 3945
              |||
Db       3733 TGA 3735

RESULT 13
AAD17761
ID   AAD17761 standard; DNA; 3822 BP.
XX
AC   AAD17761;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human novel STE20-like protein, NOV-3c encoding DNA.
XX
KW   Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;
KW   trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;
KW   immunological disorder; neurodegenerative disorder; Alzheimer's disease;
KW   Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;
KW   human immunodeficiency virus; HIV; fertility disorder; neuroprotective;
KW   cytostatic; nootropic; anti-infertility; cancer; chromosome 17;
KW   NOV-3c protein; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3822
FT                   /*tag=  a
FT                   /product= "Human novel STE20-like protein, NOV-3c"
XX
PN   WO200162928-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US006151.
XX
PR   25-FEB-2000; 2000US-0184951P.
PR   28-FEB-2000; 2000US-0185548P.
PR   01-MAR-2000; 2000US-0185967P.
PR   18-APR-2000; 2000US-0197723P.
PR   27-APR-2000; 2000US-0199957P.
PR   23-FEB-2001; 2001US-00789390.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Vernet CAM,  Fernandes E,  Shimkets RA,  Macdougall J,  Spaderna SK;
XX
DR   WPI; 2001-582051/65.
DR   P-PSDB; AAE10613.
XX
PT   New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like
PT   polypeptide for diagnosing and treating pathological disorders, such as
PT   Parkinson's disease and for use in pharmocogenomics.
XX
PS   Claim 9; Page 58-59; 189pp; English.
XX
CC   The invention relates to novel human polypeptides referred as NOV-X and
CC   their corresponding nucleic acid sequences. NOV-X collectively include
CC   NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-
CC   3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and
CC   NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin
CC   inhibitor-like polypeptides. NOV-X is used to identify a potential
CC   therapeutic agent that can modulate its activity and can be used for
CC   treating a pathology related to aberrant expression or aberrant
CC   physiological interactions of NOV-X. NOV-X or its DNA is used to
CC   determine the presence or predisposition to a disease associated with
CC   altered levels of NOV-X. NOV-X, its DNA and its antibody are used to
CC   treat or prevent a pathology associated with NOV-X. The pathological
CC   states that can be treated or prevented are haematopoietic, cancer,
CC   immunological, tumour, neurodegenerative (e.g. Alzheimer's and
CC   Parkinson's disease), human immunodeficiency virus (HIV) illness and
CC   fertility disorders. NOV-X and its DNA are used in pharmacogenomics for
CC   predictive medicine. NOV-X DNA is used in gene therapy. The present
CC   sequence is a DNA encoding human novel STE20-like protein, NOV-3c. NOV-3c
CC   gene is located at chromosome 17
XX
SQ   Sequence 3822 BP; 904 A; 1129 C; 1165 G; 624 T; 0 U; 0 Other;

  Query Match             82.9%;  Score 3275.6;  DB 5;  Length 3822;
  Best Local Similarity   90.9%;  Pred. No. 0;
  Matches 3682;  Conservative    0;  Mismatches   29;  Indels  339;  Gaps    5;

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Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
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Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
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Db        241 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 300

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
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Db        301 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Db        361 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 480

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 540

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 660

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
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Db     661 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGTGACATGCACCCCATGCGA 720

Qy     727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db     721 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 780

Qy     787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db     781 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 840

Qy     847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db     841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy     907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db     901 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 960

Qy     967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db     961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

Qy    1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db    1021 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1080

Qy    1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db    1081 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1140

Qy    1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db    1141 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1200

Qy    1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
Db    1201 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1260

Qy    1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db    1261 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1320

Qy    1327 GAGCGGCGGCAGGCGGAGCGTGAGCA---------------------------------- 1352
Db    1321 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGGAGCAG 1380

Qy    1353 -----------------------------------------------------GGAATAC 1359
Db    1381 CGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGGCCCTGCTGCTGGAATAC 1440

Qy    1360 AAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAG 1419
Db    1441 AAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAG 1500

Qy    1420 GAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAG 1479
Db    1501 GAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAG 1560

Qy    1480 CAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG 1539
Db    1561 CAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG 1620

Qy    1540 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAG 1599
Db    1621 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAG----------------------- 1657

Qy    1600 CAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATC 1659
Db    1658 ----------------------------------------------TGGCACACCGGGTC 1671

Qy    1660 CCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCG 1719
Db    1672 CCACTGAAGCCATATGCAGCACCTGTACCCCGATCCC----------------------- 1708

Qy    1720 GTGGAGCCCCAGGAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCT 1779
Db    1709 -------------------------AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCT 1743

Qy    1780 GCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGT 1839
Db    1744 GCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGT 1803

Qy    1840 GCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGC 1899
Db    1804 GCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGC 1863

Qy    1900 CCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGG 1959
Db    1864 CCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGG 1923

Qy    1960 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 2019
Db    1924 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 1983

Qy    2020 GCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCA 2079
Db    1984 GCAGTCCGTGCC------------------------------------------------ 1995

Qy    2080 GAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCC 2139
Db    1996 ------------------------------------------------------------ 1995

Qy    2140 TCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTT 2199
Db    1996 ---AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTT 2052

Qy    2200 CCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCC 2259
Db    2053 CCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTC 2112

Qy    2260 TCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGAC 2319
Db    2113 TCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGAC 2172

Qy    2320 CACCGCTCACGGCCAGGCCGGCCCGCA-----------------------GACTTTGTG 2355
Db    2173 CACCGCTCACGGCCAGGCCGGCCCGCAAGCTATAAGCGAGCAATTGGTGAGGACTTTGTG 2232

Qy    2356 TTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTAC 2415
Db    2233 TTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTAC 2292

Qy    2416 TCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGG 2475
Db    2293 TCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGG 2352

Qy    2476 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2535
Db    2353 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2412

Qy    2536 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2595
Db    2413 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2472

Qy    2596 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2655
Db    2473 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2532

Qy    2656 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2715
Db    2533 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2592

Qy    2716 AAAGGCCAAAGCCCACCCTCGAAGGATGGAGTGGTGACTACCAGTCTCGTGGGCTGGTA 2775
Db    2593 AAAGGCCAAAGCCCACCCTCGAAGGATGGAGTGGTGACTACCAGTCTCGTGGGCTGGTA 2652
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Qy       2776 AAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGA 2835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2653 AAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGA 2712

Qy       2836 GGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGAC 2895
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2713 GGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGAC 2772

Qy       2896 CAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGG 2955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2773 CAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGG 2832

Qy       2956 GCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTC 3015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2833 GCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTC 2892

Qy       3016 TGTGCAGCCCTTTGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTG 3075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2893 TGTGCAGCCCTTTGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTG 2952

Qy       3076 GACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATG 3135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2953 GACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATG 3012

Qy       3136 GATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGG 3195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3013 GATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGG 3072

Qy       3196 GTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAG 3255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3073 GTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAG 3132

Qy       3256 AAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAA 3315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3133 AAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAA 3192

Qy       3316 TACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGG 3375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3193 TACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGG 3252

Qy       3376 GCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGC 3435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3253 GCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGC 3312

Qy       3436 CCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCC 3495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3313 CCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCC 3372

Qy       3496 AGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCT 3555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3373 AGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCT 3432

Qy       3556 GTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGC 3615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3433 GTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGC 3492

Qy       3616 ATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATC 3675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3493 ATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATC 3552

Qy       3676 ATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCC 3735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3553 ATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCC 3612

Qy       3736 AACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCAC 3795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3613 AACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCAC 3672

Qy       3796 CTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAAT 3855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3673 CTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAAT 3732

Qy       3856 GACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACT 3915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3733 GACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACT 3792

Qy       3916 CTGAACCGTAACTGCATCATGAACTGGTGA 3945
              ||||||||||||||||||||||||||||||
Db       3793 CTGAACCGTAACTGCATCATGAACTGGTGA 3822
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RESULT 14
AAC98909
ID   AAC98909 standard; cDNA; 2345 BP.
XX
AC   AAC98909;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:137.
XX
KW   Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;
KW   diagnosis; identification; cytostatic; neuroprotective; nootropic;
KW   immunomodulatory; relaxant; contraceptive; gynaecological;
KW   antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW   linkage analysis; tissue identification; tissue typing; forensic; neural;
KW   immune system; muscular; reproductive; gastrointestinal; pulmonary;
KW   cardiovascular; renal; proliferative; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055320-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005989.
XX
PR   12-MAR-1999;   99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-579444/54.
DR   P-PSDB; AAB54144.
XX
PT   New nucleic acid that is a pancreatic cancer antigen for preventing,
PT   treating, or ameliorating a medical condition, particular pancreatic
PT   cancer, or for use in assays for diagnosing a pathological condition.
XX
PS   Claim 1; Page 596-597; 1379pp; English.
XX
CC   AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC   proteins, called pancreatic cancer antigens, given in AAB54008 to
CC   AAB54466. The human pancreatic cancer antigens have cytostatic,
CC   neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC   gynaecological, cardiant and antiinflammatory activities, and can be used
CC   in gene therapy. The polynucleotide and proteins can be used for
CC   preventing, treating, or ameliorating a medical condition or in assays
CC   for diagnosing a pathological condition or a susceptibility to one in a
CC   subject. Binding partners to the proteins and the activity of the
CC   proteins can be identified. The pancreatic cancer antigens can be used to
CC   detect, treat or prevent pancreatic disorders, especially cancer.
CC   Agonists and antagonists to the antigens can be screened for. The
CC   pancreatic cancer antigen polynucleotides can be used to design nucleic
CC   acid hybridisation probes that can be used in chromosome mapping, linkage
CC   analysis, tissue identification and/or typing and a variety of forensic
CC   and diagnostic methods. The proteins can be used to generate antibodies
CC   which are used to purify, detect and target the polypeptides, including
CC   both in vivo and in vitro diagnostic and therapeutic methods. The
CC   proteins can be used to treat or prevent neural, immune system, muscular,
CC   reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC   proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC   sequences used in the exemplification of the present invention
XX
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SQ   Sequence 2345 BP; 499 A; 693 C; 671 G; 467 T; 0 U; 15 Other;

  Query Match             38.0%;  Score 1502.6;  DB 3;  Length 2345;
  Best Local Similarity   99.2%;  Pred. No. 6.9e-278;
  Matches 1527;  Conservative    3;  Mismatches    8;  Indels    2;  Gaps    2;

Qy       2413 TACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGC 2472
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TATTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGC 60

Qy       2473 GGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGC 2532
              |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db         61 GGCCAGCAGAGGGGAGCAGAGATACCCYTGGGGGCCGCAGCGATGGGGATACAGACAGC 120

Qy       2533 GTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGG 2592
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCA-CACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGG 179

Qy       2593 GGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGAC 2652
              |  | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GCGGNCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGAC 239

Qy       2653 AGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAAC 2712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAAC 299

Qy       2713 AGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGT-GACTACCAGTCTCGTGGGCT 2771
              ||||||||||||||||||||||||||||||||||||||| ||||||||||:|||||||||
Db        300 AGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTNGACTACCAGTYTCGTGGGCT 359

Qy       2772 GGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCC 2831
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        360 GGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATTTACCAGCC 419

Qy       2832 TGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCT 2891
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        420 TGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGTT 479

Qy       2892 CGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACAC 2951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACAC 539

Qy       2952 CCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGAT 3011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGAT 599

Qy       3012 CCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTT 3071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTT 659

Qy       3072 GCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCA 3131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCA 719

Qy       3132 GATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACT 3191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 GATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACT 779

Qy       3192 GCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGA 3251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 GCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGA 839

Qy       3252 GAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGT 3311
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db        840 GAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTKTTGT 899

Qy       3312 GAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGC 3371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 GAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGC 959

Qy       3372 CTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCA 3431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 CTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCA 1019

Qy       3432 CCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGG 3491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 CCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGG 1079

Qy       3492 CTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACAT 3551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1080 CTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACAT 1139

Qy       3552 CCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGA 3611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 CCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGA 1199

Qy       3612 CGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCG 3671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 CGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCG 1259

Qy       3672 CATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTG 3731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 CATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTG 1319

Qy       3732 CTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGG 3791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 CTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGG 1379

Qy       3792 CCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCG 3851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 CCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCG 1439

Qy       3852 GAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCAT 3911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1440 GAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCAT 1499

Qy       3912 GACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              ||||||||||||||||||||||||||||||||  ||||
Db       1500 GACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 1539


RESULT 15
AAF84940
ID   AAF84940 standard; DNA; 3996 BP.
XX
AC   AAF84940;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Nucleotide sequence of cell cycle protein Tnik isoform 2.
XX
KW   Cell cycle protein; Tnik; germinal center kinase; Nck; Traf2; cell cycle;
KW   tumour necrosis factor receptor associated factor 2; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3996
FT                   /*tag=  a
FT                   /transl_except= "(pos:"3994. .3996, aa: Glx) /product=
FT                   "Tnik
XX
PN   WO200129197-A2.
XX
PD   26-APR-2001.
XX
PF   23-OCT-2000; 2000WO-US041455.
XX
PR   21-OCT-1999;    99US-00425324.
XX
PA   (RIGE-) RIGEL PHARM INC.
XX
PI   Luo Y,  Fu CA,  Shen M;
XX
DR   WPI; 2001-300333/31.
DR   P-PSDB; AAB68217.
```

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XX
PT   Novel germinal center kinase cell cycle polypeptide useful for screening
PT   modulators of cell cycle and for use in diagnostics and therapeutics.
XX
PS   Claim 1; Fig 22; 96pp; English.
XX
CC   The present sequence encodes an isoform of a human cell cycle protein
CC   designated Tnik. Tnik is a member of the germinal center kinase family.
CC   Tnik binds to tumour necrosis factor (TNF) receptor associated factor 2
CC   (Traf2) or the adapter protein Nck. Tnik polypeptides and polynucleotides
CC   are useful for screening for compounds that are modulators of cell cycle,
CC   and in therapeutics. The Tnik polynucleotide is also useful in gene
CC   therapy
XX
SQ   Sequence 3996 BP; 1203 A; 911 C; 1064 G; 818 T; 0 U; 0 Other;

  Query Match             35.6%;  Score 1407.2;  DB 4;  Length 3996;
  Best Local Similarity   62.5%;  Pred. No. 1.4e-259;
  Matches 2528;  Conservative    0;  Mismatches 1363;  Indels  153;  Gaps   15;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
Db          1 ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGAC 60
Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
Db         61 CCTGCAGGGATCTTTGAATTGGTGGAACTTGTTGGAAATGGAACATACGGGCAAGTTTAT 120
Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
Db        121 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGGTTATGGATGTCACAGGG 180
Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
Db        181 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACCGG 240
Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
Db        241 AATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCACCAGGCATGGATGACCAA 300
Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db        301 CTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCGACCTGATCAAGAACACA 360
Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db        361 AAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGCAGGGAAATCTTACGGGGG 420
Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db        421 CTGAGTCACCTGCACCAGCATAAAGTGATTCATCGAGATATTAAAGGGCAAAATGTCTTG 480
Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db        481 CTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCAGTGCTCAGCTTGATCGA 540
Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db        541 ACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGATGGCACCAGAAGTTATT 600
Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
Db        601 GCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTGACTTGTGGTCTTTGGGT 660
Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db        661 ATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCACCCCATGAGA 720
Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db        721 GCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGTCTAAGAAGTGGTCAAAA 780
Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db        781 AAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCACAGCCAGCGACCAGCAACA 840
Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db        841 GAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAATGAGCGACAGGTCCGCATT 900
Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db        901 CAACTCAAGGACCATATTGATAGAACAAAGAAGAAGCGAGGAGAAAAAGATGAGACAGAG 960
Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db        961 TATGAGTACAGTGGAAGTGAGGAAGAAGAGGAGGAGAAT---GACTCAGGAGAGCCCAGC 1017
Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db       1018 TCCATCCTGAATCTGCCAGGGGAGTCGACGCTGCGGAGGGACTTTCTGAGGCTGCAGCTG 1077
Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db       1078 GCCAACAAGGAGCGTTCTGAGGCCCTA------CGGAGGCAGCAGCTGGAGCAGCAGCAG 1131
Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db       1132 CGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTCAGAAGCGCATCGAGGAG 1191
Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
Db       1192 CAGAAAGAGCAGAGGCGGCGGCTGGAGGAGCAACAAAGGCGAGAGAAGGAGCTGCGGAAG 1251
Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db       1252 CAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGG------AGCAGATGCGCCGGGAGGAG 1305
Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
Db       1306 GAGAGGAGGCGTGCGGAGCATGAACAGGAATATAAGCGCAAACAATTGGAAGAACAGAGA 1365
Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
Db       1366 CAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAAGAAAGAGACTACTTAGTTTCCCTTCAG 1425
Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
Db       1426 CATCAGCGGCAGGAGCAG-----------------------------AGGCCTGTGGAG 1455
Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
Db       1456 AAGAAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTGAGAAGCCAGCATGGGCC 1515
Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
Db       1516 AAGGAGGTAGAAGAACGGTCAAGGCTCAACCGGCAAAGTTCCCCTGCCATGCCTCA---C 1572
Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCC---------AGGCCTCCCCAGGG 1677
Db       1573 AAGGTTGCCAACAGGATATCTGACCCCAACCTGCCCCCAAGGTCGGAGTCCTTCAGCATT 1632
Qy       1678 CCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAG------ 1731
Db       1633 AGTGGAGTTCAGCCTGCTCGAACACCCCCCATGCTCAGACCAGTCGATCCCCAGATCCCA 1692
Qy       1732 ---GAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCA 1788
Db       1693 CATCTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCTCCCAGTCAGTGCACGAG 1752
Qy       1789 GCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGA 1848
Db       1753 CAGCCCACAAAGGGCCTCTCTGGGTTTCAGGAGGCTCTGAACGTGACCTCCCACCGCGTG 1812
Qy       1849 GCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCC------- 1901
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Db   1813 GAGATGCCACGCCAGAACTCAGATCCCACCTCGGAAAATCCTCTCTCCCCACTCGCATT 1872

Qy   1902 --------GAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCT 1953

Db   1873 GAAAAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCT 1932

Qy   1954 CAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCA 2013

Db   1933 CAAAGAACAACTTCTATATCCCCAGCATTAGCCAGAAAGAATTCTCCTGGGAATGGTAGT 1992

Qy   2014 GCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGC--AAA 2071

Db   1993 GCTCTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGA 2052

Qy   2072 GGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGC 2131

Db   2053 ACTGAGCCCATCTTGGAGAGCCCCTTGCAGAGGACCAGCAGTGGCAGTTCCTCCAGCTCC 2112

Qy   2132 CCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGG----GAACGCTCG 2187

Db   2113 AGCACCCCTAGCTCCCAGCCCAGCTCCCAAGGAGGCTCCCAGCCTGGATCACAAGCAGGA 2172

Qy   2188 GACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAAC 2247

Db   2173 TCCAGTGAACGCACCAGAGTTCGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTTCCC 2232

Qy   2248 CGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCC 2307

Db   2233 CATGAGCCTGCCAAGGTGAAACCAGAAGAATCCAGGGACATTACCCGGCCCAGTCGACCA 2292

Qy   2308 AAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAG 2367

Db   2293 GCTAGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAGCCAAAGAACTAAGAGAA 2352

Qy   2368 CGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGC 2427

Db   2353 CTCCGGATTGAAGAAACAAACCGCCCAATGAAGAAGGTGACTGATTACTCCTCCTCCAGT 2412

Qy   2428 GAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGG 2487

Db   2413 GAGGAGTCAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGG 2472

Qy   2488 A--------------------------------GCAGAGATACCCCTGGGGGCCGCAGC 2514

Db   2473 ACAGTGGCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAG 2532

Qy   2515 GATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGG 2574

Db   2533 CAGTACAATGTGGGAATGGTGGGGACGCATGGGCTGGAGACCTCTCATGCGGACAGTTTC 2592

Qy   2575 ACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGG 2634

Db   2593 AGCGGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAGAGAAGAAG 2652

Qy   2635 AACCTGCTGCATGCTGACAGCAATGGGT---------ACACAAACCTGCCTGACGTGGTC 2685

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Qy   2686 CAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAA------GCCCACCCTCGAAG 2739

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Db   2953 CTCAATGAAGCAAGAAAGATTTCGGTGGTAAATGTAAACCCAACCAACATTCGGCCTCAT 3012

Qy   2962 AGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCA 3021

Db   3013 AGCGACACACCAGAAATCAGAAAATACAAGAAACGATTCAACTCAGAAATACTTTGTGCA 3072

Qy   3022 GCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGA 3081

Db   3073 GCTCTGTGGGGTGTAAACCTTCTGGTGGGGACTGAAAATGGCCTGATGCTTTTGGACCGA 3132

Qy   3082 AGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTG 3141

Db   3133 AGTGGGCAAGGCAAAGTCTATAATCTGATCAACCGGAGGCGATTTCAGCAGATGGATGTG 3192

Qy   3142 CTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTAT 3201

Db   3193 CTAGAGGGACTGAATGTCCTTGTGACAATTTCAGGAAAGAAGAATAAGCTACGAGTTTAC 3252

Qy   3202 TACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAG 3261

Db   3253 TATCTTTCATGGTTAAGAAACAGAATACTACATAATGACCCAGAAGTAGAAAAGAAACAA 3312

Qy   3262 GGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAG 3321

Db   3313 GGCTGGATCACTGTTGGGGACTTGGAAGGCTGTATACATTATAAAGTTGTTAAATATGAA 3372

Qy   3322 CGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCC 3381

Db   3373 AGGATCAAATTTTTGGTGATTGCCTTAAAGAATGCTGTGGAAATATATGCTTGGGCTCCT 3432

Qy   3382 AAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTG 3441

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Qy   3442 CTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCT 3501

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Qy   3502 GGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCAC 3561

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Qy   3562 ATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAG 3621

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Qy   3682 GATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAG 3741

Db   3733 GATGTGGTGCTCCAATGGGGAGAAATGCCCACGTCTGTGGCCTACATTCATTCCAATCAG 3792

Qy   3742 ATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGAC 3801

Db   3793 ATAATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTTGGAT 3852

Qy   3802 GGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAG 3861

Db   3853 GGAGTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAG 3912

Qy   3862 GTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAAC 3921

Db   3913 GTATTTTTTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTTTTTCATGACCCTCAAC 3972

Qy   3922 CGTAACTGCATCATGAACTGGTGA 3945

Db   3973 AGAAATTCCATGATGAACTGGTAA 3996
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Search completed: March 2, 2004, 10:12:35
Job time : 1049 secs

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OM nucleic - nucleic search, using sw model

Run on:          March  2, 2004, 12:59:16 ; Search time 70 Seconds
                                            (without alignments)
                                            9508.433 Million cell updates/sec

Title:           US-10-029-115-1
Perfect score:   3951
Sequence:        1 gcccttatgggcgacccagc.........tcatgaactggtgaaagggc 3951

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        164199 seqs, 84230614 residues

Total number of hits satisfying chosen parameters:      328398

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_NA_New:*
                 1:  /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3601	91.1	4863	6	US-10-764-503-30	Sequence 30, Appl
	2	818.6	20.7	3786	5	US-09-744-794C-46	Sequence 46, Appl
	3	214.2	5.4	1975	1	PCT-US04-03417-41	Sequence 41, Appl
	4	214.2	5.4	1975	6	US-10-772-636-41	Sequence 41, Appl
	5	141	3.6	2778	5	US-09-744-794C-33	Sequence 33, Appl
	6	134.8	3.4	11924	1	PCT-US03-31219-7	Sequence 7, Appli
	7	134.8	3.4	12242	1	PCT-US03-31219-6	Sequence 6, Appli
	8	115	2.9	445	6	US-10-767-701-920	Sequence 920, App
	9	112.4	2.8	2838	6	US-10-770-726-27	Sequence 27, Appl
	10	92.2	2.3	484	6	US-10-767-701-28242	Sequence 28242, A
	11	86	2.2	11409	6	US-10-767-471-603	Sequence 603, App
	12	86	2.2	14800	6	US-10-767-471-195	Sequence 195, App
	13	83.4	2.1	14321	6	US-10-767-471-191	Sequence 191, App
	14	83.4	2.1	14641	6	US-10-767-471-193	Sequence 193, App
	15	83.4	2.1	14760	6	US-10-767-471-192	Sequence 192, App
	16	83.4	2.1	24841	6	US-10-767-471-10753	Sequence 10753, A
	17	83.4	2.1	72779	6	US-10-767-471-10639	Sequence 10639, A
	18	79.6	2.0	2309	6	US-10-767-471-482	Sequence 482, App
	19	79.4	2.0	14859	6	US-10-767-471-10846	Sequence 10846, A
	20	79.4	2.0	67163	6	US-10-767-471-10712	Sequence 10712, A
	21	78.6	2.0	789	6	US-10-767-701-6073	Sequence 6073, Ap
	22	77.8	2.0	679	6	US-10-767-701-4740	Sequence 4740, Ap
	23	72.8	1.8	660	6	US-10-767-701-2317	Sequence 2317, Ap
	24	72.8	1.8	3218	6	US-10-451-467A-63	Sequence 63, Appl
	25	69.6	1.8	166020	6	US-10-767-471-10806	Sequence 10806, A
c	26	66.2	1.7	5921	1	PCT-US04-02188-18	Sequence 18, Appl
c	27	66.2	1.7	5921	6	US-10-764-425-18	Sequence 18, Appl
	28	66.2	1.7	111469	6	US-10-767-471-10820	Sequence 10820, A
	29	66	1.7	2213	6	US-10-770-726-31	Sequence 31, Appl
c	30	65.6	1.7	1021	6	US-10-767-701-11316	Sequence 11316, A
	31	64.2	1.6	201	6	US-10-767-471-10130	Sequence 10130, A
	32	64.2	1.6	201	6	US-10-767-471-38286	Sequence 38286, A
c	33	62.2	1.6	803755	6	US-10-767-471-10700	Sequence 10700, A
	34	61.6	1.6	6900	1	PCT-US04-02188-13	Sequence 13, Appl
	35	61.6	1.6	6900	6	US-10-764-425-13	Sequence 13, Appl
c	36	61.6	1.6	106707	1	PCT-US03-34223-8	Sequence 8, Appli
c	37	60.6	1.5	520	6	US-10-767-701-1270	Sequence 1270, Ap
	38	60.2	1.5	583	6	US-10-767-701-4088	Sequence 4088, Ap
c	39	60	1.5	1139	6	US-10-767-701-2898	Sequence 2898, Ap
	40	59.2	1.5	713	6	US-10-767-701-1473	Sequence 1473, Ap
	41	59.2	1.5	1578	6	US-10-417-884A-1441	Sequence 1441, Ap
	42	58.6	1.5	201	6	US-10-767-471-3749	Sequence 3749, Ap
	43	58.6	1.5	201	6	US-10-767-471-3826	Sequence 3826, Ap
	44	58.6	1.5	201	6	US-10-767-471-3904	Sequence 3904, Ap
	45	58.6	1.5	201	6	US-10-767-471-3994	Sequence 3994, Ap

ALIGNMENTS

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RESULT 1
US-10-764-503-30
; Sequence 30, Application US/10764503
; GENERAL INFORMATION:
;  APPLICANT: Levanon Erez, et al.
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING NATURALLY OCCURRING ANTISENSE
;  TITLE OF INVENTION:  TRANSCRIPTS AND METHODS, KITS AND ARRAYS UTILIZING SAME
;  FILE REFERENCE: 26946
;  CURRENT APPLICATION NUMBER: US/10/764,503
;  CURRENT FILING DATE:  2004-01-27
;  PRIOR APPLICATION NUMBER: US 09/718,407
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: US 09/732,938
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/785,439
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: US 09/907,923
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 09/993,398
;  PRIOR FILING DATE: 2001-11-26
;  PRIOR APPLICATION NUMBER: US 10/201,605
;  PRIOR FILING DATE: 2002-7-24
;  PRIOR APPLICATION NUMBER: PCT/IL02/00904
;  PRIOR FILING DATE: 2002-11-11
;  PRIOR APPLICATION NUMBER: US 10/441,281
;  PRIOR FILING DATE: 2003-5-20
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 4863
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-764-503-30

  Query Match             91.1%;  Score 3601;  DB 6;  Length 4863;
  Best Local Similarity   95.0%;  Pred. No. 0;
  Matches 3829;  Conservative    0;  Mismatches    5;  Indels  195;  Gaps    3;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
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Db        185 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 244

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
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Db        245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 304

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
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Db        305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 364
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Qy      187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Db      365 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 424

Qy      247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
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Db      425 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 484

Qy      307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
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Db      485 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 544

Qy      367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Qy      487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Qy      547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
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Qy      607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
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Db      785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy      667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
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Db      845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy      727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Db      905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy      787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
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Db      965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy      847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
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Db     1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy      907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
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Qy      967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
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Qy     1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
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Db     1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

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Db     1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
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Db     1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy     1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
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Qy     1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
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Qy     1745 ----------------------------------------------------------AG 1746
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Qy     1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
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Qy     2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db     2270 ------------------------------------------------------------ 2269

Qy     2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
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Qy     2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
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Qy     2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
            ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
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Qy       2347 ------------------------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
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Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
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Db       2714 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2773

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Qy       2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
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Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
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Db       2894 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2953

Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
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Db       2954 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 3013

Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
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Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
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Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
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Db       3554 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3613

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
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Db       3614 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3673

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
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Db       3734 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3793

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Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3762
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Db       4094 TGACGGGGC 4102
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RESULT 2
US-09-744-794C-46
; Sequence 46, Application US/09744794C
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; HILLMAN, Jennifer L.;
; APPLICANT: LAL, Preeti G.; TANG, Y. Tom;
; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
; APPLICANT: BAUGHN, Mariah R.; PATTERSON, Chandra S.;
; APPLICANT: BANDMAN, Olga; AU-YOUNG, Janice K.;
; APPLICANT: GORGONE, Gina A.; YUE, Henry;
; APPLICANT: AZIMZAI, Yalda; REDDY, Roopa M.;
; APPLICANT: LU, Dyung Aina M.; SHIH, Leo L.
; TITLE OF INVENTION: HUMAN CELL SURFACE RECEPTORS
; FILE REFERENCE: PF-0565 USN
; CURRENT APPLICATION NUMBER: US/09/744,794C
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PERL Program
; SEQ ID NO 46
;   LENGTH: 3786
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 2299715CB1
US-09-744-794C-46

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  Query Match             20.7%;  Score 818.6;  DB 5;  Length 3786;
  Best Local Similarity   56.2%;  Pred. No. 4.1e-168;
  Matches 2219;  Conservative    0;  Mismatches 1189;  Indels  537;  Gaps   15;
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Db      200 CCTGCTGGGATTTTTGAGCTGGTGGAAGTGGTTGGAAATGGCACCTATGGACAAGTCTAT 259
Qy      127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
Db      260 AAGGGTCGACATGTTAAAACGGGTCAGTTGGCAGCCATCAAAGTTATGGATGTCACTGAG 319
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Db      500 AAAGGGAACACACTCAAAGAAGACTGGATCGCTTACATCTCCAGAGAAATCCTGAGGGGA 559
Qy      427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db      560 CTGGCACATCTTCACATTCATCATGTGATTCACCGGGATATCAAGGGCCAGAATGTGTTG 619
Qy      487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db      620 CTGACTGAGAATGCAGGGGTGAAACTTGTTGACTTTGGTGTGAGTGCTCAGCTGGACAGG 679
Qy      547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db      680 ACTGTGGGGCGGAGAAATACGTTCATAGGCACTCCCTACTGGATGGCTCCTGAGGTCATC 739
Qy      607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
Db      740 GCCTGTGATGAGAACCCAGATGCCACCTATGATTACAGAAGTGATCTTTGGTCTTGTGGC 799
Qy      667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db      800 ATTACAGCCATTGAGATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCATCCAATGAGA 859
Qy      727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db      860 GCACTGTTTCTCATTCCCAGAAACCCTCCTCCCCGGCTGAAGTCAAAAAAATGGTCGAAG 919
Qy      787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db      920 AAGTTTTTTAGTTTTATAGAAGGGTGCCTGGTGAAGAATTACATGCAGCGGCCCTCTACA 979
Qy      847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db      980 GAGCAGCTTTTGAAACATCCTTTTATAAGGGATCAGCCAAATGAAAGGCAAGTTAGAATC 1039
Qy      907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db     1040 CAGCTTAAGGATCATATAGATCGTACCAGGAAGAAGAGAGGCGAGAAAGATGAAACTGAG 1099
Qy      967 TATGAGTACAGCGGCAGCGAGGAGGAA---GATGACAGCCATGGAGAGGAAGGAGAGCCA 1023
Db     1100 TATGAGTACAGTGGGAGTGAGGAAGAAGAGGAGGAAGTGCCTGAACAGGAAGGAGAGCCA 1159
Qy     1024 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1083
Db     1160 AGTTCCATTGTGAACGTGCCTGGTGAGTCTACTCTTCGCCGAGATTTCCTGAGACTGCAG 1219

Qy     1084 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1143
Db     1220 CAGGAGAACAAGGAACGTTCCGAGGCTCTTCGGAGACAACAGTTACTACAGGAGCAACAG 1279
Qy     1144 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1203
Db     1280 CTCCGGGAGCAGGAAGAATATAAAAGGCAACTGCTGGCAGAGAGACAGAAGCGGATTGAG 1339
Qy     1204 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1263
Db     1340 CAGCAGAAAGAACAGAGGCGACGGCTAGAAGAGCAACAAAGGAGAGAGCGGGAAGCTAGA 1399
Qy     1264 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1323
Db     1400 AGGCAGCAGGAACGTGAACAGCGAAGGAGAGAACAAGAAGAAAAGAGGCGTCTAGAGGAG 1459
Qy     1324 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1383
Db     1460 TTGGAGAGA--------------------------AGGCGCAAAGAAGAAGAGGAGAGG 1492
Qy     1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
Db     1493 AGACGGGCAGAAGAAGAAAAGAGGAGAGTTGAAAGAGAACAGGAGTATATCAGG---CGA 1549
Qy     1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1503
Db     1550 CAGCTAGAAGAGGAGCAGCGGCACTTGGAAGTCCTTCAGCAGCAGCTGCTCCAGGAGCAG 1609
Qy     1504 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1563
Db     1610 GCCATGTTACTGCATGACCATAGGAGGCCGCACCCGCAGCACTC---------------- 1653
Qy     1564 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1623
Db     1654 ----------------------------GCAGCAGCCGCCACCACCGCAGCAGGAAAGG 1684
Qy     1624 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1683
Db     1685 AGCAAGCCAAGCTTCCATGCTCCCGAGCCCAAAGCCCACTACGAGCCTGCTGACCGAGCG 1744
Qy     1684 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1743
Db     1745 CGAGAGGTTCCTGTGAGAACAACATCTCGCTCCCCTGTTCTGTC---------------- 1788
Qy     1744 AAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1803
Db     1789 ----CCGTCGAGATTCCCCACTGCAGGGCAGTGGGCAGCAGAATAGCCAGGCAGGACAGA 1844
Qy     1804 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1863
Db     1845 GAAAC-------------------------------------------TCCACCAG 1857
Qy     1864 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 1923
Db     1858 TATTGAGCCCAGGCTTCTGTGGG------------------------------------ 1880
Qy     1924 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 1983
Db     1881 ------------------------------------------------------------ 1880
Qy     1984 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2043
Db     1881 ------AGAGAGTGGAGAAGCTGGTGCCCAGACCTGGCAGT------------------- 1915
Qy     2044 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2103
Db     1916 -----------------------------------------------GGCAGCTCCTCAG 1928
Qy     2104 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2163
Db     1929 GGTCCAGCAACTCAGGATCCCAGCCCGGGTCTCACCCTGGGTCTCAGAGTGGCTCCGGGG 1988
Qy     2164 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2223
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Db       1989 AACGCTTCAGAGTGAGA----TCATCATCCAAGTCTGAAGGCTCTCCATCTCAGCGCCTG 2044

Qy       2224 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2283
Db       2045 GAAAATGCAGTGAAAAAACCTGAAGATAAAAAGGAAGTTTTCAGACCCCTCAAGCCTGCT 2104

Qy       2284 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2343
Db       2105 GATCTGACCGCACTGGCCAAAGAGCTTCGAGCAGTGGAAGATGTACGGCC---------- 2154

Qy       2344 GCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAG 2403
Db       2155 ----------------------ACCTCACAAAGTAACGGACTACTCCTCATCCAGTGAGG 2192

Qy       2404 GCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAA 2463
Db       2193 AGTCGGG----GACGACGGATGAGGAGGACGACGATGTGGAGCAGGAAGGGGCTGACGAG 2248

Qy       2464 GGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGAT 2523
Db       2249 TCCACCTCAGGACCAGAGGACACCAGAGCAGCGTCATCTCTGAATTTGAGCAATGGTGAA 2308

Qy       2524 ACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCC 2583
Db       2309 ACGGAATCTGTGAAAACCATGATTGTCCATGATGATGTAGAAAGTGAGCCGGCCATGACC 2368

Qy       2584 CCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTG 2643
Db       2369 CCATCCAAGGAGGGCACTCTAATCGTCCGCCAGACTCAGTCCGCTAGTAGCACACTCCAG 2428

Qy       2644 CATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCC 2703
Db       2429 AA-----------------ACACAAATCTTCCTCCTCCTTTACACCTTTTATAGACCCC- 2470

Qy       2704 ACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCT 2763
Db       2471 --------------------------------------------AGATTACTACAGATTT 2486

Qy       2764 CGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATC 2823
Db       2487 CTCCATCTAGCGGAACAACAGTGACATCTGTGGTGGGATTTTCCTGTGATGGGATGAGAC 2546

Qy       2824 TACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGC 2883
Db       2547 CAGAAGCCATAAG----------------------------------------------- 2559

Qy       2884 ACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCC 2943
Db       2560 -----------------GCAAGATCCTACCCGGAAAGGCTCAGTGGTCAATGTGAATCCT 2602

Qy       2944 ACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAAC 3003
Db       2603 ACCAACACTAGGCCACAGAGTGACACCCCGGAGATTCGTAAATACAAGAAGAGGTTTAAC 2662

Qy       3004 TCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGG 3063
Db       2663 TCTGAGATTCTGTGTGCTGCCTTATGGGGAGTGAATTTGCTAGTGGGTACAGAGAGTGGC 2722

Qy       3064 CTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGC 3123
Db       2723 CTGATGCTGCTGGACAGAAGTGGCCAAGGGAAGGTCTATCCTCTTATCAACCGAAGACGA 2782

Qy       3124 TTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGG 3183
Db       2783 TTTCAACAAATGGACGTACTTGAGGGCTTGAATGTCTTGGTGACAATATCTGGCAAAAAG 2842

Qy       3184 AACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCA 3243
Db       2843 GATAAGTTACGTGTCTACTATTTGTCCTGGTTAAGAAATAAAATACTTCACAATGATCCA 2902

Qy       3244 GAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTAC 3303
Db       2903 GAAGTTGAGAAGAAGCAGGGATGGACAACCGTAGGGGATTTGGAAGGATGTGTACATTAT 2962

Qy       3304 CGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAG 3363
Db       2963 AAAGTTGTAAAATATGAAAGAATCAAATTTCTGGTGATTGCTTTGAAGAGTTCTGTGGAA 3022

Qy       3364 GTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGAC 3423
Db       3023 GTCTATGCGTGGGCACCAAAGCCATATCACAAATTTATGGCCTTTAAGTCATTTGGAG-- 3080

Qy       3424 CTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTC 3483
Db       3081 -------------------------------------------------------AATTG 3085

Qy       3484 ATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGAC 3543
Db       3086 GTACATGGATCCTGTGCTGGATTCCATGCTGTTGATGTGGATTCAGGATCAGTCTATGAC 3145

Qy       3544 ATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCC 3603
Db       3146 ATTTATCTACCAACACATATCCAGTGTAGCATCAAACCCCATGCAATCATCATCCTCCCC 3205

Qy       3604 AACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACG 3663
Db       3206 AATACAGATGGAATGGAGCTTCTGGTGTGCTATGAAGATGAGGGGGTTTATGTAAACACA 3265

Qy       3664 TACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCC 3723
Db       3266 TATGGAAGGATCACCAAGGATGTAGTTCTACAGTGGGGAGAGATGCCTACATCAGTAGCA 3325

Qy       3724 TACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTG 3783
Db       3326 TATATTCGATCCAATCAGACAATGGGCTGGGGAGAGAAGGCCATAGAGATCCGATCTGTG 3385

Qy       3784 GAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTG 3843
Db       3386 GAAACTGGTCACTTGGATGGTGTGTTCATGCACAAAAGGGCTCAAAGACTAAAATTCTTG 3445

Qy       3844 TGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTT 3903
Db       3446 TGTGAACGCAATGACAAGGTGTTCTTTGCCTCTGTTCGGTCTGGTGGCAGCAGTCAGGTT 3505

Qy       3904 TACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAG 3948
Db       3506 TATTTCATGACCTTAGGCAGGACTTCTCTTCTGAGCTGGTAGAAG 3550
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RESULT 3
PCT-US04-03417-41
; Sequence 41, Application PC/TUS0403417
; GENERAL INFORMATION:
;  APPLICANT: Kelly, Louise M.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Farlow, Deborah
;  APPLICANT:  Healy, Aileen
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;  TITLE OF INVENTION:  HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
;  TITLE OF INVENTION:  21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
;  TITLE OF INVENTION:  9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
;  TITLE OF INVENTION:  9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
;  TITLE OF INVENTION:  53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
;  TITLE OF INVENTION:  5014
;  FILE REFERENCE: MPI03-015
;  CURRENT APPLICATION NUMBER: PCT/US04/03417
;  CURRENT FILING DATE:  2004-02-05
;  PRIOR APPLICATION NUMBER: US 60/445,241
;  PRIOR FILING DATE: 2003-02-05
;  PRIOR APPLICATION NUMBER: US 60/448,389
;  PRIOR FILING DATE: 2003-02-18
;  PRIOR APPLICATION NUMBER: US 60/456,320
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/460,279
;  PRIOR FILING DATE: 2003-04-03
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;  PRIOR APPLICATION NUMBER: US 60/465,924
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: US 60/470,052
;  PRIOR FILING DATE: 2003-05-13
;  PRIOR APPLICATION NUMBER: US 60/498,106
;  PRIOR FILING DATE: 2003-08-26
;  PRIOR APPLICATION NUMBER: US 60/500,179
;  PRIOR FILING DATE: 2003-09-04
;  PRIOR APPLICATION NUMBER: US 60/502,909
;  PRIOR FILING DATE: 2003-09-15
;  PRIOR APPLICATION NUMBER: US 60/510,351
;  PRIOR FILING DATE: 2003-10-10
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 1975
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (127)...(1407)
PCT-US04-03417-41

  Query Match             5.4%;  Score 214.2;  DB 1;  Length 1975;
  Best Local Similarity   55.5%;  Pred. No. 1.2e-37;
  Matches  576;  Conservative    0;  Mismatches  398;  Indels   63;  Gaps    6;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
Db        115 GGCGGCGCGGCCATGGCTCACCTCCGGGGATTTGCAAACCAGCACTCTCGAGTGGACCCT 174

Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
Db        175 GAGGAGCTCTTCACCAAGCTCGACCGCATTGGCAAGGGCTCGTTTGGGGAGGTCTACAAG 234

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
Db        235 GGCATCGATAACCACACAAAGGAGGTGGTGGCCATCAAGATCATCGACCTGGAGGAGGCC 294

Qy        190 GAGGAGGA---AGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
Db        295 GAGGATGAGATCGAGGACATCCAGCAGGAGATCACTGTCCTCAGTCAGTGCGACAGCCCC 354

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
Db        355 TACATCACCCGCTACTTTGGCTCCTACCTAAAGAGCA------------------CCAAG 396

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db        397 CTATGGATCATCATGGAGTACCTGGGCGGCGGCTCAGCACTGGACTTGCT---------T 447

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db        448 AAACCAGGTCCCCTGGAGGAGACATACATTGCCACGATCCTGCGGGAGATTCTGAAGGGC 507

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db        508 CTGGATTATCTGCACTCCGAACGCAAGATCCACCGAGACATCAAAGCTGCCAACGTGCTA 567

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db        568 CTCTCGGAGCAGGGTGACGTGAAGCTGGCGGACTTTGGGGTAGCAGGGCAGCTCACAGAC 627

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db        628 ACGCAGATTAAGAGGAACACATTCGTGGGCACCCCCTTCTGGATGGCACCTGAGGTCATC 687

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
Db        688 AAGC---------------AGTCGGCCTACGACTTCAAGGCTGACATCTGGTCCCTGGGC 732

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db        733 ATCACAGCCATCGAGCTGGCCAAGGGGGAGCCTCCAAACTCTGACCTCCACCCCATGCGC 792

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db        793 GTCCTGTTCCTGATTCCCAAGAACAGCCCACCCACACTGGAGGGCCAGCACAG---CAAG 849

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db        850 CCCTTCAAGGAGTTCGTGGAGGCCTGCCTCAACAAAGACCCCCGATTCCGGCCCACGGCC 909

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db        910 AAGGAGCTCCTGAAGCACAAGTTCATCACACGCTACACCAAGAAGACCTCCTTCCTCACG 969

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db        970 GAGCTCATCGA--------------CCGCTATAAGCGCTGGAAGTCAGAGGGGCATGGC 1014

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db       1015 GAGGAGTCCAGCTCTGAGGACTCTGACATTGATGGCGAGGCGGAGGACGGGGAGCAGGGC 1074

Qy       1027 TCCATCATGAACGTGCC 1043
Db       1075 CCCATCTGGACGTTCCC 1091

RESULT 4
US-10-772-636-41
; Sequence 41, Application US/10772636
; GENERAL INFORMATION:
;  APPLICANT: Kelly, Louise M.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Farlow, Deborah
;  APPLICANT:  Healy, Aileen
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;  TITLE OF INVENTION:  HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
;  TITLE OF INVENTION:  21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
;  TITLE OF INVENTION:  9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
;  TITLE OF INVENTION:  9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
;  TITLE OF INVENTION:  53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
;  TITLE OF INVENTION:  5014
;  FILE REFERENCE: MPI03-015P1RNOMNIM
;  CURRENT APPLICATION NUMBER: US/10/772,636
;  CURRENT FILING DATE:  2004-02-05
;  PRIOR APPLICATION NUMBER: US 60/445,241
;  PRIOR FILING DATE: 2003-02-05
;  PRIOR APPLICATION NUMBER: US 60/448,389
;  PRIOR FILING DATE: 2003-02-18
;  PRIOR APPLICATION NUMBER: US 60/456,320
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/460,279
;  PRIOR FILING DATE: 2003-04-03
;  PRIOR APPLICATION NUMBER: US 60/465,924
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: US 60/470,052
;  PRIOR FILING DATE: 2003-05-13
;  PRIOR APPLICATION NUMBER: US 60/498,106
;  PRIOR FILING DATE: 2003-08-26
;  PRIOR APPLICATION NUMBER: US 60/500,179
;  PRIOR FILING DATE: 2003-09-04
;  PRIOR APPLICATION NUMBER: US 60/502,909
;  PRIOR FILING DATE: 2003-09-15
;  PRIOR APPLICATION NUMBER: US 60/510,351
;  PRIOR FILING DATE: 2003-10-10
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 1975
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (127)...(1407)
US-10-772-636-41

  Query Match             5.4%;  Score 214.2;  DB 6;  Length 1975;
  Best Local Similarity   55.5%;  Pred. No. 1.2e-37;
  Matches  576;  Conservative    0;  Mismatches  398;  Indels   63;  Gaps    6;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
Db        115 GGCGGCGCGGCCATGGCTCACCTCCGGGGATTTGCAAACCAGCACTCTCGAGTGGACCCT 174

Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
Db        175 GAGGAGCTCTTCACCAAGCTCGACCGCATTGGCAAGGGCTCGTTTGGGGAGGTCTACAAG 234

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
Db        235 GGCATCGATAACCACACAAAGGAGGTGGTGGCCATCAAGATCATCGACCTGGAGGAGGCC 294

Qy        190 GAGGAGGA---AGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
Db        295 GAGGATGAGATCGAGGACATCCAGCAGGAGATCACTGTCCTCAGTCAGTGCGACAGCCCC 354

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
Db        355 TACATCACCCGCTACTTTGGCTCCTACCTAAAGAGCA------------------CCAAG 396

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db        397 CTATGGATCATCATGGAGTACCTGGGCGGCGGCTCAGCACTGGACTTGCT---------T 447

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db        448 AAACCAGGTCCCCTGGAGGAGACATACATTGCCACGATCCTGCGGGAGATTCTGAAGGGC 507

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db        508 CTGGATTATCTGCACTCCGAACGCAAGATCCACCGAGACATCAAAGCTGCCAACGTGCTA 567

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db        568 CTCTCGGAGCAGGGTGACGTGAAGCTGGCGGACTTTGGGGTAGCAGGGCAGCTCACAGAC 627

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db        628 ACGCAGATTAAGAGGAACACATTCGTGGGCACCCCCTTCTGGATGGCACCTGAGGTCATC 687

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
Db        688 AAGC---------------AGTCGGCCTACGACTTCAAGGCTGACATCTGGTCCCTGGGC 732

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db        733 ATCACAGCCATCGAGCTGGCCAAGGGGGAGCCTCCAAACTCTGACCTCCACCCCATGCGC 792

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db        793 GTCCTGTTCCTGATTCCCAAGAACAGCCCACCCACACTGGAGGGCCAGCACAG---CAAG 849

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db        850 CCCTTCAAGGAGTTCGTGGAGGCCTGCCTCAACAAAGACCCCCGATTCCGGCCCACGGCC 909

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db        910 AAGGAGCTCCTGAAGCACAAGTTCATCACACGCTACACCAAGAAGACCTCCTTCCTCACG 969

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db        970 GAGCTCATCGA---------------CCGCTATAAGCGCTGGAAGTCAGAGGGGCATGGC 1014

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db       1015 GAGGAGTCCAGCTCTGAGGACTCTGACATTGATGGCGAGGCGGAGGACGGGGAGCAGGGC 1074

Qy       1027 TCCATCATGAACGTGCC 1043
Db       1075 CCCATCTGGACGTTCCC 1091

RESULT 5
US-09-744-794C-33
; Sequence 33, Application US/09744794C
; GENERAL INFORMATION:
;  APPLICANT: INCYTE CORPORATION; HILLMAN, Jennifer L.;
;  APPLICANT:  LAL, Preeti G.; TANG, Y. Tom;
;  APPLICANT:  CORLEY, Neil C.; GUEGLER, Karl J.;
;  APPLICANT:  BAUGHN, Mariah R.; PATTERSON, Chandra S.;
;  APPLICANT:  BANDMAN, Olga; AU-YOUNG, Janice K.;
;  APPLICANT:  GORGONE, Gina A.; YUE, Henry;
;  APPLICANT:  AZIMZAI, Yalda; REDDY, Roopa M.;
;  APPLICANT:  LU, Dyung Aina M.; SHIH, Leo L.
;  TITLE OF INVENTION: HUMAN CELL SURFACE RECEPTORS
;  FILE REFERENCE: PF-0565 USN
;  CURRENT APPLICATION NUMBER: US/09/744,794C
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PERL Program
; SEQ ID NO 33
;   LENGTH: 2778
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 2197671CB1
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1) ... (2778)
;   OTHER INFORMATION: a, t, c, g, or other
US-09-744-794C-33

  Query Match             3.6%;  Score 141;  DB 5;  Length 2778;
  Best Local Similarity   51.8%;  Pred. No. 9e-22;
  Matches  476;  Conservative    0;  Mismatches  395;  Indels   48;  Gaps    5;

Qy         64 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 123
Db        110 GACCCAGAAGAGCTTTTTACAAAACTAGAGAAAATTGGGAAGGGCTCCTTTGGAGAGGTG 169

Qy        124 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 183
Db        170 TTCAAAGGCATTGACAATCGGACTCAGAAAGTGGTTGCCATAAAGATCATTGATCTGGAA 229

Qy        184 GAGGACGAGGAGGA---AGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC 240
Db        230 GAAGCTGAAGATGAGATAGAGGACATTCAACAAGAAATCACAGTGCTGAGTCAGTGTGAC 289

Qy        241 CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGAT 300
Db        290 AGTCCATATGTAACCAAATATTATGGATCCTATCTGAAG------------------GAT 331

Qy        301 GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG 360
Db        332 ACAAAATTATGGATAATAATGGAATATCTTGGTGGAGGCTCCGCACTAGATCTATT---- 387

Qy        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420
Db        388 -----AGAACCTGGCCGATTAGATGAAACCCAGATCGCTACTATATTAAGAGAAATACTG 442

Qy        421 AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT 480
Db        443 AAAGGACTCGATTATCTCCATTCGGAGAAGAAAATCCACAGAGACATTAAAGCGGCCAAC 502

Qy        481 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG 540
```

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              || |||||| | ||| |||  ||||| ||||| | ||| ||||| |||  ||  ||||||
Db        503 GTCCTGCTGTCTGAGCATGGCGAGGTGAAGCTGGCGGACTTTGGCGTGGCTGGCCAGCTG 562

Qy        541 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG 600
                    ||||  |  || | ||||||| ||| | || || || | ||||||||| || |||
Db        563 ACAGACACCCAGATCAAAAGGAACACCTTCGTGGGCACCCCATTCTGGATGGCACCCGAG 622

Qy        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660
              ||||||                        | | ||||||| |  |   || || |||||
Db        623 GTCATCAAAC---------------AGTCGGCCTATGACTCGAAGGCAGACATCTGGTCC 667

Qy        661 CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 720
              || || || ||||| || ||    ||||     || |   || ||||  |  ||  ||||||||
Db        668 CTGGGCATAACAGCTATTGAACTTGCAAGAGGGGAACCACCTCATTCCGAGCTGCACCCC 727

Qy        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780
              |||  ||    |  ||||||||||| ||||   || || |  |  |    || |  |
Db        728 ATGAAAGTTTTATTCCTCATTCCAAAGAACAACCCACCGACGTTGGAAGGAAACTACAG- 786

Qy        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840
                 |||    ||| || ||  | ||  | ||| |  |  |||               | ||
Db        787 --TAAACCCCTCAAGGAGTTTGTGGAGGCCTGTTTGAATAAGGAGCCGAGCTTTAGACCC 844

Qy        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC 900
                |  |  || || |||||     || ||  |    |  | | | |           |
Db        845 ACTGCTAAGGAGTTATTGAAGCACAAGTTTATACTACGCAATGCAAAGAAAACTTCCTAC 904

Qy        901 CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG 960
                 | | |||| |  |||            | |||         |||  | |  |   ||  |
Db        905 TTGACCGAGCTCATCGACAGGTACAAGAGATGGAAGGCCGAGCAGAGCCATGACGACTCG 964

Qy        961 ACAGAATATGAGTACAGCG 979
              |      | || | |  ||
Db        965 AGCTCCGAGGATTCCGACG 983
```

RESULT 6
PCT-US03-31219-7
; Sequence 7, Application PC/TUS0331219
; GENERAL INFORMATION:
; APPLICANT: Schering Aktiengesellschaft
; APPLICANT: Parry, Gordon
; APPLICANT: Vogel, David
; APPLICANT: Whitlow, Marc
; APPLICANT: Wu, Qingyu
; TITLE OF INVENTION: Modified Hepsin Molecules Having a Subtitute Activation Sequence
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 53038AWOM1
; CURRENT APPLICATION NUMBER: PCT/US03/31219
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/416,038
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 11924
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: plasmid 3
PCT-US03-31219-7

```
  Query Match              3.4%;  Score 134.8;  DB 1;  Length 11924;
  Best Local Similarity   52.1%;  Pred. No. 3.1e-20;
  Matches  301;  Conservative    0;  Mismatches  277;  Indels    0;  Gaps    0;

Qy        935 GGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAG 994
              || || ||| ||  |||      |||||    |  | | | |      ||    ||| |||| |
Db       6773 GGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGG 6832

Qy        995 ATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGA 1054
              | |     |     ||||| || ||    |           | | | ||  |  ||| |   |
Db       6833 AGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGC 6892

Qy       1055 CTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAA 1114
                   |     ||||    |     |    ||| || |    |  || |   |      | |
Db       6893 AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGG 6952

Qy       1115 AACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACC 1174
                ||| ||||| ||   |   |||| ||||| ||     |    |   ||||  ||       | |
Db       6953 GGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGG 7012

Qy       1175 TGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGG 1234
                |  |||   || |||||  | |     ||| || || ||| | ||  ||      | | |||
Db       7013 AGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG 7072

Qy       1235 AGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGC 1294
              ||    |||   | || ||  |   || || ||  ||||||| ||| |||| ||| |||  |
Db       7073 AGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGG 7132

Qy       1295 TGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGG 1354
                || | |    |||||     || |  | ||||||  || |  ||||| || ||  |||||||
Db       7133 AGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGG 7192

Qy       1355 AATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGC 1414
                |     ||  |   ||||  | |||||  || | | ||      |      |  || ||||| |
Db       7193 AGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGG 7252

Qy       1415 AGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGA 1474
                ||||||||| |    |     ||      |||| ||||| |   ||   |||| ||   |||
Db       7253 GGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGG 7312

Qy       1475 AACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAG 1512
                | ||| ||   |||| ||      | |        |||   || ||
Db       7313 AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAG 7350
```

RESULT 7
PCT-US03-31219-6
; Sequence 6, Application PC/TUS0331219
; GENERAL INFORMATION:
; APPLICANT: Schering Aktiengesellschaft
; APPLICANT: Parry, Gordon
; APPLICANT: Vogel, David
; APPLICANT: Whitlow, Marc
; APPLICANT: Wu, Qingyu
; TITLE OF INVENTION: Modified Hepsin Molecules Having a Subtitute Activation Sequence
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 53038AWOM1
; CURRENT APPLICATION NUMBER: PCT/US03/31219
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/416,038
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 12242
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: plasmid 2
PCT-US03-31219-6

```
  Query Match              3.4%;  Score 134.8;  DB 1;  Length 12242;
  Best Local Similarity   52.1%;  Pred. No. 3.2e-20;
  Matches  301;  Conservative    0;  Mismatches  277;  Indels    0;  Gaps    0;

Qy        935 GGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAG 994
              || || ||| ||  |||      |||||    |  | | | |      ||    ||| |||| |
Db       7091 GGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGG 7150

Qy        995 ATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGA 1054
              | |     |     ||||| || ||    |           | | | ||  |  ||| |   |
Db       7151 AGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGC 7210

Qy       1055 CTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAA 1114
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Db       7211 AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGG 7270

Qy       1115 AACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACC 1174

Db       7271 GGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGG 7330

Qy       1175 TGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGG 1234

Db       7331 AGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG 7390

Qy       1235 AGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGC 1294

Db       7391 AGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGG 7450

Qy       1295 TGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGG 1354

Db       7451 AGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGG 7510

Qy       1355 AATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGC 1414

Db       7511 AGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGG 7570

Qy       1415 AGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGA 1474

Db       7571 GGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGG 7630

Qy       1475 AACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAG 1512

Db       7631 AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAG 7668
```

RESULT 8
US-10-767-701-920
; Sequence 920, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 920
;   LENGTH: 445
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1326_1
US-10-767-701-920

```
  Query Match             2.9%;  Score 115;  DB 6;  Length 445;
  Best Local Similarity   60.0%;  Pred. No. 2.1e-16;
  Matches  237;  Conservative    0;  Mismatches  140;  Indels   18;  Gaps    2;

Qy        298 GATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTA 357

Db         64 GAGGACTACCTATGGATAGTTATGGAGTACTGTGGTGGTGGAAGTGTTGCTGATTTGATA 123

Qy        358 AAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATC 417

Db        124 GGCATCACAGAGG---AGCCTCTTGATGAATCCCAAATAGCTTATATATGTAGAGAAGCA 180

Qy        418 CTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAG 477

Db        181 CTAAAGGGCCTTGCTTACCTGCACTCCATTTTTAAAGTTCATAGAGATATTAAGGGTGGC 240

Qy        478 AATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAG 537

Db        241 AACATTCTTCTAACTGAGCAAGGCGAGGTGAAGTTGGGTGATTTTGGTGTAGCTGCCCAG 300

Qy        538 CTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCA 597

Db        301 CTGACAAGAACCATGTCAAAGCGCAACACGTTCATTGGTACTCCACATTGGATGGCACCA 360

Qy        598 GAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGG 657

Db        361 GAGGTCAT---------------TCAAGAAAGTCGTTATGATGGAAAGGTAGATGTTTGG 405

Qy        658 TCTCTAGGAATCACAGCCATCGAGATGGCAGAGGG 692

Db        406 GCATTACGTGTATCTGCAATTGAGATGGCAGAGGG 440
```

RESULT 9
US-10-770-726-27
; Sequence 27, Application US/10770726
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
;   LENGTH: 2838
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-770-726-27

```
  Query Match             2.8%;  Score 112.4;  DB 6;  Length 2838;
  Best Local Similarity   51.8%;  Pred. No. 1.4e-15;
  Matches  322;  Conservative    0;  Mismatches  276;  Indels   24;  Gaps    2;

Qy        301 GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG 360

Db       1375 GACGAGCTCTGGGTGGTCATGGAGTTCCTGGAAGGAGGCGCCCTCACCGACATCGTCACC 1434

Qy        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420

Db       1435 CACAC---------CAGGATGAACGAGGAGCAGATCGCGGCCGTGTGCCTTGCAGTGCTG 1485

Qy        421 AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT 480

Db       1486 CAGGCCCTGTCGGTGCTCCACGCCCAGGGCGTCATCCACCGGGACATCAAGAGCGACTCG 1545

Qy        481 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG 540

Db       1546 ATCCTGCTGACCCATGATGGCAGGGTGAAGCTGTCAGACTTTGGGTTCTGCGCCCAGGTG 1605

Qy        541 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG 600

Db       1606 AGCAAGGAAGTGCCCCGAAGGAAGTCGCTGGTCGGCACGCCCTACTGGATGGCCCCAGAG 1665

Qy        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660

Db       1666 CTCATCTCCCGCCTT--------------CCCTACGGGCCAGAGGTAGACATCTGGTCG 1710

Qy        661 CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 720

Db       1711 CTGGGGATAATGGTGATTGAGATGGTGGACGGAGAGCCCCCCTACTTCAACGAGCCACCC 1770

Qy        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780

Db       1771 CTCAAAGCCATGAAGATGATTCGGGACAACCTGCCACCCCGACTGAAGAACCTGCACAAG 1830

Qy        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840

Db       1831 GTGTCGCCATCCCTGAAGGGCTTCCTGGACCGCCTGCTGGTGCGAGACCCTGCCCAGCGG 1890
```

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Qy        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC 900

Db       1891 GCCACGGCAGCCGAGCTGCTGAAGCACCCATTCCTGGCCAAGGCAGGGCCGCCTGCCAGC 1950

Qy        901 CGCATCCAGCTTAAGGACCACA 922

Db       1951 ATCGTGCCCCTCATGCGCCAGA 1972
```

RESULT 10
US-10-767-701-28242
; Sequence 28242, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 28242
;   LENGTH: 484
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 7536127
US-10-767-701-28242

```
  Query Match             2.3%;  Score 92.2;  DB 6;  Length 484;
  Best Local Similarity   53.0%;  Pred. No. 1.8e-11;
  Matches  258;  Conservative    0;  Mismatches  208;  Indels   21;  Gaps    2;

Qy         54 CGCCCTGCGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTA 113

Db         14 CTCCACGGAAGACCCCGAGGCCGTGTTCGAGTTGCAGGAGAAGCTCGGGAAGGGGTCATA 73

Qy        114 CGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCAT 173

Db         74 CGGCATGGTTTACAAAGGGCGCAACCGCACCACTAATGAGACTCTGGCCGTCAAAATACT 133

Qy        174 GGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTA 233

Db        134 TGCCCTCGACGACGAGGCTACGCTAAAGGCTGTGCGGGGTGAGATCAAGATATTAGCGAC 193

Qy        234 CTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGG 293

Db        194 GTGCAACCATGCCAACATCGTGCGCTACGGGGGCAGCTACTTCAAG-------------- 239

Qy        294 AAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCT 353

Db        240 ----GACGAGAAGCTTTGGATCTGCATGGAGTACTGTGGAGGAGGATCGGTGAGTGATCT 295

Qy        354 GGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGA 413

Db        296 GTGCGTGATTCTG---GACTCAGGCCTCCAGGAAGACCAAATAGCTATCATTTGTCGCGA 352

Qy        414 GATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGG 473

Db        353 GGCTCTCAAGGGCCTCAACTACCTCCACAACGGCACCAAAATCCACAGAGACATCAAGGG 412

Qy        474 GCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGC 533

Db        413 CGGCAATATCCTCCTCACCGAAAGCGGCGATGTGAAGTTGGCCGATTTCGGGGTGTCGGC 472

Qy        534 TCAGCTG 540

Db        473 AACGCTG 479
```

RESULT 11
US-10-767-471-603
; Sequence 603, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 603
;   LENGTH: 11409
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-767-471-603

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  Query Match             2.2%;  Score 86;  DB 6;  Length 11409;
  Best Local Similarity   51.7%;  Pred. No. 1.1e-09;
  Matches  246;  Conservative    1;  Mismatches  220;  Indels    9;  Gaps    2;

Qy       1039 GTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAAAATAAGAGC 1098

Db       4106 GAGCGTGAGAAGGAGAAGCTCCAACAGGAGGCCAAACTGCTGCAGCTCAAGTCTGAGGAG 4165

Qy       1099 AACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGAGACCCCGAG 1158

Db       4166 ATGCAGACGGTGCAGCAGGAGCAGCTGCTGCAGGAGACGCAGGCCCTGCAGCAAAGCTTC 4225

Qy       1159 GCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAG 1218

Db       4226 CTCTCTGAAAAGGACAGCCTGCTACAGCGGGAGCGCTTCATCGAGCAGGAGAAGGCCAAG 4285

Qy       1219 CG---GCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAG 1275

Db       4286 CTGGAGCAGCTCTTCCAGGACGAGGTGGCCAAGGCMCAGCAGCTGCGTGAGGAGCAGCAG 4345

Qy       1276 AAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTG------CGGCGGGAGGAGGAG 1329

Db       4346 CGGCAGCAGCAGCAGATGGAGCAGGAACGGCAGCGGCTGGTGGCCAGCATGGAGGAGGCG 4405

Qy       1330 CGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAG 1389

Db       4406 CGGCGGCGGCAGCATGAGGCCGAGGAGGGCGTGCGGCGCAAGCAGGAGGAGCTGCAGCAG 4465

Qy       1390 TCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAG 1449

Db       4466 YTGGAGCAGCAGCGGCGGCAGCAGGAGGAGCTGCTGGCTGAGGAGAACCAGAGGCTGCGT 4525

Qy       1450 CAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGA 1505

Db       4526 GAGCAGCTGCAGCTCCTGGAGGAGCAGCACCGGGCCGCGCTGGCGCACTCAGAGGA 4581
```

RESULT 12
US-10-767-471-195
; Sequence 195, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 195
;   LENGTH: 14800
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-767-471-195

```
  Query Match             2.2%;  Score 86;  DB 6;  Length 14800;
  Best Local Similarity   51.7%;  Pred. No. 1.2e-09;
```

```
  Matches  246;  Conservative    1;  Mismatches  220;  Indels    9;  Gaps    2;

Qy       1039 GTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAAAATAAGAGC 1098
              | || ||    ||  ||  ||  || |  | ||||        | ||| ||||      |  | ||
Db       7498 GAGCGTGAGAAGGAGAAGCTCCAACAGGAGGCCAAACTGCTGCAGCTCAAGTCTGAGGAG 7557

Qy       1099 AACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGAGACCCCGAG 1158
                |        ||     |  |||||| || ||  | ||  ||||   | ||   |    |
Db       7558 ATGCAGACGGTGCAGCAGGAGCAGCTGCTGCAGGAGACGCAGGCCCTGCAGCAAAGCTTC 7617

Qy       1159 GCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAG 1218
                          ||  ||   ||||  |||||| ||||     ||| ||| || ||||||   ||
Db       7618 CTCTCTGAAAAGGACAGCCTGCTACAGCGGGAGCGCTTCATCGAGCAGGAGAAGGCCAAG 7677

Qy       1219 CG---GCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAG 1275
              |     ||  | |  |   ||||  |    |        ||  |  | ||| |||   ||  |||| ||
Db       7678 CTGGAGCAGCTCTTCCAGGACGAGGTGGCCAAGGCMCAGCAGCTGCGTGAGGAGCAGCAG 7737

Qy       1276 AAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTG------CGGCGGGAGGAGGAG 1329
                 | |||||||||  |   | |  ||||   ||||   |||          |  |||||||| |
Db       7738 CGGCAGCAGCAGCAGATGGAGCAGGAACGGCAGCGGCTGGTGGCCAGCATGGAGGAGGCG 7797

Qy       1330 CGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAG 1389
              ||||||| |  | |     |    ||||    |   ||||     |||  |||||||| || ||||
Db       7798 CGGCGGCGGCAGCATGAGGCCGAGGAGGGCGTGCGGCGCAAGCAGGAGGAGCTGCAGCAG 7857

Qy       1390 TCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAG 1449
              :  || |  |  | | |||||| ||| ||  ||  ||  |     ||        || ||
Db       7858 YTGGAGCAGCAGCGGCGGCAGCAGGAGGAGCTGCTGGCTGAGGAGAACCAGAGGCTGCGT 7917

Qy       1450 CAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGA 1505
                 |||| | |||||  | |     || | || | |      || |    |    | | |||
Db       7918 GAGCAGCTGCAGCTCCTGGAGGAGCAGCACCGGGCCGCGCTGGCGCACTCAGAGGA 7973
```

RESULT 13
US-10-767-471-191
; Sequence 191, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 14321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-191

```
  Query Match             2.1%;  Score 83.4;  DB 6;  Length 14321;
  Best Local Similarity   51.0%;  Pred. No. 4.2e-09;
  Matches  196;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy       1115 AACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACC 1174
               | | || |||| ||  ||||   | ||||||   |    ||  |    | | |    ||  |   |
Db       7382 AGCTGCTGCAGGAGACGCAGGCCCTGCAGCAAAGCTTCCTCTCTGAAAAGGACAGCCTGC 7441

Qy       1175 TGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGG 1234
              | |  ||   ||||                 ||| ||   |||  ||||| || |   |  ||| |
Db       7442 TACAGCGGGAGCGCTTCATCGAGCAGGAGAAGGCCAAGCTGGAGCAGCTCTTCCAGGACG 7501

Qy       1235 AGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGC 1294
              ||         |     ||| |   ||     | ||| ||||   | || ||||||||   |   ||
Db       7502 AGGTGGCCAAGGCMCAGCAGCTGCGTGAGGAGCAGCAGCGGCAGCAGCAGCAGATGGAGC 7561

Qy       1295 TGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGG 1354
               |||        ||  |     ||        |  ||||||   |||||  |  ||| ||||    |
Db       7562 AGGAACGGCAGCGGCTGGTGGCCAGCATGGAGGAGGCGCGGCGGCGGCAGCATGAGGCCG 7621

Qy       1355 AATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGC 1414
              |  |         |  ||     | ||||| ||| ||||               |  ||| ||| || ||
Db       7622 AGGAGGGCGTGCGGCGCAAGCAGGAGGAGCTGCAGCAGYTGGAGCAGCAGCGGCGGCAGC 7681

Qy       1415 AGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGA 1474
              || ||||||               ||   || |   || ||    | |||| |||||   ||  ||
Db       7682 AGGAGGAGCTGCTGGCTGAGGAGAACCAGAGGCTGCGTGAGCAGCTGCAGCTCCTGGAGG 7741

Qy       1475 AACAGCAGCAGCAGCAGCTCCTGC 1498
              | ||||| | |       |||    ||
Db       7742 AGCAGCACCGGGCCGCGCTGGCGC 7765
```

RESULT 14
US-10-767-471-193
; Sequence 193, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 14641
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-193

```
  Query Match             2.1%;  Score 83.4;  DB 6;  Length 14641;
  Best Local Similarity   51.0%;  Pred. No. 4.3e-09;
  Matches  196;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy       1115 AACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACC 1174
               | | || |||| ||  ||||   | ||||||   |    ||  |    | | |    ||  |   |
Db       7702 AGCTGCTGCAGGAGACGCAGGCCCTGCAGCAAAGCTTCCTCTCTGAAAAGGACAGCCTGC 7761

Qy       1175 TGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGG 1234
              | |  ||   ||||                 ||| ||   |||  ||||| || |   |  ||| |
Db       7762 TACAGCGGGAGCGCTTCATCGAGCAGGAGAAGGCCAAGCTGGAGCAGCTCTTCCAGGACG 7821

Qy       1235 AGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGC 1294
              ||         |     ||| |   ||     | ||| ||||   | || ||||||||   |   ||
Db       7822 AGGTGGCCAAGGCMCAGCAGCTGCGTGAGGAGCAGCAGCGGCAGCAGCAGCAGATGGAGC 7881

Qy       1295 TGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGG 1354
               |||        ||  |     ||        |  ||||||   |||||  |  ||| ||||    |
Db       7882 AGGAACGGCAGCGGCTGGTGGCCAGCATGGAGGAGGCGCGGCGGCGGCAGCATGAGGCCG 7941

Qy       1355 AATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGC 1414
              |  |         |  ||     | ||||| ||| ||||               |  ||| ||| || ||
Db       7942 AGGAGGGCGTGCGGCGCAAGCAGGAGGAGCTGCAGCAGYTGGAGCAGCAGCGGCGGCAGC 8001

Qy       1415 AGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGA 1474
              || ||||||               ||   || |   || ||    | |||| |||||   ||  ||
Db       8002 AGGAGGAGCTGCTGGCTGAGGAGAACCAGAGGCTGCGTGAGCAGCTGCAGCTCCTGGAGG 8061

Qy       1475 AACAGCAGCAGCAGCAGCTCCTGC 1498
              | ||||| | |       |||    ||
Db       8062 AGCAGCACCGGGCCGCGCTGGCGC 8085
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RESULT 15
US-10-767-471-192
; Sequence 192, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471

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;  CURRENT FILING DATE:  2004-01-30
;  NUMBER OF SEQ ID NOS: 50231
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 192
;   LENGTH: 14760
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-767-471-192

  Query Match             2.1%;  Score 83.4;  DB 6;  Length 14760;
  Best Local Similarity   51.0%;  Pred. No. 4.3e-09;
  Matches  196;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy       1115 AACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACC 1174

Db       7540 AGCTGCTGCAGGAGACGCAGGCCCTGCAGCAAAGCTTCCTCTCTGAAAAGGACAGCCTGC 7599

Qy       1175 TGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGG 1234

Db       7600 TACAGCGGGAGCGCTTCATCGAGCAGGAGAAGGCCAAGCTGGAGCAGCTCTTCCAGGACG 7659

Qy       1235 AGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGC 1294

Db       7660 AGGTGGCCAAGGCMCAGCAGCTGCGTGAGGAGCAGCAGCGGCAGCAGCAGCAGATGGAGC 7719

Qy       1295 TGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGG 1354

Db       7720 AGGAACGGCAGCGGCTGGTGGCCAGCATGGAGGAGGCGCGGCGGCGGCAGCATGAGGCCG 7779

Qy       1355 AATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGC 1414

Db       7780 AGGAGGGCGTGCGGCGCAAGCAGGAGGAGCTGCAGCAGYTGGAGCAGCAGCGGCGGCAGC 7839

Qy       1415 AGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGA 1474

Db       7840 AGGAGGAGCTGCTGGCTGAGGAGAACCAGAGGCTGCGTGAGCAGCTGCAGCTCCTGGAGG 7899

Qy       1475 AACAGCAGCAGCAGCAGCTCCTGC 1498

Db       7900 AGCAGCACCGGGCCGCGCTGGCGC 7923

Search completed: March  2, 2004, 17:17:01
Job time : 92 secs
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OM nucleic - nucleic search, using sw model

Run on:         March  2, 2004, 17:17:09 ; Search time 8003 Seconds
                                           (without alignments)
                                           17371.030 Million cell updates/sec

Title:          US-10-029-115-1
Perfect score:  3951
Sequence:       1 gcccttatgggcgacccagc..........tcatgaactggtgaaagggc 3951

Scoring table:  OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched:       37577330 seqs, 17593059518 residues

Word size :      0

Total number of hits satisfying chosen parameters:      75154660

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3951	100.0	3951	43	US-10-029-115-1	Sequence 1, Appli
	2	3288	83.2	3951	1	PCT-US02-33845-2	Sequence 2, Appli
	3	2201	55.7	5014	1	PCT-US03-37730-22	Sequence 22, Appl
	4	2099	53.1	4989	1	PCT-US03-37730-26	Sequence 26, Appl
	5	2048	51.8	5191	89	US-60-324-185-5555	Sequence 5555, Ap
	6	1907	48.3	4033	43	US-10-029-115-5	Sequence 5, Appli
	7	1787	45.2	4133	54	US-10-725-121-11	Sequence 11, Appl
	8	1787	45.2	4133	54	US-10-725-329-11	Sequence 11, Appl
	9	1787	45.2	4133	54	US-10-725-330-11	Sequence 11, Appl
	10	1787	45.2	4133	64	US-60-081-784-11	Sequence 11, Appl
	11	1714	43.4	4032	1	PCT-US02-33845-6	Sequence 6, Appli
	12	1701	43.1	3888	1	PCT-US02-01048-37	Sequence 37, Appl
	13	1701	43.1	3888	1	PCT-US03-37730-21	Sequence 21, Appl
	14	1701	43.1	3888	52	US-10-466-162-37	Sequence 37, Appl
	15	1701	43.1	4436	46	US-10-170-235-34328	Sequence 34328, A
	16	1701	43.1	4553	25	US-09-607-200-6297	Sequence 6297, Ap
	17	1701	43.1	4557	32	US-09-770-174-3346	Sequence 3346, Ap
	18	1701	43.1	4557	32	US-09-770-175-7824	Sequence 7824, Ap
	19	1701	43.1	4878	1	PCT-US03-37730-25	Sequence 25, Appl
	20	1701	43.1	5040	1	PCT-US03-26635-80	Sequence 80, Appl
	21	1689	42.7	4863	1	PCT-US01-04098A-831	Sequence 831, App
	22	1689	42.7	4863	1	PCT-US02-01048-35	Sequence 35, Appl
	23	1689	42.7	4863	1	PCT-IL02-00904-30	Sequence 30, Appl
	24	1689	42.7	4863	27	US-09-654-936A-65	Sequence 65, Appl
	25	1689	42.7	4863	42	US-09-993-398-30	Sequence 30, Appl
	26	1689	42.7	4863	47	US-10-201-605-30	Sequence 30, Appl
	27	1689	42.7	4863	48	US-10-258-899A-831	Sequence 831, App
	28	1689	42.7	4863	48	US-10-293-244-831	Sequence 831, App
	29	1689	42.7	4863	51	US-10-441-281-30	Sequence 30, Appl
	30	1689	42.7	4863	52	US-10-466-162-35	Sequence 35, Appl
	31	1689	42.7	4902	1	PCT-US03-37730-27	Sequence 27, Appl
	32	1689	42.7	5051	1	PCT-US03-26635-81	Sequence 81, Appl
	33	1683	42.6	4414	43	US-10-029-115-3	Sequence 3, Appli
	34	1650	41.8	4631	107	US-60-500-337-1177	Sequence 1177, Ap
	35	1650	41.8	4881	107	US-60-500-337-1176	Sequence 1176, Ap
	36	1650	41.8	4982	107	US-60-500-337-1175	Sequence 1175, Ap
	37	1599	40.5	3735	32	US-09-789-390-12	Sequence 12, Appl
	38	1599	40.5	3822	32	US-09-789-390-10	Sequence 10, Appl
	39	1599	40.5	3912	32	US-09-789-390-8	Sequence 8, Appli
	40	1599	40.5	3999	32	US-09-789-390-6	Sequence 6, Appli
	41	1599	40.5	5073	1	PCT-US03-13124-44	Sequence 44, Appl
	42	1587	40.2	4905	107	US-60-500-337-1178	Sequence 1178, Ap
c	43	1537	38.9	4560	24	US-09-577-410-7885	Sequence 7885, Ap
	44	1436	36.3	2906	84	US-60-278-258-2193	Sequence 2193, Ap
	45	1436	36.3	3345	77	US-60-213-359-474	Sequence 474, App
	46	1340	33.9	7132	1	PCT-US01-08631-24011	Sequence 24011, A
	47	1337	33.8	1482	32	US-09-789-390-64	Sequence 64, Appl
	48	1337	33.8	1649	32	US-09-789-390-62	Sequence 62, Appl
	49	1337	33.8	1717	32	US-09-789-390-69	Sequence 69, Appl
	50	1337	33.8	1787	32	US-09-789-390-66	Sequence 66, Appl
	51	1271	32.2	2223	19	US-09-396-885-4571	Sequence 4571, Ap
	52	1271	32.2	2223	19	US-09-396-885A-4571	Sequence 4571, Ap
	53	1271	32.2	2223	19	US-09-396-970-7115	Sequence 7115, Ap
	54	1271	32.2	2223	20	US-09-404-549-4761	Sequence 4761, Ap
	55	1271	32.2	2223	20	US-09-404-549A-4761	Sequence 4761, Ap
	56	1271	32.2	2223	20	US-09-428-151A-9631	Sequence 9631, Ap
	57	1255	31.8	2403	32	US-09-760-475-998	Sequence 998, App
	58	1255	31.8	2403	47	US-10-227-425-998	Sequence 998, App
	59	1186	30.0	1470	74	US-60-185-213-1180	Sequence 1180, Ap
	60	1165	29.5	2480	84	US-60-278-258-2200	Sequence 2200, Ap
	61	1151	29.1	2224	20	US-09-474-436-7841	Sequence 7841, Ap
c	62	1108	28.0	3416	77	US-60-213-359-472	Sequence 472, App
	63	1030	26.1	2345	1	PCT-US00-05989-137	Sequence 137, App
	64	1030	26.1	2345	38	US-09-925-297-137	Sequence 137, App
	65	1026	26.0	1890	30	US-09-705-256A-3721	Sequence 3721, Ap
	66	1026	26.0	1890	72	US-60-164-285-3721	Sequence 3721, Ap
	67	1012	25.6	2330	17	US-09-277-214A-333	Sequence 333, App
	68	1012	25.6	2330	36	US-09-891-825-333	Sequence 333, App
	69	1001	25.3	1345	20	US-09-496-914A-9540	Sequence 9540, Ap
	70	1001	25.3	1345	24	US-09-560-875A-9540	Sequence 9540, Ap
	71	1001	25.3	1345	93	US-60-365-384-403	Sequence 403, App
	72	869	22.0	1131	1	PCT-US01-03800A-570	Sequence 570, App
	73	869	22.0	1131	1	PCT-US01-04098A-2799	Sequence 2799, Ap
	74	869	22.0	1131	20	US-09-496-914A-4308	Sequence 4308, Ap
	75	869	22.0	1131	24	US-09-560-875A-4308	Sequence 4308, Ap
	76	869	22.0	1131	48	US-10-258-899A-2799	Sequence 2799, Ap
	77	869	22.0	1131	48	US-10-276-774-570	Sequence 570, App
	78	869	22.0	1131	48	US-10-293-244-2799	Sequence 2799, Ap
	79	853	21.6	5348	73	US-60-172-373-2793	Sequence 2793, Ap
	80	760	19.2	1170	74	US-60-185-213-1168	Sequence 1168, Ap
	81	697	17.6	817	19	US-09-397-424-5209	Sequence 5209, Ap
	82	697	17.6	817	19	US-09-397-424A-5209	Sequence 5209, Ap
	83	666	16.9	4411	1	PCT-US02-33845-4	Sequence 4, Appli
	84	636	16.1	1336	27	US-09-644-867-6647	Sequence 6647, Ap
	85	636	16.1	1336	27	US-09-652-126-9857	Sequence 9857, Ap
	86	636	16.1	1336	28	US-09-667-617-2220	Sequence 2220, Ap
	87	636	16.1	1336	30	US-09-710-282-3895	Sequence 3895, Ap
	88	620	15.7	726	74	US-60-184-797-637	Sequence 637, App
	89	601	15.2	1477	77	US-60-213-178-1368	Sequence 1368, Ap
	90	595	15.1	719	74	US-60-185-213-1167	Sequence 1167, Ap
	91	575	14.6	1539	28	US-09-674-266A-37	Sequence 37, Appl
	92	563	14.2	564	23	US-09-540-229-124929	Sequence 124929,
	93	555	14.0	3152	1	PCT-US03-37730-24	Sequence 24, Appl
	94	555	14.0	3152	45	US-10-108-260A-1388	Sequence 1388, Ap
	95	553	14.0	603	27	US-09-652-126-2757	Sequence 2757, Ap
	96	551	13.9	1047	27	US-09-644-873-10259	Sequence 10259, A
	97	551	13.9	1047	27	US-09-649-166-5498	Sequence 5498, Ap
c	98	535	13.5	560	22	US-09-534-846B-19694	Sequence 19694, A
c	99	535	13.5	560	49	US-10-314-344-19694	Sequence 19694, A
c	100	532	13.5	1383	74	US-60-185-216-4887	Sequence 4887, Ap
	101	514	13.0	599	33	US-09-821-837-7089	Sequence 7089, Ap
	102	481	12.2	1279	31	US-09-726-788-6057	Sequence 6057, Ap
	103	466	11.8	475	33	US-09-821-837-8592	Sequence 8592, Ap
	104	466	11.8	576	19	US-09-371-168-4160	Sequence 4160, Ap
	105	466	11.8	576	33	US-09-801-833-4160	Sequence 4160, Ap
	106	465	11.8	496	23	US-09-540-229-115871	Sequence 115871,
	107	465	11.8	513	23	US-09-540-229-101329	Sequence 101329,
	108	464	11.7	483	27	US-09-652-816-5353	Sequence 5353, Ap
	109	463	11.7	552	19	US-09-396-885-1439	Sequence 1439, Ap
	110	463	11.7	552	19	US-09-396-885A-1439	Sequence 1439, Ap
	111	456	11.5	1368	19	US-09-396-885-4631	Sequence 4631, Ap
	112	456	11.5	1368	19	US-09-396-885A-4631	Sequence 4631, Ap
	113	456	11.5	1368	19	US-09-399-932-4625	Sequence 4625, Ap
	114	456	11.5	1368	20	US-09-474-436-6154	Sequence 6154, Ap
	115	450	11.4	990	89	US-60-324-185-5550	Sequence 5550, Ap
	116	446	11.3	613	27	US-09-652-816-5158	Sequence 5158, Ap
	117	432	10.9	572	25	US-09-607-200-537	Sequence 537, App
	118	424	10.7	502	27	US-09-644-869-6557	Sequence 6557, Ap
	119	421	10.7	422	17	US-09-293-972-19085	Sequence 19085, A
	120	421	10.7	422	37	US-09-904-939-19085	Sequence 19085, A
	121	420	10.6	510	27	US-09-644-870-7029	Sequence 7029, Ap
	122	420	10.6	510	27	US-09-652-917-2792	Sequence 2792, Ap
	123	418	10.6	420	17	US-09-277-227-3457	Sequence 3457, Ap
	124	418	10.6	420	37	US-09-909-627-3457	Sequence 3457, Ap
	125	418	10.6	445	19	US-09-399-720-12539	Sequence 12539, A
	126	418	10.6	445	38	US-09-921-378-12539	Sequence 12539, A
	127	407	10.3	517	17	US-09-277-214A-226	Sequence 226, App
	128	407	10.3	517	27	US-09-644-870-705	Sequence 705, App
	129	407	10.3	517	36	US-09-891-825-226	Sequence 226, App
	130	407	10.3	528	28	US-09-667-617-1333	Sequence 1333, Ap
	131	404	10.2	427	20	US-09-496-911-10278	Sequence 10278, A
	132	404	10.2	427	41	US-09-975-673A-10278	Sequence 10278, A
	133	403	10.2	494	24	US-09-577-410-1277	Sequence 1277, Ap
	134	400	10.1	646	17	US-09-277-214A-382	Sequence 382, App
	135	400	10.1	646	36	US-09-891-825-382	Sequence 382, App
	136	399	10.1	470	20	US-09-404-549-620	Sequence 620, App
	137	399	10.1	470	20	US-09-404-549A-620	Sequence 620, App
	138	399	10.1	470	25	US-09-617-182-629	Sequence 629, App
	139	396	10.0	3285	19	US-09-371-168-6829	Sequence 6829, Ap
	140	396	10.0	3285	33	US-09-801-833-6829	Sequence 6829, Ap
	141	393	9.9	2469	84	US-60-278-258-2205	Sequence 2205, Ap
	142	392	9.9	392	17	US-09-293-972-29254	Sequence 29254, A

	143	392	9.9	392	37	US-09-904-939-29254	Sequence 29254, A
	144	392	9.9	582	19	US-09-396-885-772	Sequence 772, App
	145	392	9.9	582	19	US-09-396-885A-772	Sequence 772, App
	146	391	9.9	600	74	US-60-184-797-636	Sequence 636, App
	147	388	9.8	414	29	US-09-699-997-7485	Sequence 7485, Ap
	148	388	9.8	419	19	US-09-397-424-3358	Sequence 3358, Ap
	149	388	9.8	419	19	US-09-397-424A-3358	Sequence 3358, Ap
	150	386	9.8	408	20	US-09-465-877-12269	Sequence 12269, A
	151	386	9.8	408	37	US-09-906-555-12269	Sequence 12269, A
	152	385	9.7	527	30	US-09-717-350-3814	Sequence 3814, Ap
c	153	379	9.6	385	20	US-09-496-911-964	Sequence 964, App
c	154	379	9.6	385	41	US-09-975-673A-964	Sequence 964, App
	155	376	9.5	498	16	US-09-235-076-102	Sequence 102, App
	156	376	9.5	498	16	US-09-248-797-8679	Sequence 8679, Ap
	157	376	9.5	498	18	US-09-332-782-102	Sequence 102, App
	158	376	9.5	498	31	US-09-737-223-102	Sequence 102, App
	159	376	9.5	498	37	US-09-918-995-102	Sequence 102, App
	160	376	9.5	498	38	US-09-925-564-8679	Sequence 8679, Ap
	161	373	9.4	405	33	US-09-824-518-2045	Sequence 2045, Ap
	162	373	9.4	502	31	US-09-726-788-2346	Sequence 2346, Ap
	163	371	9.4	424	17	US-09-277-227-3474	Sequence 3474, Ap
	164	371	9.4	424	37	US-09-909-627-3474	Sequence 3474, Ap
	165	365	9.2	580	23	US-09-540-229-109282	Sequence 109282,
	166	365	9.2	770	28	US-09-668-337-254	Sequence 254, App
	167	365	9.2	770	72	US-60-168-197-554	Sequence 554, App
	168	358	9.1	423	19	US-09-396-885-3602	Sequence 3602, Ap
	169	358	9.1	423	19	US-09-396-885A-3602	Sequence 3602, Ap
	170	357	9.0	552	24	US-09-572-411-926	Sequence 926, App
c	171	357	9.0	561	24	US-09-572-411-5591	Sequence 5591, Ap
	172	352	8.9	530	29	US-09-698-010-8437	Sequence 8437, Ap
	173	348	8.8	399	74	US-60-184-797-490	Sequence 490, App
	174	339	8.6	386	31	US-09-726-174-3220	Sequence 3220, Ap
c	175	337	8.5	617	55	US-10-756-149-1605	Sequence 1605, Ap
	176	336	8.5	464	74	US-60-185-213-1015	Sequence 1015, Ap
	177	335	8.5	459	20	US-09-457-659-1786	Sequence 1786, Ap
	178	335	8.5	459	27	US-09-652-127-5504	Sequence 5504, Ap
	179	326	8.3	380	17	US-09-287-618-31989	Sequence 31989, A
	180	325	8.2	425	31	US-09-726-810-1228	Sequence 1228, Ap
	181	323	8.2	493	18	US-09-333-909-1247	Sequence 1247, Ap
	182	323	8.2	493	33	US-09-817-500-1247	Sequence 1247, Ap
	183	320	8.1	486	20	US-09-474-436-4502	Sequence 4502, Ap
	184	319	8.1	367	31	US-09-726-174-1053	Sequence 1053, Ap
	185	318	8.0	542	22	US-09-539-802A-1050	Sequence 1050, Ap
	186	316	8.0	501	28	US-09-667-617-1438	Sequence 1438, Ap
	187	310	7.8	459	27	US-09-649-166-3517	Sequence 3517, Ap
	188	310	7.8	459	27	US-09-652-124-2640	Sequence 2640, Ap
	189	303	7.7	678	33	US-09-821-837-8555	Sequence 8555, Ap
	190	302	7.6	302	12	US-08-885-220B-5351	Sequence 5351, Ap
	191	302	7.6	302	22	US-09-534-843-15164	Sequence 15164, A
	192	300	7.6	566	25	US-09-617-081-997	Sequence 997, App
	193	289	7.3	673	20	US-09-428-151A-9322	Sequence 9322, Ap
	194	287	7.3	287	15	US-09-107-909-2420	Sequence 2420, Ap
	195	287	7.3	287	22	US-09-534-843-15139	Sequence 15139, A
	196	284	7.2	455	19	US-09-399-720-12538	Sequence 12538, A
	197	284	7.2	455	38	US-09-921-378-12538	Sequence 12538, A
	198	279	7.1	422	1	PCT-US01-08631-24006	Sequence 24006, A
	199	279	7.1	422	20	US-09-404-284-3162	Sequence 3162, Ap
	200	279	7.1	422	21	US-09-524-038-3162	Sequence 3162, Ap
	201	279	7.1	422	43	US-10-011-154-3162	Sequence 3162, Ap
	202	278	7.0	278	23	US-09-540-212A-60488	Sequence 60488, A
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c	206	276	7.0	352	6	US-08-249-651-25	Sequence 25, Appl
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c	208	276	7.0	352	37	US-09-912-293-98850	Sequence 98850, A
	209	275	7.0	421	21	US-09-528-409-5477	Sequence 5477, Ap
	210	275	7.0	421	38	US-09-933-524-5477	Sequence 5477, Ap
	211	275	7.0	421	38	US-09-933-524A-5477	Sequence 5477, Ap
	212	275	7.0	425	29	US-09-699-999-1529	Sequence 1529, Ap
	213	264	6.7	264	12	US-08-879-863-5237	Sequence 5237, Ap
	214	264	6.7	264	12	US-08-879-863A-5237	Sequence 5237, Ap
	215	264	6.7	264	22	US-09-534-843-15184	Sequence 15184, A
	216	263	6.7	389	18	US-09-338-425-1553	Sequence 1553, Ap
	217	263	6.7	389	31	US-09-726-790-1553	Sequence 1553, Ap
	218	260	6.6	405	25	US-09-616-082-457	Sequence 457, App
	219	259	6.6	471	19	US-09-396-970-4020	Sequence 4020, Ap
	220	254	6.4	510	27	US-09-644-867-607	Sequence 607, App
	221	252	6.4	252	13	US-08-936-937-1521	Sequence 1521, Ap
	222	252	6.4	252	22	US-09-534-843-15134	Sequence 15134, A
	223	252	6.4	252	56	US-60-008-131-1521	Sequence 1521, Ap
	224	252	6.4	469	20	US-09-428-151A-3163	Sequence 3163, Ap
	225	252	6.4	469	25	US-09-614-387-3706	Sequence 3706, Ap
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	227	250	6.3	302	31	US-09-721-544-16737	Sequence 16737, A
	228	242	6.1	255	23	US-09-540-229-112458	Sequence 112458,
	229	242	6.1	327	5	US-08-196-363-15580	Sequence 15580, A
	230	242	6.1	327	5	US-08-196-363A-15580	Sequence 15580, A
	231	242	6.1	327	5	US-08-196-363-15580	Sequence 15580, A
	232	242	6.1	327	34	US-09-859-490-15580	Sequence 15580, A
	233	242	6.1	327	37	US-09-912-293-219639	Sequence 219639,
	234	241	6.1	241	13	US-08-903-473-124	Sequence 124, App
	235	241	6.1	241	22	US-09-534-843-15160	Sequence 15160, A
	236	241	6.1	241	58	US-60-023-339-2238	Sequence 2238, Ap
	237	241	6.1	543	19	US-09-396-970-1006	Sequence 1006, Ap
	238	239	6.0	388	27	US-09-652-917-2202	Sequence 2202, Ap
	239	238	6.0	244	15	US-09-103-003-388	Sequence 388, App
	240	238	6.0	244	22	US-09-534-843-15117	Sequence 15117, A
	241	236	6.0	342	19	US-09-359-922-4696	Sequence 4696, Ap
	242	236	6.0	342	19	US-09-359-922-4696	Sequence 4696, Ap
	243	236	6.0	342	37	US-09-919-002-4696	Sequence 4696, Ap
	244	234	5.9	281	13	US-08-903-214-561	Sequence 561, App
	245	234	5.9	281	22	US-09-534-843-15151	Sequence 15151, A
	246	234	5.9	281	58	US-60-023-378-561	Sequence 561, App
	247	231	5.8	259	32	US-09-770-174-2627	Sequence 2627, Ap
c	248	231	5.8	259	32	US-09-770-174-2917	Sequence 2917, Ap
	249	229	5.8	415	27	US-09-644-870-4505	Sequence 4505, Ap
	250	228	5.8	3266	31	US-09-724-676-33290	Sequence 33290, A
	251	228	5.8	3266	31	US-09-724-676A-33290	Sequence 33290, A
	252	228	5.8	3379	31	US-09-724-676-33291	Sequence 33291, A
	253	228	5.8	3379	31	US-09-724-676A-33291	Sequence 33291, A
	254	228	5.8	3392	31	US-09-724-676-33292	Sequence 33292, A
	255	228	5.8	3392	31	US-09-724-676A-33292	Sequence 33292, A
	256	228	5.8	3505	31	US-09-724-676-33293	Sequence 33293, A
	257	228	5.8	3505	31	US-09-724-676A-33293	Sequence 33293, A
	258	227	5.7	375	30	US-09-710-281-987	Sequence 987, App
	259	225	5.7	427	30	US-09-716-475-6350	Sequence 6350, Ap
	260	225	5.7	7868	1	PCT-US01-01239-2238	Sequence 2238, Ap
	261	225	5.7	7868	32	US-09-760-475-3947	Sequence 3947, Ap
	262	225	5.7	7868	32	US-09-764-902-2238	Sequence 2238, Ap
	263	225	5.7	7868	47	US-10-227-425-3947	Sequence 3947, Ap
	264	225	5.7	19706	78	US-60-229-525-72	Sequence 72, Appl
c	265	225	5.7	26760	77	US-60-213-178-418	Sequence 418, App
	266	225	5.7	76567	107	US-60-500-337-19392	Sequence 19392, A
c	267	225	5.7	151398	77	US-60-212-664-231	Sequence 231, App
c	268	225	5.7	15105345	39	US-09-948-128-55	Sequence 55, Appl
c	269	224	5.7	467	1	PCT-US01-00663-53	Sequence 53, Appl
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c	271	224	5.7	467	46	US-10-182-993-51	Sequence 51, Appl
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c	275	224	5.7	467	47	US-10-203-134-54	Sequence 54, Appl
c	276	224	5.7	467	47	US-10-203-135-54	Sequence 54, Appl
c	277	224	5.7	467	47	US-10-203-136-55	Sequence 55, Appl
c	278	224	5.7	467	47	US-10-203-137-53	Sequence 53, Appl
c	279	224	5.7	467	47	US-10-203-138-51	Sequence 51, Appl
c	280	224	5.7	467	47	US-10-203-138A-51	Sequence 51, Appl
c	281	224	5.7	467	47	US-10-203-139-56	Sequence 56, Appl
c	282	224	5.7	467	80	US-60-236-359-57	Sequence 57, Appl
c	283	223	5.6	1009	16	US-09-205-070-5575	Sequence 5575, Ap
c	284	223	5.6	1009	18	US-09-340-623-5575	Sequence 5575, Ap
c	285	223	5.6	1009	36	US-09-898-888-5575	Sequence 5575, Ap
c	286	223	5.6	1009	36	US-09-898-888A-5575	Sequence 5575, Ap
c	287	222	5.6	257	1	PCT-US01-00663-13292	Sequence 13292, A
c	288	222	5.6	257	35	US-09-864-761-16888	Sequence 16888, A

c 289	222	5.6	257	46	US-10-182-993-12880	Sequence 12880, A
c 290	222	5.6	257	46	US-10-182-995-10034	Sequence 10034, A
c 291	222	5.6	257	46	US-10-182-997-9351	Sequence 9351, Ap
c 292	222	5.6	257	46	US-10-182-998-5134	Sequence 5134, Ap
c 293	222	5.6	257	47	US-10-203-134-13174	Sequence 13174, A
c 294	222	5.6	257	47	US-10-203-135-12675	Sequence 12675, A
c 295	222	5.6	257	47	US-10-203-136-13172	Sequence 13172, A
c 296	222	5.6	257	47	US-10-203-137-13292	Sequence 13292, A
c 297	222	5.6	257	47	US-10-203-138-5263	Sequence 5263, Ap
c 298	222	5.6	257	47	US-10-203-138A-5263	Sequence 5263, Ap
c 299	222	5.6	257	47	US-10-203-139-12736	Sequence 12736, A
c 300	222	5.6	257	80	US-60-236-359-7468	Sequence 7468, Ap
301	221	5.6	249	22	US-09-534-843-15163	Sequence 15163, A
302	220	5.6	445	28	US-09-666-024-135	Sequence 135, App
303	213	5.4	547	27	US-09-652-109-4332	Sequence 4332, Ap
304	212	5.4	274	13	US-08-936-937-811	Sequence 811, App
305	212	5.4	274	22	US-09-534-843-15155	Sequence 15155, A
306	212	5.4	274	56	US-60-008-131-811	Sequence 811, App
307	208	5.3	532	20	US-09-496-911-12911	Sequence 12911, A
308	208	5.3	532	41	US-09-975-673A-12911	Sequence 12911, A
309	207	5.2	428	1	PCT-US01-08631-24005	Sequence 24005, A
310	205	5.2	258	14	US-09-075-075-1313	Sequence 1313, Ap
311	205	5.2	258	22	US-09-534-843-15147	Sequence 15147, A
312	205	5.2	302	43	US-10-029-386-17518	Sequence 17518, A
313	205	5.2	500	16	US-09-234-611-17745	Sequence 17745, A
314	205	5.2	500	16	US-09-235-076-32315	Sequence 32315, A
315	205	5.2	500	17	US-09-289-768-36800	Sequence 36800, A
316	205	5.2	500	18	US-09-332-782-32315	Sequence 32315, A
317	205	5.2	500	31	US-09-737-223-32315	Sequence 32315, A
318	205	5.2	500	37	US-09-904-809-17745	Sequence 17745, A
319	205	5.2	500	37	US-09-918-995-32315	Sequence 32315, A
320	205	5.2	500	38	US-09-939-397-36800	Sequence 36800, A
321	205	5.2	507	43	US-10-029-386-3818	Sequence 3818, Ap
322	205	5.2	769	20	US-09-471-275-5411	Sequence 5411, Ap
323	205	5.2	769	20	US-09-488-725B-4672	Sequence 4672, Ap
c 324	205	5.2	17701	107	US-60-500-337-19385	Sequence 19385, A
325	204	5.2	224	13	US-08-979-854A-4087	Sequence 4087, Ap
326	204	5.2	224	22	US-09-534-843-15165	Sequence 15165, A
327	204	5.2	224	59	US-60-031-834-1053	Sequence 1053, Ap
328	202	5.1	258	23	US-09-540-766-58603	Sequence 58603, A
329	198	5.0	215	27	US-09-652-126-2628	Sequence 2628, Ap
330	195	4.9	418	20	US-09-428-151A-3950	Sequence 3950, Ap
331	195	4.9	418	25	US-09-614-387-5709	Sequence 5709, Ap
332	194	4.9	307	14	US-09-076-667-2312	Sequence 2312, Ap
333	194	4.9	307	22	US-09-534-843-15140	Sequence 15140, A
334	194	4.9	307	60	US-60-048-002-2312	Sequence 2312, Ap
335	194	4.9	403	1	PCT-US99-24206-669	Sequence 669, App
336	194	4.9	403	33	US-09-807-521-669	Sequence 669, App
337	190	4.8	410	21	US-09-528-409-34499	Sequence 34499, A
338	190	4.8	410	38	US-09-933-524-34499	Sequence 34499, A
339	190	4.8	410	38	US-09-933-524A-34499	Sequence 34499, A
340	189	4.8	308	22	US-09-534-843-15173	Sequence 15173, A
341	185	4.7	349	13	US-08-993-774-2729	Sequence 2729, Ap
342	185	4.7	349	22	US-09-534-843-15142	Sequence 15142, A
343	185	4.7	349	59	US-60-034-975-2729	Sequence 2729, Ap
c 344	184	4.7	397	17	US-09-277-214A-104	Sequence 104, App
c 345	184	4.7	397	36	US-09-891-825-104	Sequence 104, App
346	182	4.6	369	29	US-09-698-010-10566	Sequence 10566, A
347	180	4.6	422	17	US-09-274-861-1241	Sequence 1241, Ap
348	180	4.6	422	37	US-09-915-738-1241	Sequence 1241, Ap
349	180	4.6	451	27	US-09-644-873-763	Sequence 763, App
350	180	4.6	589	25	US-09-606-776-2928	Sequence 2928, Ap
351	180	4.6	589	27	US-09-644-867-4254	Sequence 4254, Ap
352	178	4.5	226	13	US-08-993-774-3050	Sequence 3050, Ap
353	178	4.5	226	22	US-09-534-843-15107	Sequence 15107, A
354	178	4.5	226	59	US-60-034-975-3050	Sequence 3050, Ap
355	178	4.5	226	74	US-60-184-797-487	Sequence 487, App
356	175	4.4	427	19	US-09-359-067-49708	Sequence 49708, A
357	174	4.4	174	13	US-08-903-214-2578	Sequence 2578, Ap
358	174	4.4	174	22	US-09-534-843-15167	Sequence 15167, A
359	174	4.4	174	58	US-60-023-378-2578	Sequence 2578, Ap
360	173	4.4	511	23	US-09-540-229-108511	Sequence 108511,
361	172	4.4	5158	32	US-09-760-475-3946	Sequence 3946, Ap
362	172	4.4	5158	47	US-10-227-425-3946	Sequence 3946, Ap
c 363	172	4.4	12400	1	PCT-US01-19835-1	Sequence 1, Appli
c 364	172	4.4	12400	1	PCT-US01-19835-91	Sequence 91, Appl
365	172	4.4	12917	107	US-60-500-337-19764	Sequence 19764, A
c 366	171	4.3	481	1	PCT-US01-00663-54	Sequence 54, Appl
c 367	171	4.3	481	35	US-09-864-761-47	Sequence 47, Appl
c 368	171	4.3	481	46	US-10-182-993-52	Sequence 52, Appl
c 369	171	4.3	481	46	US-10-182-995-47	Sequence 47, Appl
c 370	171	4.3	481	46	US-10-182-997-55	Sequence 55, Appl
c 371	171	4.3	481	46	US-10-182-998-54	Sequence 54, Appl
c 372	171	4.3	481	47	US-10-203-134-55	Sequence 55, Appl
c 373	171	4.3	481	47	US-10-203-135-55	Sequence 55, Appl
c 374	171	4.3	481	47	US-10-203-136-56	Sequence 56, Appl
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c 378	171	4.3	481	47	US-10-203-139-57	Sequence 57, Appl
c 379	171	4.3	481	80	US-60-236-359-58	Sequence 58, Appl
380	171	4.3	496	31	US-09-758-472-1729	Sequence 1729, Ap
381	171	4.3	496	47	US-10-235-926-1729	Sequence 1729, Ap
382	168	4.3	549	27	US-09-649-164-7424	Sequence 7424, Ap
383	168	4.3	1784	1	PCT-US02-27777-76	Sequence 76, Appl
384	168	4.3	1784	1	PCT-US02-27777A-76	Sequence 76, Appl
385	165	4.2	185	27	US-09-652-125A-189	Sequence 189, App
386	165	4.2	273	27	US-09-652-109-2944	Sequence 2944, Ap
387	163	4.1	244	23	US-09-540-766-56331	Sequence 56331, A
388	160	4.0	189	43	US-10-029-386-26498	Sequence 26498, A
389	160	4.0	281	27	US-09-644-870-5780	Sequence 5780, Ap
390	160	4.0	507	43	US-10-029-386-12798	Sequence 12798, A
c 391	160	4.0	565	73	US-60-171-494-508	Sequence 508, App
392	160	4.0	9301	81	US-60-245-225-113	Sequence 113, App
393	160	4.0	9301	82	US-60-258-250-33	Sequence 33, Appl
394	158	4.0	327	8	US-08-440-817-312	Sequence 312, App
395	158	4.0	327	22	US-09-534-843-15157	Sequence 15157, A
396	155	3.9	310	23	US-09-540-229-108724	Sequence 108724,
397	154	3.9	346	14	US-09-021-095-600	Sequence 600, App
398	154	3.9	346	22	US-09-534-843-15178	Sequence 15178, A
399	154	3.9	411	29	US-09-699-998-3040	Sequence 3040, Ap
400	154	3.9	3700	78	US-60-229-525-618	Sequence 618, App
401	153	3.9	236	14	US-09-035-173-64	Sequence 64, Appl
402	153	3.9	236	14	US-09-081-109-134	Sequence 134, App
403	153	3.9	236	22	US-09-534-843-15150	Sequence 15150, A
404	153	3.9	236	23	US-09-540-764-38168	Sequence 38168, A
405	153	3.9	236	49	US-10-349-781-38168	Sequence 38168, A
406	153	3.9	236	60	US-60-048-727-134	Sequence 134, App
407	151	3.8	399	5	US-08-103-744A-24	Sequence 24, Appl
408	151	3.8	399	5	US-08-103-744B-24	Sequence 24, Appl
409	151	3.8	399	5	US-08-103-744-24	Sequence 24, Appl
410	151	3.8	399	6	US-08-249-651-24	Sequence 24, Appl
411	151	3.8	399	16	US-09-249-651-24	Sequence 24, Appl
412	151	3.8	399	37	US-09-912-293-98849	Sequence 98849, A
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414	150	3.8	201	107	US-60-500-337-15873	Sequence 15873, A
415	150	3.8	201	107	US-60-500-337-15875	Sequence 15875, A
416	150	3.8	201	107	US-60-500-337-15877	Sequence 15877, A
417	150	3.8	201	107	US-60-500-337-15882	Sequence 15882, A
418	150	3.8	201	107	US-60-500-337-15883	Sequence 15883, A
419	150	3.8	201	107	US-60-500-337-15885	Sequence 15885, A
420	150	3.8	201	107	US-60-500-337-15887	Sequence 15887, A
421	150	3.8	201	107	US-60-500-337-15890	Sequence 15890, A
422	150	3.8	201	107	US-60-500-337-15891	Sequence 15891, A
423	150	3.8	201	107	US-60-500-337-15892	Sequence 15892, A
424	150	3.8	201	107	US-60-500-337-15894	Sequence 15894, A
425	150	3.8	201	107	US-60-500-337-15899	Sequence 15899, A
426	150	3.8	201	107	US-60-500-337-15900	Sequence 15900, A
427	150	3.8	201	107	US-60-500-337-15902	Sequence 15902, A
428	150	3.8	201	107	US-60-500-337-15904	Sequence 15904, A
429	150	3.8	263	29	US-09-698-014-1172	Sequence 1172, Ap
430	150	3.8	770	27	US-09-652-916-9563	Sequence 9563, Ap
431	150	3.8	770	29	US-09-698-014-4887	Sequence 4887, Ap
432	148	3.7	231	13	US-08-961-525-406	Sequence 406, App
433	148	3.7	231	58	US-60-029-857-406	Sequence 406, App
434	146	3.7	178	43	US-10-029-386-17507	Sequence 17507, A

	435	146	3.7	509	43	US-10-029-386-3807	Sequence 3807, Ap
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	437	144	3.6	254	17	US-09-293-655-852	Sequence 852, App
	438	144	3.6	254	22	US-09-534-843-15122	Sequence 15122, A
	439	144	3.6	254	64	US-60-082-030-852	Sequence 852, App
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c	442	142	3.6	179	46	US-10-182-993-12881	Sequence 12881, A
c	443	142	3.6	179	46	US-10-182-995-10035	Sequence 10035, A
c	444	142	3.6	179	46	US-10-182-997-9352	Sequence 9352, Ap
c	445	142	3.6	179	46	US-10-182-998-5135	Sequence 5135, Ap
c	446	142	3.6	179	47	US-10-203-134-13175	Sequence 13175, A
c	447	142	3.6	179	47	US-10-203-135-12676	Sequence 12676, A
c	448	142	3.6	179	47	US-10-203-136-13173	Sequence 13173, A
c	449	142	3.6	179	47	US-10-203-137-13293	Sequence 13293, A
c	450	142	3.6	179	47	US-10-203-138-5264	Sequence 5264, Ap
c	451	142	3.6	179	47	US-10-203-138A-5264	Sequence 5264, Ap
c	452	142	3.6	179	47	US-10-203-139-12737	Sequence 12737, A
c	453	142	3.6	179	80	US-60-236-359-7469	Sequence 7469, Ap
	454	142	3.6	456	30	US-09-710-282-1689	Sequence 1689, Ap
	455	140	3.5	378	20	US-09-489-036-32839	Sequence 32839, A
	456	140	3.5	378	39	US-09-943-143-32839	Sequence 32839, A
c	457	140	3.5	612	73	US-60-171-494-386	Sequence 386, App
	458	137	3.5	258	74	US-60-184-774-439	Sequence 439, App
	459	136	3.4	240	14	US-09-076-667-4069	Sequence 4069, Ap
	460	136	3.4	240	22	US-09-534-843-15106	Sequence 15106, A
	461	136	3.4	240	60	US-60-048-002-4069	Sequence 4069, Ap
	462	134	3.4	829	77	US-60-213-359-3624	Sequence 3624, Ap
	463	132	3.3	272	23	US-09-540-229-112313	Sequence 112313,
	464	130	3.3	201	107	US-60-500-337-83206	Sequence 83206, A
	465	130	3.3	201	107	US-60-500-337-83229	Sequence 83229, A
	466	130	3.3	387	1	PCT-US01-01239-531	Sequence 531, App
	467	130	3.3	387	1	PCT-US01-08631-24007	Sequence 24007, A
	468	130	3.3	387	32	US-09-764-902-531	Sequence 531, App
c	469	128	3.2	140	1	PCT-US01-00663-13291	Sequence 13291, A
c	470	128	3.2	140	35	US-09-864-761-16887	Sequence 16887, A
c	471	128	3.2	140	46	US-10-182-993-12879	Sequence 12879, A
c	472	128	3.2	140	46	US-10-182-995-10033	Sequence 10033, A
c	473	128	3.2	140	46	US-10-182-997-9350	Sequence 9350, Ap
c	474	128	3.2	140	46	US-10-182-998-5133	Sequence 5133, Ap
c	475	128	3.2	140	47	US-10-203-134-13173	Sequence 13173, A
c	476	128	3.2	140	47	US-10-203-135-12674	Sequence 12674, A
c	477	128	3.2	140	47	US-10-203-136-13171	Sequence 13171, A
c	478	128	3.2	140	47	US-10-203-137-13291	Sequence 13291, A
c	479	128	3.2	140	47	US-10-203-138-5262	Sequence 5262, Ap
c	480	128	3.2	140	47	US-10-203-138A-5262	Sequence 5262, Ap
c	481	128	3.2	140	47	US-10-203-139-12735	Sequence 12735, A
c	482	128	3.2	140	80	US-60-236-359-7467	Sequence 7467, Ap
	483	128	3.2	234	23	US-09-540-766-57998	Sequence 57998, A
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c	485	128	3.2	465	35	US-09-864-761-45	Sequence 45, Appl
c	486	128	3.2	465	46	US-10-182-993-50	Sequence 50, Appl
c	487	128	3.2	465	46	US-10-182-995-45	Sequence 45, Appl
c	488	128	3.2	465	46	US-10-182-997-53	Sequence 53, Appl
c	489	128	3.2	465	46	US-10-182-998-52	Sequence 52, Appl
c	490	128	3.2	465	47	US-10-203-134-53	Sequence 53, Appl
c	491	128	3.2	465	47	US-10-203-135-53	Sequence 53, Appl
c	492	128	3.2	465	47	US-10-203-136-54	Sequence 54, Appl
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c	496	128	3.2	465	47	US-10-203-139-55	Sequence 55, Appl
c	497	128	3.2	465	80	US-60-236-359-56	Sequence 56, Appl
	498	128	3.2	488	72	US-60-162-245-1518	Sequence 1518, Ap
	499	128	3.2	489	72	US-60-162-245-977	Sequence 977, App
	500	128	3.2	489	72	US-60-169-868-2080	Sequence 2080, Ap
	501	128	3.2	489	72	US-60-169-868-2560	Sequence 2560, Ap
	502	127	3.2	287	12	US-08-826-428-5	Sequence 5, Appli
	503	127	3.2	287	22	US-09-534-843-15131	Sequence 15131, A
	504	127	3.2	287	57	US-60-014-305-5	Sequence 5, Appli
	505	127	3.2	287	57	US-60-017-170-5	Sequence 5, Appli
	506	126	3.2	250	13	US-08-992-868-3739	Sequence 3739, Ap
	507	126	3.2	250	22	US-09-534-843-15116	Sequence 15116, A
	508	125	3.2	334	47	US-10-218-140-4625	Sequence 4625, Ap
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	510	122	3.1	258	22	US-09-539-800B-10390	Sequence 10390, A
	511	122	3.1	258	22	US-09-539-800C-10390	Sequence 10390, A
	512	120	3.0	190	12	US-08-856-624-1892	Sequence 1892, Ap
	513	120	3.0	190	22	US-09-534-843-15171	Sequence 15171, A
	514	119	3.0	258	22	US-09-534-843-15175	Sequence 15175, A
	515	118	3.0	245	13	US-08-903-214-2566	Sequence 2566, Ap
	516	118	3.0	245	22	US-09-534-843-15143	Sequence 15143, A
	517	118	3.0	245	58	US-60-023-378-2566	Sequence 2566, Ap
	518	117	3.0	266	14	US-09-032-271-114	Sequence 114, App
	519	117	3.0	266	22	US-09-534-843-15123	Sequence 15123, A
	520	117	3.0	266	59	US-60-038-585-114	Sequence 114, App
	521	116	2.9	205	22	US-09-539-806-42094	Sequence 42094, A
	522	116	2.9	205	22	US-09-539-806B-42094	Sequence 42094, A
	523	115	2.9	246	12	US-08-866-372-667	Sequence 667, App
	524	115	2.9	246	22	US-09-534-843-15162	Sequence 15162, A
	525	115	2.9	246	57	US-60-018-881-667	Sequence 667, App
c	526	115	2.9	620	74	US-60-187-387-668	Sequence 668, App
	527	113	2.9	270	22	US-09-534-846B-19695	Sequence 19695, A
	528	113	2.9	270	49	US-10-314-344-19695	Sequence 19695, A
	529	113	2.9	504	19	US-09-396-885-1640	Sequence 1640, Ap
	530	113	2.9	504	19	US-09-396-885A-1640	Sequence 1640, Ap
	531	112	2.8	539	20	US-09-474-436-239	Sequence 239, App
	532	109	2.8	237	13	US-08-984-691-1019	Sequence 1019, Ap
	533	109	2.8	237	22	US-09-534-843-15136	Sequence 15136, A
	534	109	2.8	570	1	PCT-US01-08631-24009	Sequence 24009, A
	535	109	2.8	570	1	PCT-US01-08631-30154	Sequence 30154, A
	536	109	2.8	1954	1	PCT-US01-08631-27353	Sequence 27353, A
	537	105	2.7	229	9	US-08-504-732-43	Sequence 43, Appl
	538	105	2.7	250	23	US-09-540-229-113912	Sequence 113912,
	539	104	2.6	394	24	US-09-586-248-206	Sequence 206, App
	540	104	2.6	457	18	US-09-342-216-360	Sequence 360, App
	541	104	2.6	457	18	US-09-342-216A-360	Sequence 360, App
	542	104	2.6	457	37	US-09-908-601-360	Sequence 360, App
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	544	103	2.6	177	23	US-09-540-229-101998	Sequence 101998,
	545	100	2.5	186	15	US-09-103-003-223	Sequence 223, App
	546	100	2.5	186	22	US-09-534-843-15170	Sequence 15170, A
	547	100	2.5	201	107	US-60-500-337-15874	Sequence 15874, A
	548	100	2.5	201	107	US-60-500-337-15876	Sequence 15876, A
	549	100	2.5	201	107	US-60-500-337-15884	Sequence 15884, A
	550	100	2.5	201	107	US-60-500-337-15886	Sequence 15886, A
	551	100	2.5	201	107	US-60-500-337-15888	Sequence 15888, A
	552	100	2.5	201	107	US-60-500-337-15893	Sequence 15893, A
	553	100	2.5	201	107	US-60-500-337-15903	Sequence 15903, A
	554	100	2.5	201	107	US-60-500-337-83188	Sequence 83188, A
	555	100	2.5	422	51	US-10-421-961A-666	Sequence 666, App
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c	557	99	2.5	666	72	US-60-162-245-797	Sequence 797, App
c	558	99	2.5	666	72	US-60-169-868-1968	Sequence 1968, Ap
	559	99	2.5	2023	1	PCT-US01-01239-2240	Sequence 2240, Ap
	560	99	2.5	2023	32	US-09-760-475-3950	Sequence 3950, Ap
	561	99	2.5	2023	32	US-09-764-902-2240	Sequence 2240, Ap
	562	99	2.5	2023	47	US-10-227-425-3950	Sequence 3950, Ap
	563	98	2.5	385	72	US-60-162-245-1899	Sequence 1899, Ap
	564	98	2.5	386	72	US-60-169-868-3184	Sequence 3184, Ap
	565	96	2.4	269	13	US-08-962-919-1800	Sequence 1800, Ap
	566	96	2.4	269	22	US-09-534-843-15183	Sequence 15183, A
	567	95	2.4	201	107	US-60-500-337-83183	Sequence 83183, A
	568	94	2.4	466	16	US-09-235-076-15062	Sequence 15062, A
	569	94	2.4	466	16	US-09-248-797-33744	Sequence 33744, A
	570	94	2.4	466	18	US-09-332-782-15062	Sequence 15062, A
	571	94	2.4	466	31	US-09-737-223-15062	Sequence 15062, A
	572	94	2.4	466	37	US-09-918-995-15062	Sequence 15062, A
	573	94	2.4	466	38	US-09-925-564-33744	Sequence 33744, A
	574	93	2.4	201	107	US-60-500-337-83239	Sequence 83239, A
	575	92	2.3	277	23	US-09-540-229-124994	Sequence 124994,
	576	91	2.3	3866	47	US-10-218-140-5559	Sequence 5559, Ap
	577	90	2.3	277	32	US-09-796-692-3604	Sequence 3604, Ap
	578	90	2.3	277	32	US-09-796-692A-3604	Sequence 3604, Ap
	579	90	2.3	277	43	US-10-040-862-3604	Sequence 3604, Ap
	580	90	2.3	277	44	US-10-057-475B-3604	Sequence 3604, Ap

	581	90	2.3	277	46	US-10-154-884B-3604	Sequence 3604, Ap
	582	90	2.3	277	75	US-60-190-479-691	Sequence 691, App
	583	90	2.3	465	16	US-09-234-611-7923	Sequence 7923, Ap
	584	90	2.3	465	16	US-09-248-797-33743	Sequence 33743, A
	585	90	2.3	465	37	US-09-904-809-7923	Sequence 7923, Ap
	586	90	2.3	465	38	US-09-925-564-33743	Sequence 33743, A
	587	90	2.3	601	39	US-09-947-907-16716	Sequence 16716, A
	588	89	2.3	89	22	US-09-534-843-15176	Sequence 15176, A
	589	89	2.3	409	75	US-60-196-711-940	Sequence 940, App
	590	89	2.3	409	75	US-60-196-711-941	Sequence 941, App
	591	88	2.2	201	107	US-60-500-337-15870	Sequence 15870, A
	592	88	2.2	201	107	US-60-500-337-15880	Sequence 15880, A
	593	88	2.2	201	107	US-60-500-337-15889	Sequence 15889, A
	594	88	2.2	201	107	US-60-500-337-15897	Sequence 15897, A
	595	88	2.2	201	107	US-60-500-337-15901	Sequence 15901, A
	596	88	2.2	215	74	US-60-184-774-438	Sequence 438, App
	597	88	2.2	221	15	US-09-107-910-2740	Sequence 2740, Ap
	598	88	2.2	221	22	US-09-534-843-15109	Sequence 15109, A
	599	87	2.2	201	107	US-60-500-337-83284	Sequence 83284, A
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	601	87	2.2	278	22	US-09-534-843-15105	Sequence 15105, A
	602	87	2.2	289	74	US-60-184-797-645	Sequence 645, App
	603	87	2.2	541	73	US-60-170-374-946	Sequence 946, App
	604	86	2.2	201	107	US-60-500-337-83223	Sequence 83223, A
	605	86	2.2	357	31	US-09-726-788-5004	Sequence 5004, Ap
	606	86	2.2	453	72	US-60-160-209-905	Sequence 905, App
	607	86	2.2	478	72	US-60-162-245-1814	Sequence 1814, Ap
	608	86	2.2	479	72	US-60-162-245-554	Sequence 554, App
	609	86	2.2	645	74	US-60-185-216-964	Sequence 964, App
	610	86	2.2	698	89	US-60-324-185-5552	Sequence 5552, Ap
	611	86	2.2	881	31	US-09-758-439-171	Sequence 171, App
	612	86	2.2	881	47	US-10-201-915-171	Sequence 171, App
	613	86	2.2	961	73	US-60-172-373-15871	Sequence 15871, A
c	614	86	2.2	32768	76	US-60-206-600-56	Sequence 56, Appl
c	615	86	2.2	32768	76	US-60-207-316-9	Sequence 9, Appli
c	616	86	2.2	32768	76	US-60-208-129-64	Sequence 64, Appl
c	617	86	2.2	32768	76	US-60-208-965-77	Sequence 77, Appl
c	618	86	2.2	32768	76	US-60-208-973-75	Sequence 75, Appl
c	619	86	2.2	32768	76	US-60-208-973-76	Sequence 76, Appl
c	620	86	2.2	32768	77	US-60-213-177-178	Sequence 178, App
c	621	86	2.2	32768	78	US-60-229-525-196	Sequence 196, App
c	622	86	2.2	32768	79	US-60-230-445-684	Sequence 684, App
	623	85	2.2	193	77	US-60-217-080-23739	Sequence 23739, A
	624	85	2.2	375	77	US-60-217-080-23173	Sequence 23173, A
c	625	85	2.2	406	74	US-60-186-662-181	Sequence 181, App
	626	85	2.2	420	8	US-08-401-791A-10359	Sequence 10359, A
	627	85	2.2	420	8	US-08-401-791B-10359	Sequence 10359, A
	628	85	2.2	420	37	US-09-912-293-126709	Sequence 126709,
	629	84	2.1	271	14	US-09-065-521-3370	Sequence 3370, Ap
	630	84	2.1	271	22	US-09-534-843-15159	Sequence 15159, A
	631	83	2.1	201	107	US-60-500-337-83287	Sequence 83287, A
	632	82	2.1	274	17	US-09-294-093A-829	Sequence 829, App
	633	82	2.1	274	17	US-09-294-093B-723	Sequence 723, App
	634	82	2.1	274	18	US-09-304-517A-44395	Sequence 44395, A
	635	82	2.1	274	19	US-09-371-146A-44395	Sequence 44395, A
	636	82	2.1	274	34	US-09-839-976-723	Sequence 723, App
	637	82	2.1	274	34	US-09-839-976A-723	Sequence 723, App
	638	82	2.1	274	42	US-09-985-678-44395	Sequence 44395, A
	639	82	2.1	274	64	US-60-082-567-723	Sequence 723, App
	640	78	2.0	601	39	US-09-947-907-16717	Sequence 16717, A
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c	642	77	1.9	77	1	PCT-IB03-04491-18461	Sequence 18461, A
	643	77	1.9	146	27	US-09-659-737A-12	Sequence 12, Appl
	644	77	1.9	201	107	US-60-500-337-83177	Sequence 83177, A
	645	77	1.9	201	107	US-60-500-337-83178	Sequence 83178, A
	646	77	1.9	201	107	US-60-500-337-83189	Sequence 83189, A
	647	77	1.9	201	107	US-60-500-337-83190	Sequence 83190, A
	648	75	1.9	120	22	US-09-539-806-41291	Sequence 41291, A
	649	75	1.9	120	22	US-09-539-806B-41291	Sequence 41291, A
	650	75	1.9	201	107	US-60-500-337-83237	Sequence 83237, A
	651	73	1.8	413	13	US-08-971-050-577	Sequence 577, App
	652	73	1.8	413	13	US-08-971-050-577	Sequence 577, App
	653	73	1.8	413	13	US-08-971-050C-577	Sequence 577, App
	654	73	1.8	413	37	US-09-912-292-5765	Sequence 5765, Ap
	655	72	1.8	304	5	US-08-196-363-4712	Sequence 4712, Ap
	656	72	1.8	304	5	US-08-196-363A-4712	Sequence 4712, Ap
	657	72	1.8	304	5	US-08-196-363-4712	Sequence 4712, Ap
	658	72	1.8	304	34	US-09-859-490-4712	Sequence 4712, Ap
	659	72	1.8	304	37	US-09-912-293-70700	Sequence 70700, A
c	660	71	1.8	288	23	US-09-540-233D-91226	Sequence 91226, A
	661	70	1.8	201	107	US-60-500-337-83274	Sequence 83274, A
	662	70	1.8	216	25	US-09-617-081-853	Sequence 853, App
	663	69	1.7	201	107	US-60-500-337-83238	Sequence 83238, A
	664	69	1.7	283	21	US-09-513-999C-33195	Sequence 33195, A
	665	69	1.7	285	13	US-08-905-144-146	Sequence 146, App
	666	69	1.7	285	23	US-09-547-599C-781	Sequence 781, App
	667	69	1.7	285	53	US-10-631-402-781	Sequence 781, App
	668	69	1.7	285	53	US-10-631-441-781	Sequence 781, App
	669	69	1.7	285	53	US-10-631-441A-781	Sequence 781, App
	670	68	1.7	87	1	PCT-US03-18714-18462	Sequence 18462, A
	671	68	1.7	87	1	PCT-IB03-04491-18462	Sequence 18462, A
	672	68	1.7	201	107	US-60-500-337-83232	Sequence 83232, A
	673	68	1.7	252	14	US-09-010-765-55	Sequence 55, Appl
	674	68	1.7	252	23	US-09-540-766-37767	Sequence 37767, A
	675	68	1.7	252	59	US-60-036-145-55	Sequence 55, Appl
	676	68	1.7	387	1	PCT-US01-08631-16599	Sequence 16599, A
	677	68	1.7	387	1	PCT-US02-25485-131	Sequence 131, App
	678	68	1.7	387	1	PCT-US02-25485-2135	Sequence 2135, Ap
	679	68	1.7	387	47	US-10-219-382-131	Sequence 131, App
	680	68	1.7	387	47	US-10-219-382-2125	Sequence 2125, Ap
	681	68	1.7	387	47	US-10-219-382A-131	Sequence 131, App
	682	68	1.7	387	47	US-10-219-382A-2125	Sequence 2125, Ap
	683	68	1.7	387	88	US-60-311-261-131	Sequence 131, App
	684	68	1.7	387	88	US-60-311-261-2125	Sequence 2125, Ap
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c	686	68	1.7	460	72	US-60-164-760-225	Sequence 225, App
	687	68	1.7	756	93	US-60-365-384-52	Sequence 52, Appl
	688	66	1.7	189	15	US-09-107-909-2171	Sequence 2171, Ap
	689	66	1.7	189	22	US-09-534-843-15154	Sequence 15154, A
	690	66	1.7	201	107	US-60-500-337-83290	Sequence 83290, A
	691	66	1.7	385	25	US-09-617-081-1054	Sequence 1054, Ap
	692	66	1.7	385	34	US-09-845-674-962	Sequence 962, App
	693	64	1.6	201	107	US-60-500-337-83233	Sequence 83233, A
	694	63	1.6	154	77	US-60-217-080-24235	Sequence 24235, A
c	695	62	1.6	1665	1	PCT-US03-37730-23	Sequence 23, Appl
	696	61	1.5	201	107	US-60-500-337-83235	Sequence 83235, A
	697	61	1.5	201	107	US-60-500-337-83277	Sequence 83277, A
	698	61	1.5	303	51	US-10-421-961A-4507	Sequence 4507, Ap
	699	60	1.5	201	107	US-60-500-337-83288	Sequence 83288, A
	700	59	1.5	412	77	US-60-212-356-352	Sequence 352, App
	701	58	1.5	247	14	US-09-036-589-32	Sequence 32, Appl
	702	58	1.5	247	22	US-09-534-843-15108	Sequence 15108, A
	703	58	1.5	247	59	US-60-039-128-32	Sequence 32, Appl
c	704	58	1.5	449	1	PCT-US01-00663-3715	Sequence 3715, Ap
c	705	58	1.5	449	35	US-09-864-761-10271	Sequence 10271, A
c	706	58	1.5	449	46	US-10-182-993-3613	Sequence 3613, Ap
c	707	58	1.5	449	47	US-10-203-134-3640	Sequence 3640, Ap
c	708	58	1.5	449	47	US-10-203-135-3621	Sequence 3621, Ap
c	709	58	1.5	449	47	US-10-203-136-3690	Sequence 3690, Ap
c	710	58	1.5	449	47	US-10-203-137-3715	Sequence 3715, Ap
c	711	58	1.5	449	47	US-10-203-138-3606	Sequence 3606, Ap
c	712	58	1.5	449	47	US-10-203-138A-3606	Sequence 3606, Ap
c	713	58	1.5	449	47	US-10-203-139-3686	Sequence 3686, Ap
c	714	58	1.5	449	80	US-60-236-359-4228	Sequence 4228, Ap
	715	58	1.5	10422	77	US-60-212-356-78	Sequence 78, Appl
	716	58	1.5	32768	77	US-60-213-177-328	Sequence 328, App
c	717	57	1.4	95	1	PCT-US01-00663-16876	Sequence 16876, A
c	718	57	1.4	95	35	US-09-864-761-26906	Sequence 26906, A
c	719	57	1.4	95	46	US-10-182-993-16366	Sequence 16366, A
c	720	57	1.4	95	47	US-10-203-134-16683	Sequence 16683, A
c	721	57	1.4	95	47	US-10-203-135-16161	Sequence 16161, A
c	722	57	1.4	95	47	US-10-203-136-16723	Sequence 16723, A
c	723	57	1.4	95	47	US-10-203-137-16876	Sequence 16876, A
c	724	57	1.4	95	47	US-10-203-138-8745	Sequence 8745, Ap
c	725	57	1.4	95	47	US-10-203-138A-8745	Sequence 8745, Ap
c	726	57	1.4	95	47	US-10-203-139-16287	Sequence 16287, A

c	727	57	1.4	95	80	US-60-236-359-11551	Sequence 11551, A
	728	57	1.4	201	107	US-60-500-337-83225	Sequence 83225, A
	729	57	1.4	303	1	PCT-US01-08631-1901	Sequence 1901, Ap
	730	56	1.4	201	107	US-60-500-337-83224	Sequence 83224, A
	731	56	1.4	201	107	US-60-500-337-83236	Sequence 83236, A
	732	56	1.4	403	16	US-09-248-797-3362	Sequence 3362, Ap
	733	56	1.4	403	18	US-09-346-956-1352	Sequence 1352, Ap
	734	56	1.4	403	37	US-09-904-703-1352	Sequence 1352, Ap
	735	56	1.4	403	38	US-09-925-564-3362	Sequence 3362, Ap
	736	55	1.4	186	72	US-60-162-245-1548	Sequence 1548, Ap
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c	738	55	1.4	199	1	PCT-IB03-04491-18457	Sequence 18457, A
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	740	53	1.3	253	16	US-09-229-412-231	Sequence 231, App
	741	53	1.3	253	22	US-09-534-843-21737	Sequence 21737, A
	742	53	1.3	265	19	US-09-370-505-3936	Sequence 3936, Ap
	743	53	1.3	265	22	US-09-534-843-21738	Sequence 21738, A
	744	53	1.3	265	65	US-60-096-463-3936	Sequence 3936, Ap
	745	53	1.3	288	15	US-09-145-501-4594	Sequence 4594, Ap
	746	53	1.3	288	22	US-09-534-843-21732	Sequence 21732, A
	747	53	1.3	311	20	US-09-428-151A-6910	Sequence 6910, Ap
	748	53	1.3	514	28	US-09-667-617-1117	Sequence 1117, Ap
	749	53	1.3	3903	48	US-10-261-175A-4	Sequence 4, Appli
	750	53	1.3	4849	45	US-10-144-771-21878	Sequence 21878, A
	751	53	1.3	4849	93	US-60-360-207-21878	Sequence 21878, A
	752	51	1.3	51	89	US-60-324-185-5558	Sequence 5558, Ap
	753	51	1.3	247	31	US-09-726-174-3836	Sequence 3836, Ap
	754	51	1.3	438	27	US-09-652-916-1055	Sequence 1055, Ap
	755	51	1.3	450	6	US-08-276-163A-2615	Sequence 2615, Ap
	756	51	1.3	450	6	US-08-276-163B-2615	Sequence 2615, Ap
	757	51	1.3	450	6	US-08-276-163D-2615	Sequence 2615, Ap
	758	51	1.3	450	34	US-09-840-145-2615	Sequence 2615, Ap
	759	51	1.3	450	37	US-09-912-293-27579	Sequence 27579, A
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	761	48	1.2	265	23	US-09-540-233D-105963	Sequence 105963,
	762	47	1.2	275	30	US-09-704-424-27124	Sequence 27124, A
	763	47	1.2	337	1	PCT-US01-08631-24008	Sequence 24008, A
	764	47	1.2	337	19	US-09-362-510-33281	Sequence 33281, A
	765	47	1.2	337	19	US-09-362-510A-33281	Sequence 33281, A
	766	47	1.2	337	37	US-09-904-013-33281	Sequence 33281, A
	767	47	1.2	404	20	US-09-436-762A-34872	Sequence 34872, A
	768	47	1.2	835	107	US-60-507-481-5397	Sequence 5397, Ap
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	770	47	1.2	896	42	US-09-980-464-1	Sequence 1, Appli
	771	47	1.2	896	50	US-10-355-975-1	Sequence 1, Appli
	772	47	1.2	896	50	US-10-355-975A-1	Sequence 1, Appli
	773	46	1.2	201	107	US-60-500-337-83203	Sequence 83203, A
	774	45	1.1	332	12	US-08-822-575-432	Sequence 432, App
	775	45	1.1	332	22	US-09-534-843-15119	Sequence 15119, A
	776	45	1.1	332	57	US-60-013-744-432	Sequence 432, App
	777	45	1.1	416	32	US-09-770-175-5468	Sequence 5468, Ap
	778	44	1.1	275	15	US-09-187-860-164	Sequence 164, App
	779	44	1.1	275	23	US-09-540-233D-123206	Sequence 123206,
	780	44	1.1	447	19	US-09-371-508-2857	Sequence 2857, Ap
	781	44	1.1	447	19	US-09-371-508-2857	Sequence 2857, Ap
	782	44	1.1	447	31	US-09-747-508-2857	Sequence 2857, Ap
	783	44	1.1	501	19	US-09-371-508-2848	Sequence 2848, Ap
	784	44	1.1	501	19	US-09-371-508-2848	Sequence 2848, Ap
	785	44	1.1	501	31	US-09-747-508-2848	Sequence 2848, Ap
	786	44	1.1	1488	32	US-09-789-390-31	Sequence 31, Appl
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	788	44	1.1	1725	32	US-09-789-390-36	Sequence 36, Appl
	789	44	1.1	1788	32	US-09-789-390-33	Sequence 33, Appl
	790	44	1.1	3872	45	US-10-144-771-3896	Sequence 3896, Ap
	791	44	1.1	3872	93	US-60-360-207-3896	Sequence 3896, Ap
	792	43	1.1	115	14	US-09-050-815-2042	Sequence 2042, Ap
	793	43	1.1	115	22	US-09-534-843-15148	Sequence 15148, A
	794	42	1.1	1716	17	US-09-270-767-11940	Sequence 11940, A
	795	42	1.1	1746	72	US-60-167-217-4204	Sequence 4204, Ap
	796	42	1.1	4635	25	US-09-614-150-25097	Sequence 25097, A
	797	42	1.1	4635	25	US-09-614-150A-25097	Sequence 25097, A
	798	42	1.1	4635	75	US-60-191-637-25210	Sequence 25210, A
	799	42	1.1	4635	75	US-60-191-681-19843	Sequence 19843, A

	800	42	1.1	4741	70	US-60-146-315-131	Sequence 131, App
c	801	42	1.1	5419	72	US-60-167-217-4203	Sequence 4203, Ap
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	848	32	0.8	265	13	US-08-971-197C-5994	Sequence 5994, Ap
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ALIGNMENTS

RESULT 1
US-10-029-115-1
; Sequence 1, Application US/10029115
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: Novel Germinal Center Kinase Cell Cycle Protiens, Compositions an
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: A-70229/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 3951
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-1

  Query Match             100.0%;  Score 3951;  DB 43;  Length 3951;
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Db        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC 900

Qy        901 CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG 960

Qy        961 ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG 1020

Qy       1021 CCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTC 1080
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Db       1021 CCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTC 1080

Qy       1081 CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAG 1140

Qy       1141 CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA 1200

Qy       1201 GAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG 1260

Qy       1261 CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG 1320

Qy       1321 GAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG 1380

Qy       1381 CAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCC 1440

Qy       1441 CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCT 1500

Qy       1501 GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC 1560

Qy       1561 TGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC 1620

Qy       1621 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCC 1680

Qy       1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG 1740

Qy       1741 CACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC 1800
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Db       1741 CACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC 1800

Qy       1801 CCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGC 1860
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Db       1801 CCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGC 1860

Qy       1861 CAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC 1920
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Db       1861 CAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC 1920

Qy       1921 CGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCC 1980
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Db       1921 CGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCC 1980

Qy       1981 CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGC 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGC 2040
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Qy       2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100
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Db       2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100

Qy       2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160
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Db       2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160

Qy       2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220

Qy       2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280

Qy       2281 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGG 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGG 2340

Qy       2341 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAG 2400
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Db       2341 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAG 2400

Qy       2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460
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Db       2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460

Qy       2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520
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Db       2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520

Qy       2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580

Qy       2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640
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Db       2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640

Qy       2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700
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Db       2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700

Qy       2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760
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Db       2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760

Qy       2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820
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Db       2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820

Qy       2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880

Qy       2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940
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Db       2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940

Qy       2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000
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Db       2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000

Qy       3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060
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Db       3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060

Qy       3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120
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Db       3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120

Qy       3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180

Qy       3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240
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Db       3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240

Qy       3241 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC 3300
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Qy       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360
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Db       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360

Qy       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420
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Db       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420

Qy       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480

Qy       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540
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Db       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540

Qy       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600
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Db       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600

Qy       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660
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Qy       3661 ACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTG 3720
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Qy       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780
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Qy       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840
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Db       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840

Qy       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA 3900
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Qy       3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
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RESULT 2
PCT-US02-33845-2
; Sequence 2, Application PC/TUS0233845
; GENERAL INFORMATION:
;  APPLICANT: Rigel Pharmaceuticals, Inc.
;  APPLICANT:  Leo, Cindy
;  APPLICANT:  Luo, Ying
;  APPLICANT:  Xu, Xiang
;  APPLICANT:  Yu, Simon
;  TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE PROTEINS, COMPOSITIONS,
;  TITLE OF INVENTION:  AND METHODS OF THEIR USE
;  FILE REFERENCE: 021044-005600PC
;  CURRENT APPLICATION NUMBER: PCT/US02/33845
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: US 10/029,115
;  PRIOR FILING DATE: 2001-10-19
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;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 3951
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: misshapen/NIK-related kinase isoform 3a
PCT-US02-33845-2

  Query Match             83.2%;  Score 3288;  DB 1;  Length 3951;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 3948;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    5;

Qy          1 GCCCTTATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTG 60
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Qy        121 GTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC 180
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Qy        181 ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC 240
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Db        241 CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGAT 300

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Qy        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420
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Db        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420

Qy        421 AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT 480
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Qy        481 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG 540
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Db        541 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG 600

Qy        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660
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Db        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660

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Qy        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780
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Db        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780

Qy        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840
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Db        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840

Qy        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCAT-CCGGGACCAGCCCACGGAGCGGCAGGT 899
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Db        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCCGGGACCAGCCCACGGAGCGGCAGGT 900

Qy        900 CCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGA 959
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Db        901 CCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGA 960

Qy        960 GACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGA 1019
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Db        961 GACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGA 1020

Qy       1020 GCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCT 1079
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Qy       1080 CCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCA 1139
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Db       1081 CCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCA 1140

Qy       1140 GCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCAT 1199
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Db       1141 GCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCAT 1200

Qy       1200 AGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCA 1259
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Db       1201 AGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCA 1260

Qy       1260 GCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCG 1319
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Db       1261 GCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCG 1320

Qy       1320 GGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGA 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGA 1380

Qy       1380 GCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTC 1439
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Db       1381 GCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTC 1440

Qy       1440 CCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCC 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCC 1500

Qy       1500 TGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGC 1559
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       1501 TGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG-ATCCCGCTGACAAACCAGC 1559

Qy       1560 CTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGC 1619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1560 CTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGC 1619

Qy       1620 CAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCC 1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1620 CAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCC 1679

Qy       1680 CCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACC 1739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1680 CCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACC 1739

Qy       1740 GCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGA 1799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1740 GCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGA 1799

Qy       1800 CCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCG 1859
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Qy       1860 CCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGT 1919
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Db       1860 CCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGT 1919

Qy       1920 CCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGC 1979
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Db       1920 CCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGC 1979
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Qy       1980 CCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCG 2039
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Qy       2040 CAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCC 2099
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Db       2040 CAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCC 2099

Qy       2100 TCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAG 2159
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Db       2100 TCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGA--TCAG 2157

Qy       2160 GAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCT 2219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2158 GAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCT 2217

Qy       2220 CCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTC 2279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2218 CCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTC 2277

Qy       2280 CCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCG 2339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2340 GCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAA 2399
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Db       2338 GCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAA 2397

Qy       2400 GAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGA 2459
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Qy       2460 GGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGG 2519
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Db       2458 GGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGG 2517

Qy       2520 GGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCA 2579
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Qy       2580 GCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCT 2639
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Qy       2640 GCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTC 2699
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Db       2638 GCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTC 2697

Qy       2700 ACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCA 2759
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Db       2698 ACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCA 2757

Qy       2760 GTCTCGTGGGCTGGTAAAGGCCCCTGGC-AAGAGCTCGTTCACGATGTTTGTGGATCTAG 2818
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Db       2758 GTCTCGTGGGCTGGTAAAGGCCCCTGGCAAAGAGCTCGTTCACGATGTTTGTGGATCTAG 2817

Qy       2819 GGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAG 2878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2879 AGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGA 2938
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Qy       2939 ATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGAT 2998
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Qy       2999 TCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGA 3058
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Qy       3059 ACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGC 3118
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Qy       3119 GACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGA 3178
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Qy       3179 AAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATG 3238
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Qy       3239 ACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGC 3298
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Qy       3419 CCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCA 3478
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Qy       3479 AGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCT 3538
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Db       3478 AGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCT 3537

Qy       3539 ATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCC 3598
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Db       3538 ATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCC 3597

Qy       3599 TCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTC- 3657
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Db       3598 TCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCA 3657

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Qy       3718 GTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGC 3777
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Qy       3778 TCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAG 3837
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Qy       3898 CAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
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RESULT 3
PCT-US03-37730-22
; Sequence 22, Application PC/TUS0337730
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: MAPKs AS MODIFIERS OF THE RAC, AXIN, AND BETA-CATENIN PATHWAYS
;  TITLE OF INVENTION:  AND METHODS OF USE
;  FILE REFERENCE: EX03-089C-PC
;  CURRENT APPLICATION NUMBER: PCT/US03/37730
;  CURRENT FILING DATE:  2003-11-24
;  PRIOR APPLICATION NUMBER: US 60/429,061
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: US 60/437,163
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; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 5014
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-37730-22

  Query Match             55.7%;  Score 2201;  DB 1;  Length 5014;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
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Qy       2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
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Qy       2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
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Db       2595 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2654

Qy       2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
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Db       3015 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 3074

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
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Qy       2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
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Db       3195 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3254

Qy       3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
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Db       3255 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3314

Qy       3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3315 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3374

Qy       3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
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Qy       3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
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Qy       3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
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Db       3495 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3554

Qy       3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
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Db       3555 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3614

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Qy       3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3795 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3854

Qy       3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3855 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3914

Qy       3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3915 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3974

Qy       3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3975 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 4034

Qy       3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4035 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 4094

Qy       3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4095 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 4154

Qy       3905 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||||
Db       4155 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4195
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RESULT 4
PCT-US03-37730-26
; Sequence 26, Application PC/TUS0337730
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MAPKs AS MODIFIERS OF THE RAC, AXIN, AND BETA-CATENIN PATHWAYS
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: EX03-089C-PC
; CURRENT APPLICATION NUMBER: PCT/US03/37730
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 60/429,061
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 60/437,163
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 4989
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-37730-26

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  Query Match             53.1%;  Score 2099;  DB 1;  Length 4989;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2199;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1995 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 2054

Qy       1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2055 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 2114

Qy       1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2115 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 2174

Qy       1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2175 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2234

Qy       1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2235 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2294

Qy       2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2295 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2354

Qy       2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2355 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2414

Qy       2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2415 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2474

Qy       2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
              ||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||
Db       2475 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2534

Qy       2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2535 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2594

Qy       2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2595 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2654

Qy       2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2655 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2714

Qy       2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2715 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2774

Qy       2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2775 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2834

Qy       2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2835 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2894

Qy       2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2895 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2954

Qy       2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2955 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 3014

Qy       2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3015 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 3074

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3075 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 3134

Qy       2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3135 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 3194

Qy       2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3195 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3254

Qy       3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3255 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3314

Qy       3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3315 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3374

Qy       3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3375 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3434

Qy       3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3435 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3494

Qy       3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3495 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3554
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Qy       3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3555 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3614

Qy       3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3615 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3674

Qy       3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3675 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3734

Qy       3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3735 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3794

Qy       3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3795 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3854

Qy       3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3855 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3914

Qy       3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3915 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3974

Qy       3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3975 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 4034

Qy       3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4035 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 4094

Qy       3845 GTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
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Db       4095 GTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 4154

Qy       3905 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||||
Db       4155 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4195
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RESULT 5
US-60-324-185-5555
; Sequence 5555, Application US/60324185
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
;  TITLE OF INVENTION:  POLYMORPHISMS IDENTIFIED THEREBY
;  FILE REFERENCE: GX-0019-1 P
;  CURRENT APPLICATION NUMBER: US/60/324,185
;  CURRENT FILING DATE:  2001-09-21
;  NUMBER OF SEQ ID NOS: 35862
;  SOFTWARE: PERL Program
; SEQ ID NO 5555
;   LENGTH: 5191
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 1098431.17
US-60-324-185-5555

  Query Match             51.8%;  Score 2048;  DB 89;  Length 5191;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2198;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy       1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2205 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 2264

Qy       1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2265 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 2324

Qy       1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2325 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 2384

Qy       1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2385 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2444

Qy       1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2445 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2504

Qy       2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2505 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2564

Qy       2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2565 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2624

Qy       2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2625 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2684

Qy       2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
              ||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||
Db       2685 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2744

Qy       2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2745 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2804

Qy       2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2805 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2864

Qy       2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2865 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2924

Qy       2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2925 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2984

Qy       2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2985 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 3044

Qy       2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3045 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 3104

Qy       2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3105 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 3164

Qy       2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       3165 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCAAAGGATGGGAGTGGTGACTACCAGTCTC 3224

Qy       2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3225 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 3284

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3285 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 3344

Qy         2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3345 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 3404

Qy         2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3405 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3464

Qy         3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3465 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3524

Qy         3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3525 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3584

Qy         3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3585 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3644

Qy         3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3645 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3704

Qy         3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3705 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3764

Qy         3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3765 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3824

Qy         3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3825 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3884

Qy         3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3885 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3944

Qy         3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3945 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 4004

Qy         3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4005 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 4064

Qy         3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4065 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 4124

Qy         3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4125 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 4184

Qy         3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4185 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 4244

Qy         3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4245 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 4304

Qy         3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4305 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 4364

Qy         3905 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
                |||||||||||||||||||||||||||||||||||||||||
Db         4365 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4405
```

RESULT 6
US-10-029-115-5
; Sequence 5, Application US/10029115
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: Novel Germinal Center Kinase Cell Cycle Protiens, Compositions an
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: A-70229/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 4033
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-5

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  Query Match             48.3%;  Score 1907;  DB 43;  Length 4033;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2197;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy         1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1836 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1895

Qy         1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1896 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1955

Qy         1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1956 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 2015

Qy         1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2016 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2075

Qy         1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2076 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2135

Qy         2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2136 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2195

Qy         2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2196 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2255

Qy         2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2256 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2315

Qy         2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2316 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2375

Qy         2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2376 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2435

Qy         2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2436 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2495

Qy         2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        2496 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2555

Qy        2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
               |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        2556 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2612

Qy        2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2613 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2672

Qy        2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2673 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2732

Qy        2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2733 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2792

Qy        2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2793 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2852

Qy        2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2853 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2912

Qy        2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2913 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2972

Qy        2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2973 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 3032

Qy        2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3033 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3092

Qy        3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3093 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3152

Qy        3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3153 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3212

Qy        3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3213 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3272

Qy        3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3273 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3332

Qy        3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3333 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3392

Qy        3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3393 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3452

Qy        3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3453 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3512

Qy        3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3513 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3572

Qy        3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
               |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        3573 TCTATGGCTCCAGTGCTGGCTTCCATGCTGCGGATGTCGACTCGGGGAACAGCTATGACA 3632

Qy        3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3633 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3692

Qy        3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3693 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3752

Qy        3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3753 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3812

Qy        3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3813 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3872

Qy        3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3873 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3932

Qy        3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3933 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3992

Qy        3905 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
               |||||||||||||||||||||||||||||||||||||||||
Db        3993 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4033


RESULT 7
US-10-725-121-11
; Sequence 11, Application US/10725121
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0328
;  CURRENT APPLICATION NUMBER: US/10/725,121
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: US/09/688,188B
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 09/291,417
;  PRIOR FILING DATE: 1999-04-14
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-725-121-11

  Query Match             45.2%;  Score 1787;  DB 54;  Length 4133;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2177;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy        1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1784 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1843

Qy        1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1844 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1903

Qy        1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1904 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1963

Qy        1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1964 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2023

Qy    1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2024 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2083

Qy    2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2084 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2143

Qy    2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2144 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2203

Qy    2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2204 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2263

Qy    2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
           ||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||
Db    2264 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2323

Qy    2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2324 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2383

Qy    2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2384 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2443

Qy    2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2444 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2503

Qy    2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
           |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db    2504 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2560

Qy    2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2561 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2620

Qy    2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2621 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2680

Qy    2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2681 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2740

Qy    2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2741 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2800

Qy    2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2801 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2860

Qy    2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2861 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2920

Qy    2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2921 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2980

Qy    2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2981 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3040

Qy    3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3041 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3100

Qy    3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3101 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3160

Qy    3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3161 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3220

Qy    3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    3221 ACAAACTGCGGGTGTATTACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3280

Qy    3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3281 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3340

Qy    3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3341 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3400

Qy    3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3401 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3460

Qy    3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3461 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3520

Qy    3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3521 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3580

Qy    3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3581 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3640

Qy    3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3641 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3700

Qy    3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3701 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3760

Qy    3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3761 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3820

Qy    3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3821 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3880

Qy    3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3881 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3940

Qy    3905 ACTTCATGACTCTGAACCGTAAC 3927
           |||||||||||||||||||||||
Db    3941 ACTTCATGACTCTGAACCGTAAC 3963
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RESULT 8
US-10-725-329-11
; Sequence 11, Application US/10725329
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0328
;  CURRENT APPLICATION NUMBER: US/10/725,329
;  CURRENT FILING DATE:  2003-12-02
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;  PRIOR APPLICATION NUMBER: US/09/688,188B
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 09/291,417
;  PRIOR FILING DATE: 1999-04-14
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-725-329-11

  Query Match             45.2%;  Score 1787;  DB 54;  Length 4133;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2177;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy       1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1784 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1843

Qy       1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1844 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1903

Qy       1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1904 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1963

Qy       1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1964 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2023

Qy       1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2024 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2083

Qy       2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2084 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2143

Qy       2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2144 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2203

Qy       2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2204 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2263

Qy       2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
              ||||||||||||||||||||||||||||||||| |||||||||| |||||||||||||||
Db       2264 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2323

Qy       2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2324 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2383

Qy       2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2384 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2443

Qy       2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2444 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2503

Qy       2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
              |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       2504 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2560

Qy       2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2561 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2620

Qy       2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2621 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2680

Qy       2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
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Db       2681 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2740

Qy       2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2741 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2800

Qy       2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2801 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2860

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2861 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2920

Qy       2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2921 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2980

Qy       2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2981 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3040

Qy       3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3041 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3100

Qy       3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3101 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3160

Qy       3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3161 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3220

Qy       3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
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Db       3221 ACAAACTGCGGGTGTATTACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3280

Qy       3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3281 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3340

Qy       3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3341 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3400

Qy       3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3401 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3460

Qy       3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3461 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3520

Qy       3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3521 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3580

Qy       3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3581 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3640

Qy       3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3641 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3700
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Qy       3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGAGATGCCTACTTCTGTGGCCT 3724
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Db       3701 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGAGATGCCTACTTCTGTGGCCT 3760

Qy       3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
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Db       3761 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3820

Qy       3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
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Db       3821 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3880

Qy       3845 GTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
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Db       3881 GTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3940

Qy       3905 ACTTCATGACTCTGAACCGTAAC 3927
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Db       3941 ACTTCATGACTCTGAACCGTAAC 3963


RESULT 9
US-10-725-330-11
; Sequence 11, Application US/10725330
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0328
;  CURRENT APPLICATION NUMBER: US/10/725,330
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: US/09/688,188B
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 09/291,417
;  PRIOR FILING DATE: 1999-04-14
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-725-330-11

  Query Match             45.2%;  Score 1787;  DB 54;  Length 4133;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2177;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy       1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1784 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1843

Qy       1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
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Db       1844 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1903

Qy       1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1904 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1963

Qy       1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1964 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2023

Qy       1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2024 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2083

Qy       2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
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Db       2084 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2143

Qy       2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
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Db       2144 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2203

Qy       2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
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Db       2204 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2263

Qy       2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
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Db       2264 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2323

Qy       2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
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Db       2324 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2383

Qy       2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2384 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2443

Qy       2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
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Db       2444 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2503

Qy       2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
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Db       2504 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2560

Qy       2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
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Db       2561 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2620

Qy       2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
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Db       2621 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2680

Qy       2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
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Db       2681 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2740

Qy       2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2741 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2800

Qy       2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2801 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2860

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2861 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2920

Qy       2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2921 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2980

Qy       2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2981 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3040

Qy       3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3041 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3100

Qy       3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3101 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3160

Qy       3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3161 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3220
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Qy        3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
               |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        3221 ACAAACTGCGGGTGTATTACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3280

Qy        3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGACATGGAGGGCTGCGGGCACTACC 3304
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3281 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGACATGGAGGGCTGCGGGCACTACC 3340

Qy        3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3341 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3400

Qy        3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3401 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3460

Qy        3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3461 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3520

Qy        3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3521 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3580

Qy        3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3581 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3640

Qy        3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3641 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3700

Qy        3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3701 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3760

Qy        3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3761 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3820

Qy        3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3821 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3880

Qy        3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3881 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3940

Qy        3905 ACTTCATGACTCTGAACCGTAAC 3927
               |||||||||||||||||||||||
Db        3941 ACTTCATGACTCTGAACCGTAAC 3963
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RESULT 10
US-60-081-784-11
; Sequence 11, Application US/60081784
; GENERAL INFORMATION:
;   APPLICANT: GREGORY PLOWMAN and
;   APPLICANT: RICARDO MARTINEZ
;   TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;   NUMBER OF SEQUENCES: 95
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Lyon & Lyon
;   STREET: 633 West Fifth Street
;   STREET: Suite 4700
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: U.S.A.
;   ZIP: 90071-2066
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   MEDIUM TYPE: storage
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: IBM P.C. DOS 5.0
;   SOFTWARE: FastSEQ for Windows 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/60/081,784
;   FILING DATE: Filed Herewith
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Warburg, Richard J.
;   REGISTRATION NUMBER: 32,327
;   REFERENCE/DOCKET NUMBER: 232/279
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (213) 489-1600
;   TELEFAX: (213) 955-0440
;   TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4133 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   FEATURE:
;   OTHER INFORMATION: Mammalian (Human) ZC3
US-60-081-784-11

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  Query Match             45.2%;  Score 1787;  DB 64;  Length 4133;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2177;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy        1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1784 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1843

Qy        1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1844 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1903

Qy        1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1904 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1963

Qy        1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1964 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2023

Qy        1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2024 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2083

Qy        2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2084 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2143

Qy        2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2144 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2203

Qy        2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2204 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2263

Qy        2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCTCCTCCAAACTGGACAGCTCCCCTG 2284
               |||||||||||||||||||||||||||||||||||| |||||||||| |||||||||||||
Db        2264 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2323

Qy        2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2324 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2383

Qy        2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        2384 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2443

Qy        2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2444 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2503

Qy        2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCTGGGGGCCGCAGCGATGGGGATA 2524
               ||||||||||||||||||||||||||||||||||||||||||||   |||||||||||||
Db        2504 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCTGGGGGCC---GCGATGGGGATA 2560

Qy        2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2561 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2620

Qy        2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2621 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2680

Qy        2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2681 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2740

Qy        2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2741 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2800

Qy        2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2801 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2860

Qy        2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2861 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2920

Qy        2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2921 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2980

Qy        2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2981 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3040

Qy        3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3041 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3100

Qy        3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3101 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3160

Qy        3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3161 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3220

Qy        3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
               |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        3221 ACAAACTGCGGGTGTATTACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3280

Qy        3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3281 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3340

Qy        3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3341 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3400

Qy        3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3401 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3460

Qy        3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3461 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3520

Qy        3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3521 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3580

Qy        3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3581 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3640

Qy        3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3641 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3700

Qy        3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3701 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3760

Qy        3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3761 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3820

Qy        3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3821 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3880

Qy        3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3881 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3940

Qy        3905 ACTTCATGACTCTGAACCGTAAC 3927
               |||||||||||||||||||||||
Db        3941 ACTTCATGACTCTGAACCGTAAC 3963


RESULT 11
PCT-US02-33845-6
; Sequence 6, Application PC/TUS0233845
; GENERAL INFORMATION:
;  APPLICANT: Rigel Pharmaceuticals, Inc.
;  APPLICANT:  Leo, Cindy
;  APPLICANT:  Luo, Ying
;  APPLICANT:  Xu, Xiang
;  APPLICANT:  Yu, Simon
;  TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE PROTEINS, COMPOSITIONS,
;  TITLE OF INVENTION:  AND METHODS OF THEIR USE
;  FILE REFERENCE: 021044-005600PC
;  CURRENT APPLICATION NUMBER: PCT/US02/33845
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: US 10/029,115
;  PRIOR FILING DATE: 2001-10-19
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 4032
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: misshapen/NIK-related Kinase isoform c
PCT-US02-33845-6

  Query Match             43.4%;  Score 1714;  DB 1;  Length 4032;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2154;  Conservative    0;  Mismatches    4;  Indels    3;  Gaps    1;

Qy        1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1836 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1895

Qy        1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1896 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1955

Qy        1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
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Db   1956 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTTCCGC 2015

Qy   1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
Db   2016 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2075

Qy   1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
Db   2076 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2135

Qy   2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
Db   2136 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2195

Qy   2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
Db   2196 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2255

Qy   2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
Db   2256 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2315

Qy   2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
Db   2316 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2375

Qy   2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
Db   2376 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2435

Qy   2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
Db   2436 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2495

Qy   2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
Db   2496 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2555

Qy   2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
Db   2556 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2612

Qy   2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
Db   2613 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2672

Qy   2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
Db   2673 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2732

Qy   2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
Db   2733 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2792

Qy   2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
Db   2793 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2852

Qy   2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
Db   2853 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2912

Qy   2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
Db   2913 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2972

Qy   2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
Db   2973 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 3032

Qy   2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
Db   3033 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3092

Qy   3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
Db   3093 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3152

Qy   3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
Db   3153 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3212

Qy   3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
Db   3213 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3272

Qy   3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
Db   3273 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3332

Qy   3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
Db   3333 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3392

Qy   3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
Db   3393 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3452

Qy   3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
Db   3453 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3512

Qy   3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
Db   3513 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3572

Qy   3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
Db   3573 TCTATGGCTCCAGTGCTGGCTTCCATGCTGCGGATGTCGACTCGGGGAACAGCTATGACA 3632

Qy   3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
Db   3633 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3692

Qy   3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
Db   3693 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3752

Qy   3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
Db   3753 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3812

Qy   3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
Db   3813 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3872

Qy   3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
Db   3873 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3932

Qy   3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
Db   3933 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3992

Qy   3905 A 3905
Db   3993 A 3993
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RESULT 12
PCT-US02-01048-37
; Sequence 37, Application PC/TUS0201048
; GENERAL INFORMATION:
; APPLICANT: EXLIXIS, INC.
; TITLE OF INVENTION: Modulating Insulin Receptor Signaling

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;  FILE REFERENCE: EX02-001C-PC
;  CURRENT APPLICATION NUMBER: PCT/US02/01048
;  CURRENT FILING DATE:  2002-01-11
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 3888
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-01048-37

  Query Match             43.1%;  Score 1701;  DB 1;  Length 3888;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1801;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2143 AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCA 2202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCA 2145

Qy       2203 GCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCC 2262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2146 GCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCC 2205

Qy       2263 TCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCAC 2322
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2206 TCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCAC 2265

Qy       2323 CGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 CGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2325

Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2385

Qy       2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2445

Qy       2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2505

Qy       2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2565

Qy       2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2625

Qy       2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2685

Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2745

Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2746 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2805

Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2806 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2865

Qy       2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2866 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2925

Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGTCAACCTG 3042
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2926 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGTCAACCTG 2985

Qy       3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2986 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3045

Qy       3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3046 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3105

Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3106 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3165

Qy       3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3166 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3225

Qy       3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3226 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3285

Qy       3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3286 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3345

Qy       3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3346 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3405

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3406 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3465

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3466 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3525

Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3526 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3585

Qy       3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3586 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3645

Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3646 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3705

Qy       3763 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3706 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3765

Qy       3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3766 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3825

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3826 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3885

Qy       3943 TGA 3945
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Db       3886 TGA 3888

RESULT 13
PCT-US03-37730-21
; Sequence 21, Application PC/TUS0337730
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
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;  TITLE OF INVENTION: MAPKs AS MODIFIERS OF THE RAC, AXIN, AND BETA-CATENIN PATHWAYS
;  TITLE OF INVENTION:  AND METHODS OF USE
;  FILE REFERENCE: EX03-089C-PC
;  CURRENT APPLICATION NUMBER: PCT/US03/37730
;  CURRENT FILING DATE:  2003-11-24
;  PRIOR APPLICATION NUMBER: US 60/429,061
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: US 60/437,163
;  PRIOR FILING DATE: 2002-12-30
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 3888
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-37730-21

  Query Match             43.1%;  Score 1701;  DB 1;  Length 3888;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1801;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2143 AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCA 2202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCA 2145

Qy       2203 GCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCC 2262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2146 GCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCC 2205

Qy       2263 TCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCAC 2322
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2206 TCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCAC 2265

Qy       2323 CGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 CGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2325

Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2385

Qy       2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2445

Qy       2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2505

Qy       2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2565

Qy       2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2625

Qy       2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2685

Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2745

Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2746 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2805

Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2806 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2865

Qy       2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2866 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2925

Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2926 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 2985

Qy       3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2986 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3045

Qy       3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3046 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3105

Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3106 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3165

Qy       3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3166 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3225

Qy       3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3226 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3285

Qy       3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3286 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3345

Qy       3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3346 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3405

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3406 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3465

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3466 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3525

Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3526 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3585

Qy       3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3586 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3645

Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3646 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3705

Qy       3763 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3706 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3765

Qy       3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3766 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3825

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3826 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3885

Qy       3943 TGA 3945
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Db       3886 TGA 3888
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RESULT 14
US-10-466-162-37
; Sequence 37, Application US/10466162
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: Modulating Insulin Receptor Signaling
;  FILE REFERENCE: EX02-001C-PC
;  CURRENT APPLICATION NUMBER: US/10/466,162
;  CURRENT FILING DATE:  2003-07-11
;  PRIOR APPLICATION NUMBER: US 60/261,335
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US 60/261,694
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US 60/261,532
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US  60/261,361
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US  60/261,531
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US  60/261,457
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US  60/261,226
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US  60/261,304
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US  60/261,459
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US  60/261,456
;  PRIOR FILING DATE: 2001-01-12
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 3888
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-466-162-37

  Query Match            43.1%;  Score 1701;  DB 52;  Length 3888;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1801;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2143 AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCA 2202
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Qy       2203 GCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCC 2262
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Db       2146 GCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCC 2205

Qy       2263 TCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCAC 2322
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Qy       2323 CGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
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Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
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Qy       2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
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Qy       2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
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Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
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Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
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Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
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Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
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Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
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; Sequence 34328, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 34328
;   LENGTH: 4436
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-170-235-34328

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  Matches 1801;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy        2203 GCCTCTCACGGCACCTCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGAGCCTCC 2262
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(without alignments)
9646.236 Million cell updates/sec

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Perfect score: 3951
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 164199 seqs, 84230614 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328398

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1689	42.7	4863	6	US-10-764-503-30	Sequence 30, Appl
	2	26	0.7	219	1	PCT-US03-13184-20	Sequence 20, Appl
	3	26	0.7	219	6	US-10-424-986-20	Sequence 20, Appl
	4	26	0.7	549	1	PCT-US03-13184-19	Sequence 19, Appl
	5	26	0.7	549	6	US-10-424-986-19	Sequence 19, Appl
	6	26	0.7	676	6	US-10-767-701-26464	Sequence 26464, A
	7	26	0.7	3786	5	US-09-744-794C-46	Sequence 46, Appl
c	8	24	0.6	81440	6	US-10-451-467A-659	Sequence 659, App
	9	23	0.6	789	6	US-10-767-701-6073	Sequence 6073, Ap
c	10	22	0.6	196	5	US-09-941-492A-63	Sequence 63, Appl
	11	22	0.6	829	6	US-10-767-701-10485	Sequence 10485, A
	12	22	0.6	1123	6	US-10-767-701-11901	Sequence 11901, A
	13	22	0.6	1137	1	PCT-US04-02974-37	Sequence 37, Appl
	14	22	0.6	1137	6	US-10-770-668-37	Sequence 37, Appl
c	15	22	0.6	1139	6	US-10-767-701-2898	Sequence 2898, Ap
	16	21	0.5	561	6	US-10-767-701-1671	Sequence 1671, Ap
	17	21	0.5	1201	6	US-10-767-701-8758	Sequence 8758, Ap
	18	21	0.5	2120	6	US-10-451-467A-99	Sequence 99, Appl
	19	21	0.5	2342	6	US-10-451-467A-277	Sequence 277, App
	20	20	0.5	380	7	US-60-539-605-1	Sequence 1, Appli
c	21	20	0.5	422	6	US-10-767-701-290	Sequence 290, App
c	22	20	0.5	534	6	US-10-767-701-9406	Sequence 9406, Ap
	23	20	0.5	546	6	US-10-767-701-17879	Sequence 17879, A
	24	20	0.5	592	6	US-10-632-150-31	Sequence 31, Appl
	25	20	0.5	594	6	US-10-767-701-6154	Sequence 6154, Ap
	26	20	0.5	674	6	US-10-767-701-8311	Sequence 8311, Ap
	27	20	0.5	696	7	US-60-539-605-11	Sequence 11, Appl
	28	20	0.5	732	7	US-60-539-605-9	Sequence 9, Appli
	29	20	0.5	748	6	US-10-767-701-12843	Sequence 12843, A
	30	20	0.5	756	7	US-60-539-605-15	Sequence 15, Appl
	31	20	0.5	787	6	US-10-767-701-2200	Sequence 2200, Ap
	32	20	0.5	789	7	US-60-539-605-3	Sequence 3, Appli
	33	20	0.5	789	7	US-60-539-605-17	Sequence 17, Appl
	34	20	0.5	927	7	US-60-539-605-5	Sequence 5, Appli
c	35	20	0.5	1045	6	US-10-767-701-12721	Sequence 12721, A
c	36	20	0.5	1210	6	US-10-767-701-11200	Sequence 11200, A
	37	20	0.5	1434	6	US-10-767-701-11204	Sequence 11204, A
c	38	20	0.5	2220	6	US-10-767-701-14365	Sequence 14365, A
	39	20	0.5	2339	7	US-60-539-605-2	Sequence 2, Appli
	40	20	0.5	2559	1	PCT-IB03-06177-1	Sequence 1, Appli
	41	20	0.5	3218	6	US-10-451-467A-63	Sequence 63, Appl
	42	20	0.5	4257	6	US-10-451-467A-471	Sequence 471, App
c	43	19	0.5	201	6	US-10-767-471-4689	Sequence 4689, Ap
c	44	19	0.5	201	6	US-10-767-471-4694	Sequence 4694, Ap
c	45	19	0.5	201	6	US-10-767-471-4710	Sequence 4710, Ap
	46	19	0.5	201	6	US-10-767-471-26841	Sequence 26841, A
	47	19	0.5	226	6	US-10-767-701-26492	Sequence 26492, A
	48	19	0.5	270	6	US-10-767-701-21659	Sequence 21659, A
c	49	19	0.5	272	6	US-10-767-701-24869	Sequence 24869, A
	50	19	0.5	336	6	US-10-767-701-17448	Sequence 17448, A
	51	19	0.5	433	6	US-10-767-701-30222	Sequence 30222, A
c	52	19	0.5	451	6	US-10-767-701-24910	Sequence 24910, A
	53	19	0.5	522	6	US-10-767-701-28542	Sequence 28542, A
	54	19	0.5	528	6	US-10-767-701-3354	Sequence 3354, Ap
	55	19	0.5	580	6	US-10-767-701-9627	Sequence 9627, Ap
	56	19	0.5	599	6	US-10-767-701-29331	Sequence 29331, A
	57	19	0.5	612	6	US-10-767-701-23715	Sequence 23715, A
	58	19	0.5	633	6	US-10-767-701-5477	Sequence 5477, Ap
	59	19	0.5	634	6	US-10-767-701-4658	Sequence 4658, Ap
	60	19	0.5	648	6	US-10-767-701-14003	Sequence 14003, A
c	61	19	0.5	723	6	US-10-767-701-11717	Sequence 11717, A
	62	19	0.5	799	7	US-60-542-614-1	Sequence 1, Appli
	63	19	0.5	833	6	US-10-767-701-1395	Sequence 1395, Ap
	64	19	0.5	857	6	US-10-767-701-5729	Sequence 5729, Ap
c	65	19	0.5	871	6	US-10-767-701-643	Sequence 643, App
	66	19	0.5	1095	6	US-10-767-701-12574	Sequence 12574, A
	67	19	0.5	1311	6	US-10-767-471-248	Sequence 248, App
c	68	19	0.5	1365	6	US-10-767-471-238	Sequence 238, App
	69	19	0.5	1790	6	US-10-767-471-243	Sequence 243, App
	70	19	0.5	1847	6	US-10-767-701-14989	Sequence 14989, A
	71	19	0.5	1898	6	US-10-767-701-12922	Sequence 12922, A
	72	19	0.5	3064	6	US-10-767-471-247	Sequence 247, App
	73	19	0.5	3765	6	US-10-767-471-249	Sequence 249, App
	74	19	0.5	4226	6	US-10-767-471-254	Sequence 254, App
	75	19	0.5	4312	6	US-10-767-471-252	Sequence 252, App
	76	19	0.5	4386	6	US-10-767-471-251	Sequence 251, App
	77	19	0.5	4475	6	US-10-767-471-260	Sequence 260, App
	78	19	0.5	4622	6	US-10-767-471-268	Sequence 268, App
	79	19	0.5	4658	6	US-10-767-471-266	Sequence 266, App
	80	19	0.5	6543	1	PCT-US03-09534-34	Sequence 34, Appl
c	81	19	0.5	78568	6	US-10-767-471-10897	Sequence 10897, A
	82	19	0.5	87716	6	US-10-767-471-10648	Sequence 10648, A
	83	19	0.5	123504	6	US-10-767-471-10665	Sequence 10665, A
	84	19	0.5	388939	6	US-10-417-375A-4	Sequence 4, Appli
	85	18	0.5	196	6	US-10-767-471-5490	Sequence 5490, Ap
	86	18	0.5	196	6	US-10-767-471-5506	Sequence 5506, Ap
c	87	18	0.5	201	6	US-10-767-471-17761	Sequence 17761, A
c	88	18	0.5	201	6	US-10-767-471-17762	Sequence 17762, A
	89	18	0.5	201	6	US-10-767-471-44523	Sequence 44523, A
	90	18	0.5	359	6	US-10-767-701-19152	Sequence 19152, A
	91	18	0.5	366	6	US-10-767-701-28802	Sequence 28802, A
	92	18	0.5	383	6	US-10-767-701-29915	Sequence 29915, A
	93	18	0.5	395	6	US-10-767-701-19625	Sequence 19625, A
	94	18	0.5	405	6	US-10-767-701-11997	Sequence 11997, A
	95	18	0.5	410	6	US-10-767-701-19028	Sequence 19028, A
	96	18	0.5	423	6	US-10-767-701-28392	Sequence 28392, A
	97	18	0.5	435	6	US-10-767-701-18905	Sequence 18905, A
	98	18	0.5	455	6	US-10-767-701-1357	Sequence 1357, Ap
c	99	18	0.5	456	6	US-10-767-701-21212	Sequence 21212, A

	100	18	0.5	460	6	US-10-767-701-3412	Sequence 3412, Ap
	101	18	0.5	477	6	US-10-767-701-26820	Sequence 26820, A
	102	18	0.5	494	6	US-10-767-701-3943	Sequence 3943, Ap
	103	18	0.5	496	6	US-10-767-701-29400	Sequence 29400, A
	104	18	0.5	500	6	US-10-767-701-2229	Sequence 2229, Ap
	105	18	0.5	501	6	US-10-767-701-22229	Sequence 22229, A
	106	18	0.5	502	6	US-10-767-701-15126	Sequence 15126, A
c	107	18	0.5	504	6	US-10-767-701-29196	Sequence 29196, A
	108	18	0.5	519	6	US-10-767-701-1834	Sequence 1834, Ap
	109	18	0.5	519	6	US-10-767-701-30340	Sequence 30340, A
	110	18	0.5	522	6	US-10-767-701-22746	Sequence 22746, A
	111	18	0.5	527	6	US-10-767-701-4848	Sequence 4848, Ap
	112	18	0.5	546	6	US-10-767-701-24409	Sequence 24409, A
c	113	18	0.5	547	6	US-10-767-701-31235	Sequence 31235, A
c	114	18	0.5	548	6	US-10-767-701-2682	Sequence 2682, Ap
	115	18	0.5	553	6	US-10-767-701-4587	Sequence 4587, Ap
	116	18	0.5	555	6	US-10-767-701-29633	Sequence 29633, A
	117	18	0.5	556	6	US-10-767-701-25505	Sequence 25505, A
	118	18	0.5	558	6	US-10-767-701-7755	Sequence 7755, Ap
	119	18	0.5	560	6	US-10-767-701-3299	Sequence 3299, Ap
	120	18	0.5	569	6	US-10-767-701-25170	Sequence 25170, A
	121	18	0.5	578	6	US-10-767-701-1448	Sequence 1448, Ap
c	122	18	0.5	583	6	US-10-767-701-4088	Sequence 4088, Ap
	123	18	0.5	585	6	US-10-767-701-1791	Sequence 1791, Ap
c	124	18	0.5	587	6	US-10-767-701-22738	Sequence 22738, A
	125	18	0.5	588	6	US-10-767-701-27834	Sequence 27834, A
	126	18	0.5	589	6	US-10-767-701-4344	Sequence 4344, Ap
c	127	18	0.5	611	6	US-10-767-701-23677	Sequence 23677, A
	128	18	0.5	612	6	US-10-767-701-8499	Sequence 8499, Ap
c	129	18	0.5	613	6	US-10-767-701-2244	Sequence 2244, Ap
	130	18	0.5	614	6	US-10-767-701-9197	Sequence 9197, Ap
	131	18	0.5	622	6	US-10-767-701-5072	Sequence 5072, Ap
	132	18	0.5	622	6	US-10-767-701-11817	Sequence 11817, A
c	133	18	0.5	627	6	US-10-431-598-5	Sequence 5, Appli
	134	18	0.5	631	6	US-10-767-701-9519	Sequence 9519, Ap
	135	18	0.5	633	6	US-10-767-701-1350	Sequence 1350, Ap
	136	18	0.5	634	6	US-10-767-701-3370	Sequence 3370, Ap
	137	18	0.5	645	6	US-10-767-701-25169	Sequence 25169, A
	138	18	0.5	646	6	US-10-767-701-9518	Sequence 9518, Ap
	139	18	0.5	647	6	US-10-767-701-10027	Sequence 10027, A
	140	18	0.5	650	6	US-10-767-701-6316	Sequence 6316, Ap
	141	18	0.5	657	6	US-10-767-701-4804	Sequence 4804, Ap
	142	18	0.5	659	6	US-10-767-701-682	Sequence 682, App
c	143	18	0.5	664	6	US-10-767-701-5587	Sequence 5587, Ap
	144	18	0.5	664	6	US-10-767-701-24497	Sequence 24497, A
	145	18	0.5	665	6	US-10-767-701-9677	Sequence 9677, Ap
	146	18	0.5	669	6	US-10-767-701-20280	Sequence 20280, A
	147	18	0.5	670	6	US-10-767-701-2598	Sequence 2598, Ap
c	148	18	0.5	670	6	US-10-767-701-8560	Sequence 8560, Ap
c	149	18	0.5	678	6	US-10-767-701-23778	Sequence 23778, A
	150	18	0.5	679	6	US-10-767-701-4740	Sequence 4740, Ap
c	151	18	0.5	690	6	US-10-767-701-15365	Sequence 15365, A
	152	18	0.5	693	6	US-10-767-701-4646	Sequence 4646, Ap
c	153	18	0.5	698	6	US-10-767-701-8086	Sequence 8086, Ap
	154	18	0.5	713	6	US-10-767-701-1473	Sequence 1473, Ap
c	155	18	0.5	722	6	US-10-767-701-4805	Sequence 4805, Ap
	156	18	0.5	725	6	US-10-767-701-6434	Sequence 6434, Ap
	157	18	0.5	744	6	US-10-767-701-11827	Sequence 11827, A
	158	18	0.5	746	6	US-10-767-701-2535	Sequence 2535, Ap
	159	18	0.5	746	6	US-10-767-701-14278	Sequence 14278, A
c	160	18	0.5	749	6	US-10-767-701-334	Sequence 334, App
c	161	18	0.5	806	6	US-10-767-701-15366	Sequence 15366, A
	162	18	0.5	888	6	US-10-767-701-7871	Sequence 7871, Ap
	163	18	0.5	933	6	US-10-767-701-12899	Sequence 12899, A
	164	18	0.5	943	6	US-10-767-701-3249	Sequence 3249, Ap
c	165	18	0.5	956	6	US-10-767-701-1647	Sequence 1647, Ap
c	166	18	0.5	968	6	US-10-767-701-13099	Sequence 13099, A
c	167	18	0.5	978	6	US-10-431-598-1	Sequence 1, Appli
	168	18	0.5	1006	6	US-10-767-701-13927	Sequence 13927, A
	169	18	0.5	1014	6	US-10-767-701-12490	Sequence 12490, A
c	170	18	0.5	1016	6	US-10-431-598-7	Sequence 7, Appli
	171	18	0.5	1041	6	US-10-767-701-10776	Sequence 10776, A
c	172	18	0.5	1041	6	US-10-767-701-10776	Sequence 10776, A
	173	18	0.5	1068	6	US-10-767-701-6876	Sequence 6876, Ap
	174	18	0.5	1178	6	US-10-767-701-12496	Sequence 12496, A
c	175	18	0.5	1312	6	US-10-767-701-5404	Sequence 5404, Ap
	176	18	0.5	1450	6	US-10-767-701-14606	Sequence 14606, A
	177	18	0.5	1629	6	US-10-767-701-11626	Sequence 11626, A
c	178	18	0.5	1797	6	US-10-761-033-11	Sequence 11, Appl
c	179	18	0.5	1818	6	US-10-761-033-7	Sequence 7, Appli
	180	18	0.5	1854	6	US-10-469-992-9	Sequence 9, Appli
	181	18	0.5	1863	6	US-10-767-701-14295	Sequence 14295, A
c	182	18	0.5	1866	6	US-10-761-033-3	Sequence 3, Appli
	183	18	0.5	1884	6	US-10-767-701-13198	Sequence 13198, A
c	184	18	0.5	1971	6	US-10-761-033-9	Sequence 9, Appli
c	185	18	0.5	1992	6	US-10-761-033-5	Sequence 5, Appli
c	186	18	0.5	2036	1	PCT-US04-03417-47	Sequence 47, Appl
c	187	18	0.5	2036	6	US-10-772-636-47	Sequence 47, Appl
c	188	18	0.5	2040	6	US-10-761-033-1	Sequence 1, Appli
c	189	18	0.5	2178	6	US-10-765-790-155	Sequence 155, App
c	190	18	0.5	2420	6	US-10-761-033-13	Sequence 13, Appl
	191	18	0.5	2532	6	US-10-767-701-15518	Sequence 15518, A
	192	18	0.5	2844	6	US-10-767-471-280	Sequence 280, App
	193	18	0.5	3395	5	US-09-830-915D-19	Sequence 19, Appl
	194	18	0.5	6214	6	US-10-767-471-278	Sequence 278, App
	195	18	0.5	23875	6	US-10-767-471-10867	Sequence 10867, A
c	196	18	0.5	24142	6	US-10-451-467A-651	Sequence 651, App
	197	18	0.5	29976	6	US-10-767-471-10815	Sequence 10815, A
c	198	18	0.5	30753	6	US-10-765-790-24	Sequence 24, Appl
c	199	18	0.5	40000	6	US-10-767-471-10913	Sequence 10913, A
c	200	18	0.5	40911	6	US-10-767-471-10694	Sequence 10694, A
c	201	18	0.5	41665	6	US-10-767-471-10744	Sequence 10744, A
c	202	18	0.5	54303	6	US-10-417-375A-79	Sequence 79, Appl
	203	18	0.5	66412	6	US-10-417-375A-157	Sequence 157, App
c	204	18	0.5	100608	6	US-10-417-375A-108	Sequence 108, App
c	205	18	0.5	105077	6	US-10-417-375A-15	Sequence 15, Appl
c	206	18	0.5	122673	6	US-10-765-790-33	Sequence 33, Appl
c	207	18	0.5	129297	6	US-10-765-790-89	Sequence 89, Appl
c	208	18	0.5	165097	6	US-10-765-790-77	Sequence 77, Appl
	209	18	0.5	184809	6	US-10-767-471-10627	Sequence 10627, A
c	210	18	0.5	186191	6	US-10-767-471-10794	Sequence 10794, A
c	211	18	0.5	230101	6	US-10-767-471-10691	Sequence 10691, A
	212	18	0.5	261922	6	US-10-767-471-10653	Sequence 10653, A
c	213	18	0.5	310122	6	US-10-417-375A-1	Sequence 1, Appli
	214	18	0.5	350570	6	US-10-417-375A-146	Sequence 146, App
c	215	18	0.5	1126118	6	US-10-767-471-10615	Sequence 10615, A
c	216	18	0.5	1790242	6	US-10-767-471-10805	Sequence 10805, A
c	217	17	0.4	25	6	US-10-708-204-3982	Sequence 3982, Ap
c	218	17	0.4	27	1	PCT-US03-33433-35	Sequence 35, Appl
c	219	17	0.4	28	6	US-10-708-204-3966	Sequence 3966, Ap
c	220	17	0.4	117	6	US-10-700-740-68	Sequence 68, Appl
c	221	17	0.4	138	1	PCT-US03-34801-52	Sequence 52, Appl
c	222	17	0.4	181	6	US-10-767-701-24459	Sequence 24459, A
c	223	17	0.4	187	6	US-10-767-701-27648	Sequence 27648, A
c	224	17	0.4	196	6	US-10-767-701-6473	Sequence 6473, Ap
	225	17	0.4	201	6	US-10-767-471-3741	Sequence 3741, Ap
	226	17	0.4	201	6	US-10-767-471-3749	Sequence 3749, Ap
	227	17	0.4	201	6	US-10-767-471-3775	Sequence 3775, Ap
	228	17	0.4	201	6	US-10-767-471-3787	Sequence 3787, Ap
	229	17	0.4	201	6	US-10-767-471-3818	Sequence 3818, Ap
	230	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
	231	17	0.4	201	6	US-10-767-471-3852	Sequence 3852, Ap
	232	17	0.4	201	6	US-10-767-471-3864	Sequence 3864, Ap
	233	17	0.4	201	6	US-10-767-471-3896	Sequence 3896, Ap
	234	17	0.4	201	6	US-10-767-471-3904	Sequence 3904, Ap
	235	17	0.4	201	6	US-10-767-471-3930	Sequence 3930, Ap
	236	17	0.4	201	6	US-10-767-471-3943	Sequence 3943, Ap
	237	17	0.4	201	6	US-10-767-471-3990	Sequence 3990, Ap
	238	17	0.4	201	6	US-10-767-471-3994	Sequence 3994, Ap
	239	17	0.4	201	6	US-10-767-471-4020	Sequence 4020, Ap
	240	17	0.4	201	6	US-10-767-471-4021	Sequence 4021, Ap
c	241	17	0.4	201	6	US-10-767-471-4747	Sequence 4747, Ap
c	242	17	0.4	201	6	US-10-767-471-4784	Sequence 4784, Ap
c	243	17	0.4	201	6	US-10-767-471-4958	Sequence 4958, Ap
c	244	17	0.4	201	6	US-10-767-471-5026	Sequence 5026, Ap
c	245	17	0.4	201	6	US-10-767-471-5064	Sequence 5064, Ap

c 246	17	0.4	201	6	US-10-767-471-6185	Sequence 6185, Ap
c 247	17	0.4	201	6	US-10-767-471-6190	Sequence 6190, Ap
c 248	17	0.4	201	6	US-10-767-471-6202	Sequence 6202, Ap
c 249	17	0.4	201	6	US-10-767-471-6207	Sequence 6207, Ap
c 250	17	0.4	201	6	US-10-767-471-6218	Sequence 6218, Ap
c 251	17	0.4	201	6	US-10-767-471-6223	Sequence 6223, Ap
252	17	0.4	201	6	US-10-767-471-8730	Sequence 8730, Ap
253	17	0.4	201	6	US-10-767-471-8745	Sequence 8745, Ap
254	17	0.4	201	6	US-10-767-471-8759	Sequence 8759, Ap
255	17	0.4	201	6	US-10-767-471-8774	Sequence 8774, Ap
256	17	0.4	201	6	US-10-767-471-8792	Sequence 8792, Ap
257	17	0.4	201	6	US-10-767-471-8806	Sequence 8806, Ap
258	17	0.4	201	6	US-10-767-471-8821	Sequence 8821, Ap
259	17	0.4	201	6	US-10-767-471-10055	Sequence 10055, A
260	17	0.4	201	6	US-10-767-471-10076	Sequence 10076, A
261	17	0.4	201	6	US-10-767-471-10091	Sequence 10091, A
262	17	0.4	201	6	US-10-767-471-10129	Sequence 10129, A
c 263	17	0.4	201	6	US-10-767-471-12496	Sequence 12496, A
c 264	17	0.4	201	6	US-10-767-471-12567	Sequence 12567, A
c 265	17	0.4	201	6	US-10-767-471-13755	Sequence 13755, A
266	17	0.4	201	6	US-10-767-471-23029	Sequence 23029, A
267	17	0.4	201	6	US-10-767-471-23052	Sequence 23052, A
268	17	0.4	201	6	US-10-767-471-23059	Sequence 23059, A
269	17	0.4	201	6	US-10-767-471-23102	Sequence 23102, A
c 270	17	0.4	201	6	US-10-767-471-24199	Sequence 24199, A
c 271	17	0.4	201	6	US-10-767-471-24200	Sequence 24200, A
c 272	17	0.4	201	6	US-10-767-471-24255	Sequence 24255, A
c 273	17	0.4	201	6	US-10-767-471-24257	Sequence 24257, A
c 274	17	0.4	201	6	US-10-767-471-25442	Sequence 25442, A
c 275	17	0.4	201	6	US-10-767-471-25549	Sequence 25549, A
276	17	0.4	201	6	US-10-767-471-33002	Sequence 33002, A
277	17	0.4	201	6	US-10-767-471-34369	Sequence 34369, A
c 278	17	0.4	201	6	US-10-767-471-35078	Sequence 35078, A
c 279	17	0.4	201	6	US-10-767-471-35178	Sequence 35178, A
280	17	0.4	201	6	US-10-767-471-38208	Sequence 38208, A
281	17	0.4	201	6	US-10-767-471-38229	Sequence 38229, A
282	17	0.4	201	6	US-10-767-471-38245	Sequence 38245, A
283	17	0.4	201	6	US-10-767-471-38283	Sequence 38283, A
c 284	17	0.4	201	6	US-10-767-471-39214	Sequence 39214, A
c 285	17	0.4	201	6	US-10-767-471-39229	Sequence 39229, A
c 286	17	0.4	201	6	US-10-767-471-39285	Sequence 39285, A
c 287	17	0.4	201	6	US-10-767-471-39287	Sequence 39287, A
c 288	17	0.4	201	6	US-10-767-471-39288	Sequence 39288, A
289	17	0.4	201	6	US-10-767-471-39698	Sequence 39698, A
290	17	0.4	201	6	US-10-767-471-39699	Sequence 39699, A
291	17	0.4	201	6	US-10-767-471-39700	Sequence 39700, A
292	17	0.4	201	6	US-10-767-471-39718	Sequence 39718, A
293	17	0.4	201	6	US-10-767-471-39733	Sequence 39733, A
294	17	0.4	201	6	US-10-767-471-44426	Sequence 44426, A
295	17	0.4	201	6	US-10-767-471-44443	Sequence 44443, A
296	17	0.4	201	6	US-10-767-471-44447	Sequence 44447, A
c 297	17	0.4	201	6	US-10-767-471-45383	Sequence 45383, A
c 298	17	0.4	201	6	US-10-767-471-45388	Sequence 45388, A
299	17	0.4	238	6	US-10-767-701-15870	Sequence 15870, A
c 300	17	0.4	255	6	US-10-767-701-22990	Sequence 22990, A
301	17	0.4	266	6	US-10-767-701-19118	Sequence 19118, A
302	17	0.4	314	6	US-10-767-701-30314	Sequence 30314, A
303	17	0.4	336	1	PCT-US03-13184-2	Sequence 2, Appli
304	17	0.4	336	6	US-10-424-986-2	Sequence 2, Appli
305	17	0.4	339	6	US-10-700-740-69	Sequence 69, Appl
306	17	0.4	346	6	US-10-767-701-18893	Sequence 18893, A
307	17	0.4	352	6	US-10-767-701-28943	Sequence 28943, A
308	17	0.4	355	6	US-10-767-701-19146	Sequence 19146, A
c 309	17	0.4	357	6	US-10-767-701-19038	Sequence 19038, A
310	17	0.4	363	6	US-10-767-701-17216	Sequence 17216, A
311	17	0.4	384	6	US-10-767-701-18970	Sequence 18970, A
c 312	17	0.4	390	6	US-10-770-021-374	Sequence 374, App
c 313	17	0.4	391	6	US-10-767-701-25638	Sequence 25638, A
314	17	0.4	406	6	US-10-767-701-25521	Sequence 25521, A
c 315	17	0.4	407	6	US-10-767-701-19303	Sequence 19303, A
316	17	0.4	411	6	US-10-767-701-18273	Sequence 18273, A
317	17	0.4	416	6	US-10-767-701-28694	Sequence 28694, A
318	17	0.4	421	6	US-10-767-701-21061	Sequence 21061, A
c 319	17	0.4	426	6	US-10-767-701-17752	Sequence 17752, A
c 320	17	0.4	426	6	US-10-773-236-183	Sequence 183, App
321	17	0.4	445	6	US-10-767-701-18790	Sequence 18790, A
322	17	0.4	449	6	US-10-767-701-20747	Sequence 20747, A
323	17	0.4	455	6	US-10-767-701-16556	Sequence 16556, A
324	17	0.4	455	6	US-10-767-701-22346	Sequence 22346, A
325	17	0.4	472	6	US-10-767-701-14585	Sequence 14585, A
c 326	17	0.4	473	6	US-10-767-701-28439	Sequence 28439, A
327	17	0.4	475	6	US-10-767-701-957	Sequence 957, App
328	17	0.4	477	6	US-10-767-701-22309	Sequence 22309, A
329	17	0.4	480	6	US-10-767-701-18177	Sequence 18177, A
330	17	0.4	482	6	US-10-767-701-13654	Sequence 13654, A
331	17	0.4	489	6	US-10-767-701-21098	Sequence 21098, A
332	17	0.4	490	6	US-10-767-701-15747	Sequence 15747, A
c 333	17	0.4	493	6	US-10-767-701-29436	Sequence 29436, A
334	17	0.4	493	6	US-10-767-701-31233	Sequence 31233, A
335	17	0.4	502	6	US-10-767-701-24439	Sequence 24439, A
336	17	0.4	507	6	US-10-767-701-22107	Sequence 22107, A
337	17	0.4	513	6	US-10-767-701-25544	Sequence 25544, A
338	17	0.4	514	6	US-10-767-701-1047	Sequence 1047, Ap
339	17	0.4	518	6	US-10-767-701-16187	Sequence 16187, A
340	17	0.4	519	6	US-10-767-701-4639	Sequence 4639, Ap
341	17	0.4	521	6	US-10-767-701-347	Sequence 347, App
342	17	0.4	524	6	US-10-767-701-28854	Sequence 28854, A
c 343	17	0.4	526	6	US-10-767-701-21490	Sequence 21490, A
344	17	0.4	527	6	US-10-767-701-24660	Sequence 24660, A
345	17	0.4	527	6	US-10-767-701-29434	Sequence 29434, A
346	17	0.4	528	6	US-10-767-701-3459	Sequence 3459, Ap
347	17	0.4	528	6	US-10-767-701-28700	Sequence 28700, A
c 348	17	0.4	529	6	US-10-767-701-1352	Sequence 1352, Ap
349	17	0.4	529	6	US-10-767-701-26767	Sequence 26767, A
350	17	0.4	531	6	US-10-767-701-3219	Sequence 3219, Ap
c 351	17	0.4	533	6	US-10-767-701-20525	Sequence 20525, A
352	17	0.4	534	6	US-10-767-701-2093	Sequence 2093, Ap
353	17	0.4	538	6	US-10-767-701-4099	Sequence 4099, Ap
354	17	0.4	538	6	US-10-767-701-25663	Sequence 25663, A
c 355	17	0.4	541	6	US-10-767-701-30710	Sequence 30710, A
356	17	0.4	546	6	US-10-767-701-26891	Sequence 26891, A
c 357	17	0.4	548	6	US-10-770-021-48	Sequence 48, Appl
358	17	0.4	549	6	US-10-767-701-22708	Sequence 22708, A
359	17	0.4	550	6	US-10-767-701-4187	Sequence 4187, Ap
c 360	17	0.4	553	6	US-10-767-701-1623	Sequence 1623, Ap
c 361	17	0.4	553	6	US-10-767-701-28729	Sequence 28729, A
c 362	17	0.4	556	6	US-10-767-701-31023	Sequence 31023, A
363	17	0.4	559	6	US-10-767-701-6197	Sequence 6197, Ap
364	17	0.4	562	6	US-10-767-701-26537	Sequence 26537, A
365	17	0.4	563	6	US-10-767-701-1936	Sequence 1936, Ap
366	17	0.4	564	6	US-10-767-701-30941	Sequence 30941, A
367	17	0.4	567	6	US-10-767-701-20568	Sequence 20568, A
368	17	0.4	567	6	US-10-767-701-24257	Sequence 24257, A
369	17	0.4	571	6	US-10-767-701-22450	Sequence 22450, A
370	17	0.4	571	6	US-10-767-701-25449	Sequence 25449, A
c 371	17	0.4	572	6	US-10-767-701-26285	Sequence 26285, A
372	17	0.4	575	6	US-10-767-701-15585	Sequence 15585, A
373	17	0.4	577	6	US-10-767-701-25575	Sequence 25575, A
c 374	17	0.4	578	6	US-10-767-701-15156	Sequence 15156, A
375	17	0.4	579	6	US-10-767-701-21829	Sequence 21829, A
376	17	0.4	580	6	US-10-767-701-4590	Sequence 4590, Ap
377	17	0.4	583	6	US-10-767-701-4088	Sequence 4088, Ap
c 378	17	0.4	583	6	US-10-767-701-6043	Sequence 6043, Ap
379	17	0.4	585	6	US-10-767-701-25344	Sequence 25344, A
380	17	0.4	590	6	US-10-767-701-24813	Sequence 24813, A
381	17	0.4	598	6	US-10-767-701-15161	Sequence 15161, A
382	17	0.4	598	6	US-10-767-701-23205	Sequence 23205, A
383	17	0.4	599	6	US-10-767-701-20919	Sequence 20919, A
c 384	17	0.4	604	6	US-10-767-701-6212	Sequence 6212, Ap
385	17	0.4	606	6	US-10-767-701-7068	Sequence 7068, Ap
c 386	17	0.4	606	6	US-10-767-701-30057	Sequence 30057, A
387	17	0.4	610	6	US-10-767-701-528	Sequence 528, App
388	17	0.4	613	6	US-10-767-701-6693	Sequence 6693, Ap
389	17	0.4	613	6	US-10-767-701-26438	Sequence 26438, A
390	17	0.4	614	6	US-10-767-701-22480	Sequence 22480, A
c 391	17	0.4	615	6	US-10-767-701-446	Sequence 446, App

	392	17	0.4	617	6	US-10-767-701-24499	Sequence 24499, A
	393	17	0.4	622	6	US-10-767-701-5162	Sequence 5162, Ap
	394	17	0.4	628	6	US-10-767-701-1475	Sequence 1475, Ap
	395	17	0.4	630	6	US-10-767-701-24256	Sequence 24256, A
	396	17	0.4	635	6	US-10-767-701-8878	Sequence 8878, Ap
	397	17	0.4	635	6	US-10-767-701-28748	Sequence 28748, A
c	398	17	0.4	635	6	US-10-773-236-166	Sequence 166, App
	399	17	0.4	639	6	US-10-767-701-25816	Sequence 25816, A
c	400	17	0.4	640	6	US-10-767-701-20022	Sequence 20022, A
	401	17	0.4	641	6	US-10-767-701-4739	Sequence 4739, Ap
c	402	17	0.4	643	6	US-10-767-701-23935	Sequence 23935, A
	403	17	0.4	646	6	US-10-767-701-8423	Sequence 8423, Ap
	404	17	0.4	646	6	US-10-767-701-24337	Sequence 24337, A
c	405	17	0.4	646	6	US-10-767-701-25564	Sequence 25564, A
	406	17	0.4	647	6	US-10-767-701-12518	Sequence 12518, A
c	407	17	0.4	648	6	US-10-767-701-6082	Sequence 6082, Ap
	408	17	0.4	651	6	US-10-767-701-7875	Sequence 7875, Ap
c	409	17	0.4	651	6	US-10-767-701-20291	Sequence 20291, A
c	410	17	0.4	658	6	US-10-767-701-4622	Sequence 4622, Ap
	411	17	0.4	658	6	US-10-767-701-25290	Sequence 25290, A
	412	17	0.4	660	6	US-10-767-701-2317	Sequence 2317, Ap
	413	17	0.4	664	6	US-10-767-701-21524	Sequence 21524, A
	414	17	0.4	665	6	US-10-767-701-5902	Sequence 5902, Ap
	415	17	0.4	666	6	US-10-767-701-4674	Sequence 4674, Ap
	416	17	0.4	666	6	US-10-767-701-5231	Sequence 5231, Ap
c	417	17	0.4	667	6	US-10-767-701-2774	Sequence 2774, Ap
	418	17	0.4	668	6	US-10-767-701-11335	Sequence 11335, A
	419	17	0.4	669	6	US-10-767-701-15584	Sequence 15584, A
	420	17	0.4	672	6	US-10-767-701-9244	Sequence 9244, Ap
	421	17	0.4	675	6	US-10-767-701-9163	Sequence 9163, Ap
c	422	17	0.4	675	6	US-10-767-701-25919	Sequence 25919, A
	423	17	0.4	681	6	US-10-767-701-7185	Sequence 7185, Ap
	424	17	0.4	684	6	US-10-767-701-10756	Sequence 10756, A
	425	17	0.4	692	6	US-10-767-701-14720	Sequence 14720, A
c	426	17	0.4	698	6	US-10-767-701-6049	Sequence 6049, Ap
	427	17	0.4	702	6	US-10-767-701-2548	Sequence 2548, Ap
c	428	17	0.4	704	6	US-10-767-701-3712	Sequence 3712, Ap
c	429	17	0.4	715	6	US-10-767-701-7305	Sequence 7305, Ap
	430	17	0.4	722	6	US-10-767-701-2037	Sequence 2037, Ap
c	431	17	0.4	722	6	US-10-767-701-4403	Sequence 4403, Ap
c	432	17	0.4	726	6	US-10-773-236-65	Sequence 65, Appl
c	433	17	0.4	734	6	US-10-767-701-5462	Sequence 5462, Ap
c	434	17	0.4	735	6	US-10-767-701-5312	Sequence 5312, Ap
	435	17	0.4	736	6	US-10-767-701-13868	Sequence 13868, A
	436	17	0.4	737	6	US-10-767-701-12728	Sequence 12728, A
	437	17	0.4	737	6	US-10-767-701-19718	Sequence 19718, A
c	438	17	0.4	742	6	US-10-767-701-10893	Sequence 10893, A
c	439	17	0.4	743	6	US-10-767-701-1452	Sequence 1452, Ap
c	440	17	0.4	749	6	US-10-767-701-9670	Sequence 9670, Ap
	441	17	0.4	749	6	US-10-767-701-10143	Sequence 10143, A
c	442	17	0.4	756	6	US-10-767-701-11281	Sequence 11281, A
c	443	17	0.4	757	6	US-10-767-701-1518	Sequence 1518, Ap
	444	17	0.4	761	6	US-10-767-701-1442	Sequence 1442, Ap
	445	17	0.4	765	6	US-10-767-701-9091	Sequence 9091, Ap
c	446	17	0.4	772	6	US-10-767-701-4188	Sequence 4188, Ap
	447	17	0.4	772	6	US-10-767-701-10435	Sequence 10435, A
	448	17	0.4	779	6	US-10-767-701-7956	Sequence 7956, Ap
	449	17	0.4	786	6	US-10-767-701-7932	Sequence 7932, Ap
	450	17	0.4	793	6	US-10-767-701-20286	Sequence 20286, A
c	451	17	0.4	800	6	US-10-767-701-10261	Sequence 10261, A
c	452	17	0.4	804	6	US-10-767-701-15063	Sequence 15063, A
c	453	17	0.4	805	6	US-10-767-701-6791	Sequence 6791, Ap
	454	17	0.4	810	6	US-10-767-701-8586	Sequence 8586, Ap
	455	17	0.4	811	6	US-10-767-701-9159	Sequence 9159, Ap
	456	17	0.4	823	6	US-10-767-701-13046	Sequence 13046, A
	457	17	0.4	824	6	US-10-767-701-2654	Sequence 2654, Ap
c	458	17	0.4	834	6	US-10-767-701-13697	Sequence 13697, A
c	459	17	0.4	838	6	US-10-767-701-10262	Sequence 10262, A
	460	17	0.4	841	6	US-10-767-701-13998	Sequence 13998, A
c	461	17	0.4	852	6	US-10-767-701-850	Sequence 850, App
	462	17	0.4	857	6	US-10-767-701-9672	Sequence 9672, Ap
c	463	17	0.4	863	6	US-10-767-701-14360	Sequence 14360, A
c	464	17	0.4	874	6	US-10-767-701-12304	Sequence 12304, A
	465	17	0.4	877	6	US-10-767-701-8252	Sequence 8252, Ap
	466	17	0.4	879	6	US-10-451-467A-495	Sequence 495, App
	467	17	0.4	895	6	US-10-767-701-9396	Sequence 9396, Ap
	468	17	0.4	900	6	US-10-767-701-10688	Sequence 10688, A
	469	17	0.4	920	6	US-10-767-701-11392	Sequence 11392, A
	470	17	0.4	921	6	US-10-767-701-1665	Sequence 1665, Ap
c	471	17	0.4	932	6	US-10-767-701-10977	Sequence 10977, A
	472	17	0.4	936	6	US-10-646-620A-8	Sequence 8, Appli
	473	17	0.4	945	6	US-10-767-701-10900	Sequence 10900, A
	474	17	0.4	962	6	US-10-767-701-10472	Sequence 10472, A
c	475	17	0.4	977	6	US-10-767-701-12410	Sequence 12410, A
c	476	17	0.4	987	6	US-10-767-701-14401	Sequence 14401, A
	477	17	0.4	988	6	US-10-767-701-13978	Sequence 13978, A
	478	17	0.4	994	6	US-10-767-701-5362	Sequence 5362, Ap
	479	17	0.4	1004	6	US-10-767-701-13622	Sequence 13622, A
	480	17	0.4	1018	6	US-10-767-701-5625	Sequence 5625, Ap
	481	17	0.4	1022	1	PCT-US03-13184-1	Sequence 1, Appli
	482	17	0.4	1022	6	US-10-424-986-1	Sequence 1, Appli
c	483	17	0.4	1022	6	US-10-773-236-137	Sequence 137, App
	484	17	0.4	1028	6	US-10-767-701-9054	Sequence 9054, Ap
	485	17	0.4	1028	6	US-10-767-701-15083	Sequence 15083, A
c	486	17	0.4	1029	6	US-10-767-701-11693	Sequence 11693, A
	487	17	0.4	1050	6	US-10-767-701-14529	Sequence 14529, A
	488	17	0.4	1051	6	US-10-767-701-12214	Sequence 12214, A
	489	17	0.4	1052	6	US-10-767-701-12098	Sequence 12098, A
c	490	17	0.4	1055	6	US-10-773-236-168	Sequence 168, App
c	491	17	0.4	1061	6	US-10-767-701-14361	Sequence 14361, A
	492	17	0.4	1076	6	US-10-767-701-13091	Sequence 13091, A
c	493	17	0.4	1088	6	US-10-773-236-202	Sequence 202, App
	494	17	0.4	1091	6	US-10-767-701-10763	Sequence 10763, A
	495	17	0.4	1104	1	PCT-US03-13184-25	Sequence 25, Appl
	496	17	0.4	1104	6	US-10-767-701-14359	Sequence 14359, A
	497	17	0.4	1104	6	US-10-424-986-25	Sequence 25, Appl
	498	17	0.4	1142	6	US-10-767-701-15574	Sequence 15574, A
	499	17	0.4	1154	6	US-10-767-701-9353	Sequence 9353, Ap
c	500	17	0.4	1165	6	US-10-767-701-12235	Sequence 12235, A
c	501	17	0.4	1183	6	US-10-773-236-53	Sequence 53, Appl
c	502	17	0.4	1188	6	US-10-773-236-169	Sequence 169, App
c	503	17	0.4	1195	6	US-10-773-236-167	Sequence 167, App
	504	17	0.4	1200	6	US-10-767-701-13685	Sequence 13685, A
c	505	17	0.4	1201	6	US-10-767-701-12659	Sequence 12659, A
c	506	17	0.4	1216	6	US-10-773-236-92	Sequence 92, Appl
c	507	17	0.4	1218	6	US-10-767-701-14553	Sequence 14553, A
	508	17	0.4	1224	6	US-10-767-701-12453	Sequence 12453, A
c	509	17	0.4	1231	6	US-10-767-701-4505	Sequence 4505, Ap
	510	17	0.4	1251	6	US-10-767-701-7224	Sequence 7224, Ap
	511	17	0.4	1263	6	US-10-767-701-10309	Sequence 10309, A
	512	17	0.4	1273	6	US-10-767-701-13420	Sequence 13420, A
	513	17	0.4	1274	6	US-10-767-701-12967	Sequence 12967, A
	514	17	0.4	1278	6	US-10-767-701-13540	Sequence 13540, A
c	515	17	0.4	1290	5	US-09-744-794C-57	Sequence 57, Appl
c	516	17	0.4	1325	6	US-10-767-701-12769	Sequence 12769, A
	517	17	0.4	1361	6	US-10-451-467A-305	Sequence 305, App
c	518	17	0.4	1427	6	US-10-767-701-11848	Sequence 11848, A
	519	17	0.4	1428	6	US-10-767-701-14180	Sequence 14180, A
	520	17	0.4	1439	6	US-10-767-701-12374	Sequence 12374, A
	521	17	0.4	1486	6	US-10-767-701-13707	Sequence 13707, A
	522	17	0.4	1528	6	US-10-767-701-14584	Sequence 14584, A
	523	17	0.4	1572	6	US-10-767-701-15555	Sequence 15555, A
	524	17	0.4	1593	6	US-10-767-701-15100	Sequence 15100, A
	525	17	0.4	1602	6	US-10-767-701-15564	Sequence 15564, A
	526	17	0.4	1605	6	US-10-767-701-8511	Sequence 8511, Ap
c	527	17	0.4	1621	6	US-10-767-701-12166	Sequence 12166, A
	528	17	0.4	1721	6	US-10-451-467A-261	Sequence 261, App
c	529	17	0.4	1726	1	PCT-US03-35026-18	Sequence 18, Appl
c	530	17	0.4	1779	6	US-10-767-701-15580	Sequence 15580, A
c	531	17	0.4	1836	6	US-10-772-656-11	Sequence 11, Appl
c	532	17	0.4	1869	7	US-60-542-038-22	Sequence 22, Appl
c	533	17	0.4	1890	6	US-10-772-656-15	Sequence 15, Appl
c	534	17	0.4	1899	6	US-10-679-140-15	Sequence 15, Appl
	535	17	0.4	1899	6	US-10-679-140-16	Sequence 16, Appl
c	536	17	0.4	1914	6	US-10-772-656-9	Sequence 9, Appli
c	537	17	0.4	1943	1	PCT-US04-02851-43	Sequence 43, Appl

c	538	17	0.4	1943	6	US-10-768-158-43	Sequence 43, Appl
c	539	17	0.4	1959	6	US-10-772-656-19	Sequence 19, Appl
	540	17	0.4	1960	6	US-10-767-701-14919	Sequence 14919, A
c	541	17	0.4	1968	6	US-10-772-656-13	Sequence 13, Appl
c	542	17	0.4	1973	1	PCT-US03-31120A-1	Sequence 1, Appli
c	543	17	0.4	2031	6	US-10-772-656-23	Sequence 23, Appl
c	544	17	0.4	2037	6	US-10-772-656-17	Sequence 17, Appl
	545	17	0.4	2070	6	US-10-767-701-15441	Sequence 15441, A
c	546	17	0.4	2074	6	US-10-767-701-10360	Sequence 10360, A
c	547	17	0.4	2103	6	US-10-772-656-27	Sequence 27, Appl
c	548	17	0.4	2109	6	US-10-772-656-21	Sequence 21, Appl
	549	17	0.4	2135	6	US-10-767-701-14474	Sequence 14474, A
c	550	17	0.4	2181	6	US-10-772-656-25	Sequence 25, Appl
c	551	17	0.4	2311	6	US-10-772-656-3	Sequence 3, Appli
c	552	17	0.4	2311	6	US-10-772-656-7	Sequence 7, Appli
	553	17	0.4	2334	1	PCT-US03-35026-48	Sequence 48, Appl
c	554	17	0.4	2367	6	US-10-417-884A-2884	Sequence 2884, Ap
	555	17	0.4	2384	1	PCT-US04-02851-45	Sequence 45, Appl
	556	17	0.4	2384	6	US-10-768-158-45	Sequence 45, Appl
c	557	17	0.4	2389	6	US-10-772-656-1	Sequence 1, Appli
c	558	17	0.4	2389	6	US-10-772-656-5	Sequence 5, Appli
	559	17	0.4	2614	6	US-10-767-701-14986	Sequence 14986, A
c	560	17	0.4	2693	6	US-10-679-140-12	Sequence 12, Appl
	561	17	0.4	2693	6	US-10-679-140-14	Sequence 14, Appl
c	562	17	0.4	2828	6	US-10-767-701-15465	Sequence 15465, A
c	563	17	0.4	3038	6	US-10-767-701-15095	Sequence 15095, A
	564	17	0.4	3169	6	US-10-632-815-5	Sequence 5, Appli
	565	17	0.4	3303	1	PCT-US04-03417-9	Sequence 9, Appli
	566	17	0.4	3303	6	US-10-772-636-9	Sequence 9, Appli
	567	17	0.4	3985	1	PCT-US04-02851-13	Sequence 13, Appl
	568	17	0.4	3985	6	US-10-768-158-13	Sequence 13, Appl
	569	17	0.4	4219	1	PCT-US04-02188-76	Sequence 76, Appl
	570	17	0.4	4219	6	US-10-764-425-76	Sequence 76, Appl
c	571	17	0.4	4220	6	US-10-451-467A-671	Sequence 671, App
c	572	17	0.4	4356	1	PCT-US03-27748-2	Sequence 2, Appli
c	573	17	0.4	4372	6	US-10-603-196-1	Sequence 1, Appli
c	574	17	0.4	4403	6	US-10-767-471-304	Sequence 304, App
c	575	17	0.4	4424	6	US-10-767-471-302	Sequence 302, App
c	576	17	0.4	4549	6	US-10-767-471-303	Sequence 303, App
c	577	17	0.4	5816	6	US-10-767-471-241	Sequence 241, App
c	578	17	0.4	6747	6	US-10-767-471-242	Sequence 242, App
	579	17	0.4	6798	6	US-10-765-790-38	Sequence 38, Appl
	580	17	0.4	7098	6	US-10-767-471-498	Sequence 498, App
	581	17	0.4	7240	6	US-10-767-471-499	Sequence 499, App
	582	17	0.4	7241	6	US-10-767-471-494	Sequence 494, App
c	583	17	0.4	7914	6	US-10-767-471-263	Sequence 263, App
c	584	17	0.4	7918	6	US-10-767-471-265	Sequence 265, App
c	585	17	0.4	7922	6	US-10-767-471-258	Sequence 258, App
	586	17	0.4	7976	6	US-10-767-471-493	Sequence 493, App
	587	17	0.4	8118	6	US-10-767-471-497	Sequence 497, App
	588	17	0.4	8554	6	US-10-767-471-495	Sequence 495, App
	589	17	0.4	9250	6	US-10-767-471-492	Sequence 492, App
	590	17	0.4	11409	6	US-10-767-471-603	Sequence 603, App
	591	17	0.4	14111	6	US-10-767-471-10879	Sequence 10879, A
	592	17	0.4	14321	6	US-10-767-471-191	Sequence 191, App
	593	17	0.4	14641	6	US-10-767-471-193	Sequence 193, App
	594	17	0.4	14760	6	US-10-767-471-192	Sequence 192, App
	595	17	0.4	14800	6	US-10-767-471-195	Sequence 195, App
	596	17	0.4	15251	6	US-10-451-467A-669	Sequence 669, App
	597	17	0.4	15407	6	US-10-767-471-10684	Sequence 10684, A
c	598	17	0.4	16526	6	US-10-767-471-10792	Sequence 10792, A
c	599	17	0.4	22218	6	US-10-767-471-10583	Sequence 10583, A
	600	17	0.4	23047	6	US-10-767-471-10609	Sequence 10609, A
	601	17	0.4	24841	6	US-10-767-471-10753	Sequence 10753, A
	602	17	0.4	27779	6	US-10-767-471-10841	Sequence 10841, A
c	603	17	0.4	28591	6	US-10-767-471-10834	Sequence 10834, A
	604	17	0.4	28786	6	US-10-767-471-10789	Sequence 10789, A
	605	17	0.4	34016	6	US-10-767-471-10556	Sequence 10556, A
	606	17	0.4	36989	6	US-10-767-471-10812	Sequence 10812, A
c	607	17	0.4	37255	6	US-10-767-471-10594	Sequence 10594, A
c	608	17	0.4	38092	7	US-60-542-038-23	Sequence 23, Appl
c	609	17	0.4	39320	6	US-10-767-471-10781	Sequence 10781, A
c	610	17	0.4	43692	6	US-10-767-471-10557	Sequence 10557, A
	611	17	0.4	48234	6	US-10-767-471-10706	Sequence 10706, A
	612	17	0.4	50010	6	US-10-767-471-10874	Sequence 10874, A
	613	17	0.4	51323	6	US-10-417-375A-135	Sequence 135, App
	614	17	0.4	55759	6	US-10-767-471-10656	Sequence 10656, A
	615	17	0.4	55996	6	US-10-767-471-10663	Sequence 10663, A
	616	17	0.4	72779	6	US-10-767-471-10639	Sequence 10639, A
	617	17	0.4	81440	6	US-10-451-467A-659	Sequence 659, App
c	618	17	0.4	87716	6	US-10-767-471-10648	Sequence 10648, A
	619	17	0.4	91697	6	US-10-417-375A-36	Sequence 36, Appl
	620	17	0.4	104438	6	US-10-767-471-10731	Sequence 10731, A
	621	17	0.4	134598	6	US-10-767-471-10655	Sequence 10655, A
c	622	17	0.4	134598	6	US-10-767-471-10655	Sequence 10655, A
	623	17	0.4	144232	6	US-10-767-471-10881	Sequence 10881, A
c	624	17	0.4	162329	6	US-10-767-471-10637	Sequence 10637, A
c	625	17	0.4	170546	6	US-10-767-471-10703	Sequence 10703, A
c	626	17	0.4	184809	6	US-10-767-471-10627	Sequence 10627, A
	627	17	0.4	219715	6	US-10-417-375A-63	Sequence 63, Appl
c	628	17	0.4	219715	6	US-10-417-375A-63	Sequence 63, Appl
	629	17	0.4	230101	6	US-10-767-471-10691	Sequence 10691, A
c	630	17	0.4	234734	6	US-10-767-471-10827	Sequence 10827, A
	631	17	0.4	252907	6	US-10-417-375A-66	Sequence 66, Appl
c	632	17	0.4	252907	6	US-10-417-375A-66	Sequence 66, Appl
	633	17	0.4	265113	6	US-10-767-471-10658	Sequence 10658, A
c	634	17	0.4	354592	6	US-10-765-790-70	Sequence 70, Appl
c	635	17	0.4	401433	6	US-10-765-790-79	Sequence 79, Appl
	636	17	0.4	495635	6	US-10-765-790-12	Sequence 12, Appl
	637	17	0.4	546025	6	US-10-767-471-10717	Sequence 10717, A
c	638	17	0.4	546025	6	US-10-767-471-10717	Sequence 10717, A
	639	17	0.4	705636	6	US-10-765-790-30	Sequence 30, Appl
c	640	17	0.4	765267	6	US-10-767-471-10616	Sequence 10616, A
	641	17	0.4	780759	6	US-10-767-471-10626	Sequence 10626, A
c	642	17	0.4	780759	6	US-10-767-471-10626	Sequence 10626, A
	643	17	0.4	1126118	6	US-10-767-471-10615	Sequence 10615, A
	644	16	0.4	21	6	US-10-770-726-17518	Sequence 17518, A
c	645	16	0.4	24	6	US-10-708-204-3979	Sequence 3979, Ap
c	646	16	0.4	35	5	US-09-941-492A-35	Sequence 35, Appl
c	647	16	0.4	35	5	US-09-941-492A-79	Sequence 79, Appl
c	648	16	0.4	126	6	US-10-767-701-20480	Sequence 20480, A
	649	16	0.4	162	6	US-10-767-471-9508	Sequence 9508, Ap
	650	16	0.4	162	6	US-10-767-471-9516	Sequence 9516, Ap
	651	16	0.4	162	6	US-10-767-471-9524	Sequence 9524, Ap
	652	16	0.4	162	6	US-10-767-471-9532	Sequence 9532, Ap
	653	16	0.4	163	6	US-10-767-471-9509	Sequence 9509, Ap
	654	16	0.4	163	6	US-10-767-471-9517	Sequence 9517, Ap
	655	16	0.4	163	6	US-10-767-471-9525	Sequence 9525, Ap
	656	16	0.4	163	6	US-10-767-471-9533	Sequence 9533, Ap
	657	16	0.4	164	6	US-10-767-471-9510	Sequence 9510, Ap
	658	16	0.4	164	6	US-10-767-471-9518	Sequence 9518, Ap
	659	16	0.4	164	6	US-10-767-471-9526	Sequence 9526, Ap
	660	16	0.4	164	6	US-10-767-471-9534	Sequence 9534, Ap
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	662	16	0.4	201	6	US-10-767-471-2010	Sequence 2010, Ap
	663	16	0.4	201	6	US-10-767-471-2031	Sequence 2031, Ap
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c	665	16	0.4	201	6	US-10-767-471-4219	Sequence 4219, Ap
c	666	16	0.4	201	6	US-10-767-471-4221	Sequence 4221, Ap
c	667	16	0.4	201	6	US-10-767-471-4225	Sequence 4225, Ap
c	668	16	0.4	201	6	US-10-767-471-4249	Sequence 4249, Ap
c	669	16	0.4	201	6	US-10-767-471-4253	Sequence 4253, Ap
c	670	16	0.4	201	6	US-10-767-471-4255	Sequence 4255, Ap
c	671	16	0.4	201	6	US-10-767-471-4259	Sequence 4259, Ap
c	672	16	0.4	201	6	US-10-767-471-7311	Sequence 7311, Ap
c	673	16	0.4	201	6	US-10-767-471-7316	Sequence 7316, Ap
c	674	16	0.4	201	6	US-10-767-471-7317	Sequence 7317, Ap
c	675	16	0.4	201	6	US-10-767-471-7369	Sequence 7369, Ap
c	676	16	0.4	201	6	US-10-767-471-7374	Sequence 7374, Ap
c	677	16	0.4	201	6	US-10-767-471-7375	Sequence 7375, Ap
c	678	16	0.4	201	6	US-10-767-471-7429	Sequence 7429, Ap
c	679	16	0.4	201	6	US-10-767-471-7434	Sequence 7434, Ap
c	680	16	0.4	201	6	US-10-767-471-7435	Sequence 7435, Ap
c	681	16	0.4	201	6	US-10-767-471-7487	Sequence 7487, Ap
c	682	16	0.4	201	6	US-10-767-471-7492	Sequence 7492, Ap
c	683	16	0.4	201	6	US-10-767-471-7493	Sequence 7493, Ap

c	684	16	0.4	201	6	US-10-767-471-7545	Sequence 7545, Ap
c	685	16	0.4	201	6	US-10-767-471-7548	Sequence 7548, Ap
c	686	16	0.4	201	6	US-10-767-471-7550	Sequence 7550, Ap
c	687	16	0.4	201	6	US-10-767-471-7600	Sequence 7600, Ap
c	688	16	0.4	201	6	US-10-767-471-7603	Sequence 7603, Ap
c	689	16	0.4	201	6	US-10-767-471-7605	Sequence 7605, Ap
c	690	16	0.4	201	6	US-10-767-471-7657	Sequence 7657, Ap
c	691	16	0.4	201	6	US-10-767-471-7659	Sequence 7659, Ap
c	692	16	0.4	201	6	US-10-767-471-7713	Sequence 7713, Ap
c	693	16	0.4	201	6	US-10-767-471-7714	Sequence 7714, Ap
c	694	16	0.4	201	6	US-10-767-471-9544	Sequence 9544, Ap
c	695	16	0.4	201	6	US-10-767-471-9545	Sequence 9545, Ap
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c	697	16	0.4	201	6	US-10-767-471-9560	Sequence 9560, Ap
c	698	16	0.4	201	6	US-10-767-471-9561	Sequence 9561, Ap
c	699	16	0.4	201	6	US-10-767-471-9562	Sequence 9562, Ap
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	701	16	0.4	201	6	US-10-767-471-10145	Sequence 10145, A
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	703	16	0.4	201	6	US-10-767-471-13139	Sequence 13139, A
c	704	16	0.4	201	6	US-10-767-471-14198	Sequence 14198, A
c	705	16	0.4	201	6	US-10-767-471-14299	Sequence 14299, A
c	706	16	0.4	201	6	US-10-767-471-19433	Sequence 19433, A
c	707	16	0.4	201	6	US-10-767-471-23046	Sequence 23046, A
c	708	16	0.4	201	6	US-10-767-471-23546	Sequence 23546, A
c	709	16	0.4	201	6	US-10-767-471-23552	Sequence 23552, A
c	710	16	0.4	201	6	US-10-767-471-23555	Sequence 23555, A
c	711	16	0.4	201	6	US-10-767-471-23561	Sequence 23561, A
	712	16	0.4	201	6	US-10-767-471-24426	Sequence 24426, A
	713	16	0.4	201	6	US-10-767-471-24475	Sequence 24475, A
	714	16	0.4	201	6	US-10-767-471-24529	Sequence 24529, A
	715	16	0.4	201	6	US-10-767-471-24602	Sequence 24602, A
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c	717	16	0.4	201	6	US-10-767-471-29555	Sequence 29555, A
c	718	16	0.4	201	6	US-10-767-471-29590	Sequence 29590, A
	719	16	0.4	201	6	US-10-767-471-36542	Sequence 36542, A
	720	16	0.4	201	6	US-10-767-471-36543	Sequence 36543, A
	721	16	0.4	201	6	US-10-767-471-36544	Sequence 36544, A
	722	16	0.4	201	6	US-10-767-471-36981	Sequence 36981, A
	723	16	0.4	201	6	US-10-767-471-36983	Sequence 36983, A
	724	16	0.4	201	6	US-10-767-471-36985	Sequence 36985, A
c	725	16	0.4	201	6	US-10-767-471-37065	Sequence 37065, A
c	726	16	0.4	201	6	US-10-767-471-37067	Sequence 37067, A
c	727	16	0.4	201	6	US-10-767-471-37069	Sequence 37069, A
	728	16	0.4	201	6	US-10-767-471-38296	Sequence 38296, A
	729	16	0.4	201	6	US-10-767-471-38299	Sequence 38299, A
c	730	16	0.4	201	6	US-10-767-471-38782	Sequence 38782, A
c	731	16	0.4	201	6	US-10-767-471-45558	Sequence 45558, A
	732	16	0.4	201	6	US-10-767-471-47606	Sequence 47606, A
	733	16	0.4	201	6	US-10-767-471-47607	Sequence 47607, A
c	734	16	0.4	201	6	US-10-767-471-48948	Sequence 48948, A
c	735	16	0.4	201	6	US-10-767-471-48970	Sequence 48970, A
	736	16	0.4	201	6	US-10-767-471-48980	Sequence 48980, A
	737	16	0.4	204	6	US-10-767-701-21558	Sequence 21558, A
c	738	16	0.4	204	6	US-10-767-701-25998	Sequence 25998, A
	739	16	0.4	206	6	US-10-767-701-25388	Sequence 25388, A
	740	16	0.4	212	6	US-10-767-701-1155	Sequence 1155, Ap
	741	16	0.4	237	6	US-10-767-701-16593	Sequence 16593, A
	742	16	0.4	247	6	US-10-767-701-22034	Sequence 22034, A
	743	16	0.4	247	6	US-10-767-701-28838	Sequence 28838, A
	744	16	0.4	251	6	US-10-767-701-1432	Sequence 1432, Ap
c	745	16	0.4	257	6	US-10-767-701-19493	Sequence 19493, A
	746	16	0.4	339	6	US-10-767-701-17986	Sequence 17986, A
c	747	16	0.4	340	6	US-10-767-701-27674	Sequence 27674, A
c	748	16	0.4	345	6	US-10-767-701-230	Sequence 230, App
	749	16	0.4	358	6	US-10-767-701-22841	Sequence 22841, A
c	750	16	0.4	374	6	US-10-767-701-20802	Sequence 20802, A
c	751	16	0.4	374	6	US-10-767-701-20997	Sequence 20997, A
	752	16	0.4	391	6	US-10-767-701-25638	Sequence 25638, A
	753	16	0.4	392	6	US-10-767-701-4797	Sequence 4797, Ap
c	754	16	0.4	397	6	US-10-767-701-30786	Sequence 30786, A
c	755	16	0.4	401	1	PCT-US03-34223-23	Sequence 23, Appl
c	756	16	0.4	401	1	PCT-US03-34223-24	Sequence 24, Appl
c	757	16	0.4	401	6	US-10-767-701-26902	Sequence 26902, A
	758	16	0.4	406	6	US-10-767-701-687	Sequence 687, App
c	759	16	0.4	416	6	US-10-767-701-28694	Sequence 28694, A
	760	16	0.4	425	6	US-10-767-701-1879	Sequence 1879, Ap
c	761	16	0.4	425	6	US-10-773-236-170	Sequence 170, App
	762	16	0.4	443	6	US-10-767-701-21086	Sequence 21086, A
	763	16	0.4	445	6	US-10-767-701-17312	Sequence 17312, A
	764	16	0.4	453	6	US-10-767-701-25614	Sequence 25614, A
	765	16	0.4	457	6	US-10-767-701-25071	Sequence 25071, A
	766	16	0.4	457	6	US-10-767-701-30104	Sequence 30104, A
	767	16	0.4	462	6	US-10-767-701-3118	Sequence 3118, Ap
	768	16	0.4	463	6	US-10-767-701-23815	Sequence 23815, A
	769	16	0.4	469	6	US-10-767-701-29716	Sequence 29716, A
c	770	16	0.4	476	6	US-10-767-701-27027	Sequence 27027, A
	771	16	0.4	484	6	US-10-767-701-8248	Sequence 8248, Ap
c	772	16	0.4	487	6	US-10-767-701-15034	Sequence 15034, A
	773	16	0.4	488	6	US-10-767-701-2951	Sequence 2951, Ap
c	774	16	0.4	494	6	US-10-767-701-21599	Sequence 21599, A
	775	16	0.4	496	6	US-10-767-701-29044	Sequence 29044, A
c	776	16	0.4	497	6	US-10-767-701-2690	Sequence 2690, Ap
c	777	16	0.4	497	6	US-10-767-701-16148	Sequence 16148, A
	778	16	0.4	499	6	US-10-767-701-28049	Sequence 28049, A
	779	16	0.4	500	6	US-10-767-701-26449	Sequence 26449, A
c	780	16	0.4	503	6	US-10-767-701-29148	Sequence 29148, A
c	781	16	0.4	506	6	US-10-767-701-11279	Sequence 11279, A
	782	16	0.4	507	6	US-10-767-701-1658	Sequence 1658, Ap
	783	16	0.4	509	6	US-10-767-701-4850	Sequence 4850, Ap
c	784	16	0.4	511	6	US-10-767-701-19716	Sequence 19716, A
c	785	16	0.4	512	6	US-10-767-701-25952	Sequence 25952, A
	786	16	0.4	515	6	US-10-767-701-29483	Sequence 29483, A
c	787	16	0.4	522	6	US-10-767-701-24422	Sequence 24422, A
	788	16	0.4	529	6	US-10-767-701-17847	Sequence 17847, A
	789	16	0.4	529	6	US-10-767-701-19637	Sequence 19637, A
	790	16	0.4	534	6	US-10-767-701-7280	Sequence 7280, Ap
	791	16	0.4	540	6	US-10-767-701-2640	Sequence 2640, Ap
	792	16	0.4	545	6	US-10-767-701-27961	Sequence 27961, A
c	793	16	0.4	552	6	US-10-767-701-24367	Sequence 24367, A
c	794	16	0.4	553	6	US-10-767-701-26798	Sequence 26798, A
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ALIGNMENTS

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RESULT 1
US-10-764-503-30
; Sequence 30, Application US/10764503
; GENERAL INFORMATION:
;  APPLICANT: Levanon Erez, et al.
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING NATURALLY OCCURRING ANTISENSE
;  TITLE OF INVENTION:  TRANSCRIPTS AND METHODS, KITS AND ARRAYS UTILIZING SAME
;  FILE REFERENCE: 26946
;  CURRENT APPLICATION NUMBER: US/10/764,503
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;  PRIOR FILING DATE: 2003-5-20
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;  SOFTWARE: PatentIn version 3.1
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;   LENGTH: 4863
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-764-503-30

  Query Match             42.7%;  Score 1689;  DB 6;  Length 4863;
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Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 784

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1085 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1144

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1325 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1384

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1685 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1744

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924


RESULT 2
PCT-US03-13184-20
; Sequence 20, Application PC/TUS0313184
; GENERAL INFORMATION:
;  APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
;  TITLE OF INVENTION: D1-1 NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS
;  FILE REFERENCE: CTCH-PWO-001
;  CURRENT APPLICATION NUMBER: PCT/US03/13184
;  CURRENT FILING DATE:  2003-04-28
;  PRIOR APPLICATION NUMBER: 60/375904
;  PRIOR FILING DATE: 2002-04-26
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 219
;   TYPE: DNA
;   ORGANISM: Sus scrofa
PCT-US03-13184-20

  Query Match             0.7%;  Score 26;  DB 1;  Length 219;
  Best Local Similarity   100.0%;  Pred. No. 0.0031;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||||||
Db         80 GCAGCAGCAGCAACAGCAGCAGCAGC 105


RESULT 3
US-10-424-986-20
; Sequence 20, Application US/10424986
; GENERAL INFORMATION:
;  APPLICANT: ANDERSON et. al.
;  TITLE OF INVENTION: D1-1 NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS
;  FILE REFERENCE: CTCH-P01-001
;  CURRENT APPLICATION NUMBER: US/10/424,986
;  CURRENT FILING DATE:  2003-04-28
;  PRIOR APPLICATION NUMBER: 60/375904
;  PRIOR FILING DATE: 2002-04-26
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 219
;   TYPE: DNA
;   ORGANISM: Sus scrofa
US-10-424-986-20

  Query Match             0.7%;  Score 26;  DB 6;  Length 219;
  Best Local Similarity   100.0%;  Pred. No. 0.0031;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||||||
Db         80 GCAGCAGCAGCAACAGCAGCAGCAGC 105


RESULT 4
PCT-US03-13184-19
; Sequence 19, Application PC/TUS0313184
; GENERAL INFORMATION:
;  APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
;  TITLE OF INVENTION: D1-1 NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS
;  FILE REFERENCE: CTCH-PWO-001
;  CURRENT APPLICATION NUMBER: PCT/US03/13184
;  CURRENT FILING DATE:  2003-04-28
;  PRIOR APPLICATION NUMBER: 60/375904
;  PRIOR FILING DATE: 2002-04-26
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
;   LENGTH: 549
;   TYPE: DNA
;   ORGANISM: Sus scrofa
PCT-US03-13184-19

  Query Match             0.7%;  Score 26;  DB 1;  Length 549;
  Best Local Similarity   100.0%;  Pred. No. 0.0031;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||||||
Db        188 GCAGCAGCAGCAACAGCAGCAGCAGC 213


RESULT 5
US-10-424-986-19
; Sequence 19, Application US/10424986
; GENERAL INFORMATION:
;  APPLICANT: ANDERSON et. al.
;  TITLE OF INVENTION: D1-1 NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS
;  FILE REFERENCE: CTCH-P01-001
;  CURRENT APPLICATION NUMBER: US/10/424,986
;  CURRENT FILING DATE:  2003-04-28
;  PRIOR APPLICATION NUMBER: 60/375904
;  PRIOR FILING DATE: 2002-04-26
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
;   LENGTH: 549
;   TYPE: DNA
;   ORGANISM: Sus scrofa
US-10-424-986-19

  Query Match             0.7%;  Score 26;  DB 6;  Length 549;
  Best Local Similarity   100.0%;  Pred. No. 0.0031;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||||||
Db        188 GCAGCAGCAGCAACAGCAGCAGCAGC 213


RESULT 6
US-10-767-701-26464
; Sequence 26464, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 26464
;   LENGTH: 676
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 30974808
US-10-767-701-26464

  Query Match             0.7%;  Score 26;  DB 6;  Length 676;
  Best Local Similarity   100.0%;  Pred. No. 0.0031;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||||||
Db        617 GCAGCAGCAGCAACAGCAGCAGCAGC 642


RESULT 7
US-09-744-794C-46
; Sequence 46, Application US/09744794C
; GENERAL INFORMATION:
;  APPLICANT: INCYTE CORPORATION; HILLMAN, Jennifer L.;
;  APPLICANT:  LAL, Preeti G.; TANG, Y. Tom;
;  APPLICANT:  CORLEY, Neil C.; GUEGLER, Karl J.;
;  APPLICANT:  BAUGHN, Mariah R.; PATTERSON, Chandra S.;
;  APPLICANT:  BANDMAN, Olga; AU-YOUNG, Janice K.;
;  APPLICANT:  GORGONE, Gina A.; YUE, Henry;
;  APPLICANT:  AZIMZAI, Yalda; REDDY, Roopa M.;
;  APPLICANT:  LU, Dyung Aina M.; SHIH, Leo L.
;  TITLE OF INVENTION: HUMAN CELL SURFACE RECEPTORS
;  FILE REFERENCE: PF-0565 USN
;  CURRENT APPLICATION NUMBER: US/09/744,794C
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PERL Program
; SEQ ID NO 46
;   LENGTH: 3786
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 2299715CB1
US-09-744-794C-46

  Query Match             0.7%;  Score 26;  DB 5;  Length 3786;
  Best Local Similarity   100.0%;  Pred. No. 0.0031;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAGGTCATCGCCTGTGATGAGAACCC 623
              ||||||||||||||||||||||||||
Db        731 GAGGTCATCGCCTGTGATGAGAACCC 756


RESULT 8
US-10-451-467A-659/c
; Sequence 659, Application US/10451467A
; GENERAL INFORMATION:
;  APPLICANT: CONTRERAS, ROLAND HENRI
;  APPLICANT:  EBERHARDT, INES
;  APPLICANT:  LUYTEN, WALTER HERMAN MARIA LOUIS
;  APPLICANT:  REEKMANS, RIEKA JOSEPHINA
;  TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
;  TITLE OF INVENTION:  YEAST AND FUNGI
;  FILE REFERENCE: JAB-1667
;  CURRENT APPLICATION NUMBER: US/10/451,467A
;  CURRENT FILING DATE:  2003-06-19
;  PRIOR APPLICATION NUMBER: EP 00870318.3
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: EP 01870002.1
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: EP 01870003.9
;  PRIOR FILING DATE: 2001-01-09
;  NUMBER OF SEQ ID NOS: 732
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 659
;   LENGTH: 81440
;   TYPE: DNA
;   ORGANISM: Candida albicans
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (41180)..(41180)
;   OTHER INFORMATION: N = A, G, T or C
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (41181)..(41181)
;   OTHER INFORMATION: N = A, G, T or C
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (41211)..(41211)
;   OTHER INFORMATION: N = A, G, T or C
US-10-451-467A-659

  Query Match             0.6%;  Score 24;  DB 6;  Length 81440;
  Best Local Similarity   100.0%;  Pred. No. 0.031;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 GCAGCAGCAGCAACAGCAGCAGCA 1466
              ||||||||||||||||||||||||
Db      66636 GCAGCAGCAGCAACAGCAGCAGCA 66613


RESULT 9
US-10-767-701-6073
; Sequence 6073, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 6073
;   LENGTH: 789
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS33754_1
US-10-767-701-6073

  Query Match             0.6%;  Score 23;  DB 6;  Length 789;
  Best Local Similarity   100.0%;  Pred. No. 0.096;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1446 GCAGCAGCAACAGCAGCAGCAGC 1468
              |||||||||||||||||||||||
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Db        189 GCAGCAGCAACAGCAGCAGCAGC 211


RESULT 10
US-09-941-492A-63/c
; Sequence 63, Application US/09941492A
; GENERAL INFORMATION:
;  APPLICANT: Mitchell, Lloyd
;  APPLICANT:  Garcia-Blanco, Mariano M.
;  APPLICANT:  Puttaraju, Madaiah
;  APPLICANT:  Mansfield, Gary S.
;  TITLE OF INVENTION: METHODS OF COMPOSITIONS FOR USE IN
;  TITLE OF INVENTION:  SPLICEOSOME MEDIATED RNA TRANS-SPLICING
;  FILE REFERENCE: A31304-BAE (072874.0156)
;  CURRENT APPLICATION NUMBER: US/09/941,492A
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: 09/838,858
;  PRIOR FILING DATE: 2001-04-20
;  PRIOR APPLICATION NUMBER: 09/756,096
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 09/158,863
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 09/133,717
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: 09/087,233
;  PRIOR FILING DATE: 1998-05-28
;  PRIOR APPLICATION NUMBER: 08/766,354
;  PRIOR FILING DATE: 1996-12-13
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Trans-spliced product containing Esherichia coli
;   OTHER INFORMATION: lacZ gene sequences
US-09-941-492A-63

  Query Match             0.6%;  Score 22;  DB 5;  Length 196;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1444 CAGCAGCAGCAACAGCAGCAGC 1465
              ||||||||||||||||||||||
Db        146 CAGCAGCAGCAACAGCAGCAGC 125


RESULT 11
US-10-767-701-10485
; Sequence 10485, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 10485
;   LENGTH: 829
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS16079_1
US-10-767-701-10485

  Query Match             0.6%;  Score 22;  DB 6;  Length 829;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 GCAGCAGCAGCAACAGCAGCAG 1464
              ||||||||||||||||||||||
Db        175 GCAGCAGCAGCAACAGCAGCAG 196


RESULT 12
US-10-767-701-11901
; Sequence 11901, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 11901
;   LENGTH: 1123
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS34030_1
US-10-767-701-11901

  Query Match             0.6%;  Score 22;  DB 6;  Length 1123;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1442 TGCAGCAGCAGCAACAGCAGCA 1463
              ||||||||||||||||||||||
Db        413 TGCAGCAGCAGCAACAGCAGCA 434


RESULT 13
PCT-US04-02974-37
; Sequence 37, Application PC/TUS0402974
; GENERAL INFORMATION:
;  APPLICANT: Wright, Susan C.
;  APPLICANT:  Larrick, James W.
;  APPLICANT:  Nock, Steffen R.
;  APPLICANT:  Wilson, David S.
;  TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof
;  FILE REFERENCE: ABSALUS-08804
;  CURRENT APPLICATION NUMBER: PCT/US04/02974
;  CURRENT FILING DATE:  2004-02-02
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 1137
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
PCT-US04-02974-37

  Query Match             0.6%;  Score 22;  DB 1;  Length 1137;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1447 CAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||
Db        328 CAGCAGCAACAGCAGCAGCAGC 349


RESULT 14
US-10-770-668-37
; Sequence 37, Application US/10770668
; GENERAL INFORMATION:
;  APPLICANT: Wright, Susan C.
;  APPLICANT:  Larrick, James W.
;  APPLICANT:  Nock, Steffen R.
;  APPLICANT:  Wilson, David S.
;  TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof
```

```
;  FILE REFERENCE: ABSALUS-08602
;  CURRENT APPLICATION NUMBER: US/10/770,668
;  CURRENT FILING DATE:  2004-02-02
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 1137
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-10-770-668-37

  Query Match              0.6%;  Score 22;  DB 6;  Length 1137;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1447 CAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||
Db        328 CAGCAGCAACAGCAGCAGCAGC 349


RESULT 15
US-10-767-701-2898/c
; Sequence 2898, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 2898
;   LENGTH: 1139
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS49114_1
US-10-767-701-2898

  Query Match              0.6%;  Score 22;  DB 6;  Length 1139;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1446 GCAGCAGCAACAGCAGCAGCAG 1467
              ||||||||||||||||||||||
Db        800 GCAGCAGCAACAGCAGCAGCAG 779

Search completed: March  3, 2004, 05:28:39
Job time : 85 secs
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OM nucleic - nucleic search, using sw model

Run on:         March  2, 2004, 09:53:30 ; Search time 191 Seconds
                                           (without alignments)
                                           11479.639 Million cell updates/sec

Title:          US-10-029-115-1
Perfect score:  3951
Sequence:       1 gcccttatgggcgacccagc..........tcatgaactggtgaaagggc 3951

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:      1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                               SUMMARIES
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Result            Query
  No.    Score    Match Length DB  ID                         Description
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    2     3635    92.0    4133  4  US-09-291-417D-11          Sequence 11, Appl
    3   1407.2    35.6    3996  4  US-09-645-456A-2           Sequence 2, Appli
    4   1407.2    35.6    3996  4  US-09-425-324A-2           Sequence 2, Appli
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    6   1391.2    35.2    3972  4  US-09-645-456A-6           Sequence 6, Appli
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    9   1358.6    34.4    4083  4  US-09-579-664B-7           Sequence 7, Appli
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                               ALIGNMENTS

RESULT 1
US-09-688-188B-11
; Sequence 11, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0328
;  CURRENT APPLICATION NUMBER: US/09/688,188B
;  CURRENT FILING DATE:  2000-10-16
;  PRIOR APPLICATION NUMBER: 09/291,417
;  PRIOR FILING DATE: 1999-04-14
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-688-188B-11

  Query Match             92.0%;  Score 3635;  DB 4;  Length 4133;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 3824;  Conservative    0;  Mismatches   15;  Indels  150;  Gaps    3;

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Qy        290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
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Db       3359 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3418

Qy       3383 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3419 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3478

Qy       3443 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3479 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3538

Qy       3503 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3539 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3598

Qy       3563 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3599 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3658

Qy       3623 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3659 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3718

Qy       3683 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3719 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3778

Qy       3743 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGCCACCTCGACG 3802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3779 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGCCACCTCGACG 3838

Qy       3803 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3839 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3898

Qy       3863 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3899 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3958

Qy       3923 GTAACTGCATCATGAACTGGTGAAAGGGC 3951
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RESULT 2
US-09-291-417D-11
; Sequence 11, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0329
;  CURRENT APPLICATION NUMBER: US/09/291,417D
;  CURRENT FILING DATE:  1999-04-13
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-291-417D-11

  Query Match             92.0%;  Score 3635;  DB 4;  Length 4133;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 3824;  Conservative    0;  Mismatches   15;  Indels  150;  Gaps    3;

Qy        110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
              | |  ||  ||||||  ||||||||||||||||||||||||||||||||||||||||||
Db          2 CATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 61

Qy        170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
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Qy        230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
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Db        122 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 181

Qy        290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 241

Qy        350 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 301
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Qy        410 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 361

Qy        470 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 421

Qy        530 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 589
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Db        422 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 481

Qy        590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 541

Qy        650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 601

Qy        710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 661

Qy        770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 721

Qy        830 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 889
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Db        722 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 781

Qy        890 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 949
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Db        782 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 841

Qy        950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
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Db        842 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 901

Qy       1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
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Db        902 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 961

Qy       1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1021

Qy       1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1081

Qy       1190 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1141

Qy       1250 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1201

Qy       1310 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCA----------------- 1352
              ||||||||||||||||||||||||||||||||||||| |||||
Db       1202 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACA 1261

Qy       1353 ------------------------------------------------------------ 1352

Db       1262 GGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGG 1321

Qy       1353 ----------GGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1402
                        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 CCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1381

Qy       1403 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1462
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Db       1382 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1441

Qy       1463 AGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1522
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1442 AGCAGCTTCAGAAACAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1501

Qy       1523 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1582
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Db       1502 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1561

Qy       1583 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1621

Qy       1643 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1681

Qy       1703 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA------------------ 1744
              ||||||||||||||||||||||||||||||||||||||||||
Db       1682 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAGAGCCTGGTGGCACACC 1741

Qy       1745 -------------------------------------------AGTCCCTGCAGGACCAGC 1762
                                                         |||||||||||||||||
Db       1742 GGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAGC 1801

Qy       1763 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1861

Qy       1823 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1882
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Db       1862 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1921

Qy       1883 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1981

Qy       1943 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2002
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Db       1982 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2041

Qy       2003 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2062
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Db       2042 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2101

Qy       2063 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2161

Qy       2123 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2182
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Db       2162 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2221

Qy       2183 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2222 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2281

Qy       2243 GGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2302
              |||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||||
Db       2282 GGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2341

Qy       2303 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2342 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2401

Qy       2363 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2402 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2461

Qy       2423 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2482
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Db       2462 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2521

Qy       2483 AGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCA 2542
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Db       2522 AGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATACAGACAGCGTCAGCACCA 2578

Qy       2543 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2602
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Qy       2603 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2662
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Qy       2723 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2782
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Qy       2783 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2842
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Db       2819 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2878

Qy       2843 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2902
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Db       2879 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2938

Qy       2903 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2962
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Qy       2963 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3022
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Qy       3083 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3142
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Db       3119 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3178

Qy       3143 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3202
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Qy       3203 ACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3262
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3299 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3358

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Db       3359 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3418

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Db       3419 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3478

Qy       3443 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3503 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3562
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Db       3539 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3598

Qy       3563 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3622
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Db       3599 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3658

Qy       3623 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3719 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3778

Qy       3743 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3802
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Db       3779 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3838

Qy       3803 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3862
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Db       3839 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3898

Qy       3863 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3899 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3958

Qy       3923 GTAACTGCATCATGAACTGGTGAAAGGGC 3951
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Db       3959 GTAACCGCATCATGAACTGGTGACGGGGC 3987
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RESULT 3
US-09-645-456A-2
; Sequence 2, Application US/09645456A
; Patent No. 6562580
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AN
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/645,456A
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US/09/425,324
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3996
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-645-456A-2

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  Query Match             35.6%;  Score 1407.2;  DB 4;  Length 3996;
  Best Local Similarity   62.5%;  Pred. No. 6.4e-285;
  Matches 2528;  Conservative    0;  Mismatches 1363;  Indels  153;  Gaps   15;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||     |      |||| || || |||||||| || || || || || || ||| |||||
Db          1 ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGAC 60

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||| ||||||||||   | |||||  | || || |||||||| ||||| || ||
Db         61 CCTGCAGGGATCTTTGAATTGGTGGAACTTGTTGGAAATGGAACATACGGGCAAGTTTAT 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||| |||||||||  ||| ||||| | |||||||||||| ||||||||||| | |
Db        121 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGGTTATGGATGTCACAGGG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Db        181 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACCGG 240
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Qy    247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCGGGAAACGATGACCAG 306
Db    241 AATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCACCAGGCATGGATGACCAA 300

Qy    307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db    301 CTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCGACCTGATCAAGAACACA 360

Qy    367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db    361 AAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGCAGGGAAATCTTACGGGGG 420

Qy    427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db    421 CTGAGTCACCTGCACCAGCATAAAGTGATTCATCGAGATATTAAAGGGCAAAATGTCTTG 480

Qy    487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db    481 CTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCAGTGCTCAGCTTGATCGA 540

Qy    547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db    541 ACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGATGGCACCAGAAGTTATT 600

Qy    607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
Db    601 GCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTGACTTGTGGTCTTTGGGT 660

Qy    667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db    661 ATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCACCCCATGAGA 720

Qy    727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db    721 GCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGTCTAAGAAGTGGTCAAAA 780

Qy    787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db    781 AAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCACAGCCAGCGACCAGCAACA 840

Qy    847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db    841 GAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAATGAGCGACAGGTCCGCATT 900

Qy    907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db    901 CAACTCAAGGACCATATTGATAGAACAAAGAAGAAGCGAGGAGAAAAAGATGAGACAGAG 960

Qy    967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db    961 TATGAGTACAGTGGAAGTGAGGAAGAAGAGGAGGAGAAT---GACTCAGGAGAGCCCAGC 1017

Qy   1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db   1018 TCCATCCTGAATCTGCCAGGGGAGTCGACGCTGCGGAGGGACTTTCTGAGGCTGCAGCTG 1077

Qy   1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db   1078 GCCAACAAGGAGCGTTCTGAGGCCCTA------CGGAGGCAGCAGCTGGAGCAGCAGCAG 1131

Qy   1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db   1132 CGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTCAGAAGCGCATCGAGGAG 1191

Qy   1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
Db   1192 CAGAAAGAGCAGAGGCGGCGGCTGGAGGAGCAACAAAGGCGAGAGAAGGAGCTGCGGAAG 1251

Qy   1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db   1252 CAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGG------AGCAGATGCGCCGGGAGGAG 1305

Qy   1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
Db   1306 GAGAGGAGGCGTGCGGAGCATGAACAGGAATATAAGCGCAAACAATTGGAAGAACAGAGA 1365

Qy   1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
Db   1366 CAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAAGAAAGAGACTACTTAGTTTCCCTTCAG 1425

Qy   1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
Db   1426 CATCAGCGGCAGGAGCAG----------------------------AGGCCTGTGGAG 1455

Qy   1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
Db   1456 AAGAAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTGAGAAGCCAGCATGGGCC 1515

Qy   1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
Db   1516 AAGGAGGTAGAAGAACGGTCAAGGCTCAACCGGCAAAGTTCCCCTGCCATGCCTCA---C 1572

Qy   1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCC---------AGGCCTCCCCAGGG 1677
Db   1573 AAGGTTGCCAACAGGATATCTGACCCCAACCTGCCCCCAAGGTCGGAGTCCTTCAGCATT 1632

Qy   1678 CCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAG------ 1731
Db   1633 AGTGGAGTTCAGCCTGCTCGAACACCCCCCATGCTCAGACCAGTCGATCCCCAGATCCCA 1692

Qy   1732 ---GAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCA 1788
Db   1693 CATCTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCTCCCAGTCAGTGCACGAG 1752

Qy   1789 GCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGA 1848
Db   1753 CAGCCCACAAAGGGCCTCTCTGGGTTTCAGGAGGCTCTGAACGTGACCTCCCACCGCGTG 1812

Qy   1849 GCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCC------- 1901
Db   1813 GAGATGCCACGCCAGAACTCAGATCCCACCTCGGAAAATCCTCCTCTCCCCACTCGCATT 1872

Qy   1902 --------GAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCT 1953
Db   1873 GAAAAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCT 1932

Qy   1954 CAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCA 2013
Db   1933 CAAAGAACAACTTCTATATCCCCAGCATTAGCCAGAAAGAATTCTCCTGGGAATGGTAGT 1992

Qy   2014 GCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGC--AAA 2071
Db   1993 GCTCTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGA 2052

Qy   2072 GGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGC 2131
Db   2053 ACTGAGCCCATCTTGGAGAGCCCCTTGCAGAGGACCAGCAGTGGCAGTTCCTCCAGCTCC 2112

Qy   2132 CCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGG----GAACGCTCG 2187
Db   2113 AGCACCCCTAGCTCCCAGCCCAGCTCCCAAGGAGGCTCCCAGCCTGGATCACAAGCAGGA 2172

Qy   2188 GACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAAC 2247
Db   2173 TCCAGTGAACGCACCAGAGTTCGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTTCCC 2232

Qy   2248 CGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCC 2307
Db   2233 CATGAGCCTGCCAAGGTGAAACCAGAAGAATCCAGGGACATTACCCGGCCCAGTCGACCA 2292

Qy   2308 AAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAG 2367
Db   2293 GCTAGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAGCCAAAGAACTAAGAGAA 2352

Qy   2368 CGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGC 2427
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Db   2353 CTCCGGATTGAAGAAACAAACCGCCCAATGAAGAAGGTGACTGATTACTCCTCCTCCAGT 2412

Qy   2428 GAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGG 2487
Db   2413 GAGGAGTCAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGG 2472

Qy   2488 A--------------------------------GCAGAGATACCCCTGGGGGCCGCAGC 2514
Db   2473 ACAGTGGCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAG 2532

Qy   2515 GATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGG 2574
Db   2533 CAGTACAATGTGGGAATGGTGGGGACGCATGGGCTGGAGACCTCTCATGCGGACAGTTTC 2592

Qy   2575 ACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGG 2634
Db   2593 AGCGGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAGAGAAGAAG 2652

Qy   2635 AACCTGCTGCATGCTGACAGCAATGGGT---------ACACAAACCTGCCTGACGTGGTC 2685
Db   2653 CGATCTGGCCACAGTGACAGCAATGGCTTTGCTGGCCACATCAACCTCCCTGACCTGGTG 2712

Qy   2686 CAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAA------GCCCACCCTCGAAG 2739
Db   2713 CAGCAGAGCCATTCTCCAGCTGGAACCCCGACTGAGGGACTGGGCGCGTCTCAACCCAT 2772

Qy   2740 GATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTC 2799
Db   2773 TCCCAGGAGATGGACTCTGGGACTGAATATGGCATGGGGAGCAGCACCAAAGCCTCCTTC 2832

Qy   2800 ACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCC----- 2854
Db   2833 ACCCCCTTTGTGGACCCCAGAGTATACCAGACGTCTCCCACTGATGAAGATGAAGAGGAT 2892

Qy   2855 ----------CCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAG---CTG 2901
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Qy   2902 CAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCAC 2961
Db   2953 CTCAATGAAGCAAGAAAGATTTCGGTGGTAAATGTAAACCCAACCAACATTCGGCCTCAT 3012

Qy   2962 AGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCA 3021
Db   3013 AGCGACACACCAGAAATCAGAAAATACAAGAAACGATTCAACTCAGAAATACTTTGTGCA 3072

Qy   3022 GCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGA 3081
Db   3073 GCTCTGTGGGGTGTAAACCTTCTGGTGGGGACTGAAAATGGCCTGATGCTTTTGGACCGA 3132

Qy   3082 AGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTG 3141
Db   3133 AGTGGGCAAGGCAAAGTCTATAATCTGATCAACCGGAGGCGATTTCAGCAGATGGATGTG 3192

Qy   3142 CTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTAT 3201
Db   3193 CTAGAGGGACTGAATGTCCTTGTGACAATTTCAGGAAAGAAGAATAAGCTACGAGTTTAC 3252

Qy   3202 TACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAG 3261
Db   3253 TATCTTTCATGGTTAAGAAACAGAATACTACATAATGACCCAGAAGTAGAAAAGAAACAA 3312

Qy   3262 GGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAG 3321
Db   3313 GGCTGGATCACTGTTGGGGACTTGGAAGGCTGTATACATTATAAAGTTGTTAAATATGAA 3372

Qy   3322 CGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCC 3381
Db   3373 AGGATCAAATTTTTGGTGATTGCCTTAAAGAATGCTGTGGAAATATATGCTTGGGCTCCT 3432

Qy   3382 AAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTG 3441
Db   3433 AAACCGTATCATAAATTCATGGCATTTAAGTCTTTTGCAGATCTCCAGCACAAGCCTCTG 3492

Qy   3442 CTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCT 3501
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Qy   3502 GGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCAC 3561
Db   3553 GGTTTCCATGTAATTGATGTTGATTCAGGAAACTCTTATGATATCTACATACCATCTCAT 3612

Qy   3562 ATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAG 3621
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Qy   3622 ATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAG 3681
Db   3673 ATGCTTGTTTGCTATGAGGATGAGGGGGTGTATGTAAACACCTATGGCCGGATAACTAAG 3732

Qy   3682 GATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAG 3741
Db   3733 GATGTGGTGCTCCAATGGGGAGAAATGCCCACGTCTGTGGCCTACATTCATTCCAATCAG 3792

Qy   3742 ATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGAC 3801
Db   3793 ATAATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTTGGAT 3852

Qy   3802 GGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAG 3861
Db   3853 GGAGTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAG 3912

Qy   3862 GTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAAC 3921
Db   3913 GTATTTTTTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTTTTTCATGACCCTCAAC 3972

Qy   3922 CGTAACTGCATCATGAACTGGTGA 3945
Db   3973 AGAAATTCCATGATGAACTGGTAA 3996
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RESULT 4
US-09-425-324A-2
; Sequence 2, Application US/09425324A
; Patent No. 6562591
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AN
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/425,324A
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3996
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-425-324A-2

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Query Match           35.6%;  Score 1407.2;  DB 4;  Length 3996;
Best Local Similarity 62.5%;  Pred. No. 6.4e-285;
Matches 2528;  Conservative    0;  Mismatches 1363;  Indels 153;  Gaps   15;

Qy      7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
Db      1 ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGAC 60

Qy     67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
Db     61 CCTGCAGGGATCTTTGAATTGGTGGAACTTGTTGGAAATGGAACATACGGGCAAGTTTAT 120

Qy    127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
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Db    121 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGGTTATGGATGTCACAGGG 180
Qy    187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Qy    247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
Db    241 AATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCACCAGGCATGGATGACCAA 300
Qy    307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db    301 CTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCGACCTGATCAAGAACACA 360
Qy    367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db    361 AAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGCAGGGAAATCTTACGGGGG 420
Qy    427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db    421 CTGAGTCACCTGCACCAGCATAAAGTGATTCATCGAGATATTAAAGGGCAAAATGTCTTG 480
Qy    487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db    481 CTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCAGTGCTCAGCTTGATCGA 540
Qy    547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db    541 ACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGATGGCACCAGAAGTTATT 600
Qy    607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
Db    601 GCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTGACTTGTGGTCTTTGGGT 660
Qy    667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db    661 ATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCACCCCATGAGA 720
Qy    727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db    721 GCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGTCTAAGAAGTGGTCAAAA 780
Qy    787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db    781 AAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCACAGCCAGCGACCAGCAACA 840
Qy    847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db    841 GAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAATGAGCGACAGGTCCGCATT 900
Qy    907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
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Qy    967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
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Qy   1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
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Qy   1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
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Qy   1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db   1252 CAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGG------AGCAGATGCGCCGGGAGGAG 1305
Qy   1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
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Qy   1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
Db   1366 CAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAAGAAAGAGACTACTTAGTTTCCCTTCAG 1425
Qy   1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
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Qy   1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
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Db   1516 AAGGAGGTAGAAGAACGGTCAAGGCTCAACCGGCAAAGTTCCCCTGCCATGCCTCA---C 1572
Qy   1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCC---------AGGCCTCCCCAGGG 1677
Db   1573 AAGGTTGCCAACAGGATATCTGACCCCAACCTGCCCCCAAGGTCGGAGTCCTTCAGCATT 1632
Qy   1678 CCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAG------ 1731
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Qy   1732 ---GAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCA 1788
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Qy   1789 GCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGA 1848
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Qy   1849 GCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCC------- 1901
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Qy   1902 --------GAATCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCT 1953
Db   1873 GAAAAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCT 1932
Qy   1954 CAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCA 2013
Db   1933 CAAAGAACAACTTCTATATCCCCAGCATTAGCCAGAAAGAATTCTCCTGGGAATGGTAGT 1992
Qy   2014 GCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGC--AAA 2071
Db   1993 GCTCTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGA 2052
Qy   2072 GGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGC 2131
Db   2053 ACTGAGCCCATCTTGGAGAGCCCCTTGCAGAGGACCAGCAGTGGCAGTTCCTCCAGCTCC 2112
Qy   2132 CCAACGCCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGG----GAACGCTCG 2187
Db   2113 AGCACCCCTAGCTCCCAGCCCAGCTCCCAAGGAGGCTCCCAGCCTGGATCACAAGCAGGA 2172
Qy   2188 GACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAAC 2247
Db   2173 TCCAGTGAACGCACCAGAGTTCGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTTCCC 2232
Qy   2248 CGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCC 2307
Db   2233 CATGAGCCTGCCAAGGTGAAACCAGAAGAATCCAGGGACATTACCCGGCCCAGTCGACCA 2292
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Qy   2308 AAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAG 2367
Db   2293 GCTAGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAGCCAAAGAACTAAGAGAA 2352

Qy   2368 CGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGC 2427
Db   2353 CTCCGGATTGAAGAAACAAACCGCCCAATGAAGAAGGTGACTGATTACTCCTCCTCCAGT 2412

Qy   2428 GAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGG 2487
Db   2413 GAGGAGTCAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGG 2472

Qy   2488 A-------------------------------GCAGAGATACCCCTGGGGGCCGCAGC 2514
Db   2473 ACAGTGGCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAG 2532

Qy   2515 GATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGG 2574
Db   2533 CAGTACAATGTGGGAATGGTGGGGACGCATGGGCTGGAGACCTCTCATGCGGACAGTTTC 2592

Qy   2575 ACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGG 2634
Db   2593 AGCGGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAGAGAAGAAG 2652

Qy   2635 AACCTGCTGCATGCTGACAGCAATGGGT---------ACACAAACCTGCCTGACGTGGTC 2685
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Qy   2686 CAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAA------GCCCACCCTCGAAG 2739
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Qy   2740 GATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTC 2799
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Qy   2800 ACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCC----- 2854
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Qy   2855 ----------CCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAG---CTG 2901
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Qy   2902 CAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCAC 2961
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Qy   2962 AGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCA 3021
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Qy   3142 CTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTAT 3201
Db   3193 CTAGAGGGACTGAATGTCCTTGTGACAATTTCAGGAAAGAAGAATAAGCTACGAGTTTAC 3252

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Qy   3382 AAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTG 3441
Db   3433 AAACCGTATCATAAATTCATGGCATTTAAGTCTTTTGCAGATCTCCAGCACAAGCCTCTG 3492

Qy   3442 CTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCT 3501
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US-09-645-791-2
; Sequence 2, Application US/09645791
; Patent No. 6569658
; GENERAL INFORMATION:
;  APPLICANT: Luo, Ying
;  APPLICANT:  Fu, Alan C
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AN
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: A-68344-1/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/09/645,791
;  CURRENT FILING DATE:  2000-08-24
;  PRIOR APPLICATION NUMBER: US 09/425,324
;  PRIOR FILING DATE: 1999-10-21
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 3996
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-09-645-791-2

  Query Match             35.6%;  Score 1407.2;  DB 4;  Length 3996;
  Best Local Similarity   62.5%;  Pred. No. 6.4e-285;
  Matches 2528;  Conservative    0;  Mismatches 1363;  Indels  153;  Gaps   15;
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Db       61 CCTGCAGGGATCTTTGAATTGGTGGAACTTGTTGGAAATGGAACATACGGGCAAGTTTAT 120

Qy      127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
Db      121 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGGTTATGGATGTCACAGGG 180

Qy      187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
Db      181 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACCGG 240

Qy      247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
Db      241 AATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCACCAGGCATGGATGACCAA 300

Qy      307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db      301 CTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCGACCTGATCAAGAACACA 360

Qy      367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Qy      427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
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Qy      487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db      481 CTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCAGTGCTCAGCTTGATCGA 540

Qy      547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db      541 ACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGATGGCACCAGAAGTTATT 600

Qy      607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
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Qy      667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db      661 ATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCACCCCATGAGA 720

Qy      727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db      721 GCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGTCTAAGAAGTGGTCAAAA 780

Qy      787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
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Qy      847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db      841 GAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAATGAGCGACAGGTCCGCATT 900

Qy      907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db      901 CAACTCAAGGACCATATTGATAGAACAAAGAAGAAGCGAGGAGAAAAAGATGAGACAGAG 960

Qy      967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
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Qy     1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
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Qy     1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
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Qy     1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
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Qy     1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
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Qy     1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
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Db     1366 CAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAAGAAAGAGACTACTTAGTTTCCCTTCAG 1425

Qy     1447 CAGCAGCAACAGCAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
Db     1426 CATCAGCGGCAGGAGCAG----------------------------AGGCCTGTGGAG 1455

Qy     1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
Db     1456 AAGAAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTGAGAAGCCAGCATGGGCC 1515

Qy     1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
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Qy     1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCC---------AGGCCTCCCCAGGG 1677
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Qy     1678 CCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAG------ 1731
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Qy     1732 ---GAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCA 1788
Db     1693 CATCTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCTCCCAGTCAGTGCACGAG 1752

Qy     1789 GCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGA 1848
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Qy     1849 GCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCC------- 1901
Db     1813 GAGATGCCACGCCAGAACTCAGATCCCACCTCGGAAAATCCTCCTCTCCCCACTCGCATT 1872

Qy     1902 --------GAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCT 1953
Db     1873 GAAAAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCT 1932

Qy     1954 CAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCA 2013
Db     1933 CAAAGAACAACTTCTATATCCCCAGCATTAGCCAGAAAGAATTCTCCTGGGAATGGTAGT 1992

Qy     2014 GCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGC--AAA 2071
Db     1993 GCTCTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGA 2052

Qy     2072 GGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGC 2131
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Qy     2132 CCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGG----GAACGCTCG 2187
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Qy     2188 GACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAAC 2247
Db     2173 TCCAGTGAACGCACCAGAGTTCGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTTCCC 2232

Qy     2248 CGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCC 2307
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Qy     2428 GAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGG 2487
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Qy     2488 A--------------------------------GCAGAGATACCCCTGGGGGCCGCAGC 2514
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RESULT 6
US-09-645-456A-6
; Sequence 6, Application US/09645456A
; Patent No. 6562580
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AN
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/645,456A
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US/09/425,324
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 3972
;   TYPE: DNA

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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-09-645-456A-6

  Query Match             35.2%;  Score 1391.2;  DB 4;  Length 3972;
  Best Local Similarity   62.7%;  Pred. No. 1.4e-281;
  Matches 2533;  Conservative    0;  Mismatches 1338;  Indels  169;  Gaps   17;

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Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
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Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db        301 CTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCGACCTGATCAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db        361 AAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGCAGGGAAATCTTACGGGGG 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db        421 CTGAGTCACCTGCACCAGCATAAAGTGATTCATCGAGATATTAAAGGGCAAAATGTCTTG 480

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db        481 CTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCAGTGCTCAGCTTGATCGA 540

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db        541 ACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGATGGCACCAGAAGTTATT 600

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
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Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Qy       1678 CCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGA 1737
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Qy     3206 TGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCT 3265
Db     3233 TTTCATGGTTAAGAAACAGAATACTACATAATGACCCAGAAGTAGAAAAGAAACAAGGCT 3292

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RESULT 7
US-09-425-324A-6
; Sequence 6, Application US/09425324A
; Patent No. 6562591
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AN
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/425,324A

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;  CURRENT FILING DATE:  1999-10-21
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 3972
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-09-425-324A-6

  Query Match            35.2%;  Score 1391.2;  DB 4;  Length 3972;
  Best Local Similarity  62.7%;  Pred. No. 1.4e-281;
  Matches 2533;  Conservative    0;  Mismatches 1338;  Indels  169;  Gaps   17;

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Db 2813 CCTTTGTGGACCCCAGAGTATACCAGACGTCTCCCACTGATGAAGATGAAGAGGATGAGG 2872

Qy 2855 ------CCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAG---CTGCAGT 2905
Db 2873 AATCATCAGCCGCAGCTCTGTTTACTAGCGAACTTCTTAGGCAAGAACAGGCCAAACTCA 2932

Qy 2906 ACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTG 2965
Db 2933 ATGAAGCAAGAAAGATTTCGGTGGTAAATGTAAACCCAACCAACATTCGGCCTCATAGCG 2992

Qy 2966 AGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCC 3025
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Qy 3026 TTTGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTG 3085
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Qy 3086 GGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGG 3145
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Qy 3926 ACTGCATCATGAACTGGTGA 3945
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RESULT 8
US-09-645-791-6
; Sequence 6, Application US/09645791
; Patent No. 6569658

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; GENERAL INFORMATION:
;  APPLICANT: Luo, Ying
;  APPLICANT:  Fu, Alan C
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AN
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: A-68344-1/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/09/645,791
;  CURRENT FILING DATE:  2000-08-24
;  PRIOR APPLICATION NUMBER: US 09/425,324
;  PRIOR FILING DATE: 1999-10-21
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 3972
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-09-645-791-6

  Query Match             35.2%;  Score 1391.2;  DB 4;  Length 3972;
  Best Local Similarity   62.7%;  Pred. No. 1.4e-281;
  Matches 2533;  Conservative    0;  Mismatches 1338;  Indels  169;  Gaps   17;

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Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
Db        181 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACCGG 240

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Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
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Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db        721 GCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGTCTAAGAAGTGGTCAAAA 780

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Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
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Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
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Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db       1132 CGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTCAGAAGCGCATCGAGGAG 1191

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
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Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
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Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
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Db       1456 AAGAAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTGAGAAGCCAGCATGGGCC 1515

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
Db       1516 AAGGAGGTAGAAGAACGGTCAAGGCTCAACCGGCAAAGTTCCCCTGCCATGCCTCA---C 1572

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCC---------AGGCCTCCCCAGGG 1677
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Qy       1678 CCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGA 1737
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Qy       1738 CCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCAT 1797
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Qy       1798 GACCC---------CGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGA 1848
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Db   1873 GAAAAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCT 1932
Qy   1954 CAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCA 2013
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Qy   2014 GCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCT--GCAAA 2071
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Qy   2132 CCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACA 2191
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Qy   2192 GCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCG 2251
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Qy   2312 CCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGA 2371
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Qy   2372 CTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGG 2431
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Qy   2432 AGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGA--- 2488
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RESULT 9
US-09-579-664B-7
; Sequence 7, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
;  APPLICANT: Immunex Corporation
;  APPLICANT:  Bird, Timothy A.
;  APPLICANT:  Virca, G. Duke
;  APPLICANT:  Martin, Unja
;  APPLICANT:  Anderson, Dirk M.
;  TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
;  FILE REFERENCE: 2923-A
;  CURRENT APPLICATION NUMBER: US/09/579,664B
;  CURRENT FILING DATE:  2000-05-26
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 4083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-579-664B-7

  Query Match            34.4%;  Score 1358.6;  DB 4;  Length 4083;
  Best Local Similarity   61.7%;  Pred. No. 9.2e-275;
  Matches 2532;  Conservative    0;  Mismatches 1389;  Indels  180;  Gaps   16;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
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Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Qy       1570 GAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAG 1629
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RESULT 10
US-09-645-456A-1
; Sequence 1, Application US/09645456A
; Patent No. 6562580
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AN
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/645,456A
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US/09/425,324
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 4083
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-09-645-456A-1

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  Best Local Similarity   61.7%;  Pred. No. 9.2e-275;
  Matches 2532;  Conservative    0;  Mismatches 1389;  Indels  180;  Gaps   16;

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Db    3583 GTTGATCTCACGGTAGAAGAAGGTCAAAGATTAAAGGTTATTTTTGGTTCACACACTGGT 3642

Qy    3505 TTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATC 3564
Db    3643 TTCCATGTAATTGATGTTGATTCAGGAAACTCTTATGATATCTACATACCATCTCATATT 3702
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Qy       3565 CAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATG 3624
Db       3703 CAGGGCAATATCACTCCTCATGCTATTGTCATCTTGCCTAAAACAGATGGAATGGAAATG 3762

Qy       3625 CTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGAT 3684
Db       3763 CTTGTTTGCTATGAGGATGAGGGGGTGTATGTAAACACCTATGGCCGGATAACTAAGGAT 3822

Qy       3685 GTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATA 3744
Db       3823 GTGGTGCTCCAATGGGGAGAAATGCCCACGTCTGTGGCCTACATTCATTCCAATCAGATA 3882

Qy       3745 ATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGG 3804
Db       3883 ATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTTGGATGGA 3942

Qy       3805 GTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTG 3864
Db       3943 GTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAGGTA 4002

Qy       3865 TTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGT 3924
Db       4003 TTTTTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTTTTTCATGACCCTCAACAGA 4062

Qy       3925 AACTGCATCATGAACTGGTGA 3945
Db       4063 AATTCCATGATGAACTGGTAA 4083
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RESULT 11
US-09-425-324A-1
; Sequence 1, Application US/09425324A
; Patent No. 6562591
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AN
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/425,324A
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 4083
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-09-425-324A-1

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  Query Match             34.4%;  Score 1358.6;  DB 4;  Length 4083;
  Best Local Similarity   61.7%;  Pred. No. 9.2e-275;
  Matches 2532;  Conservative    0;  Mismatches 1389;  Indels  180;  Gaps   16;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
Db          1 ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGAC 60

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
Db         61 CCTGCAGGGATCTTTGAATTGGTGGAACTTGTTGGAAATGGAACATACGGGCAAGTTTAT 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
Db        121 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGGTTATGGATGTCACAGGG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
Db        181 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACCGG 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
Db        241 AATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCACCAGGCATGGATGACCAA 300

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db        301 CTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCGACCTGATCAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db        361 AAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGCAGGGAAATCTTACGGGGG 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db        421 CTGAGTCACCTGCACCAGCATAAAGTGATTCATCGAGATATTAAAGGGCAAAATGTCTTG 480

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db        481 CTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCAGTGCTCAGCTTGATCGA 540

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db        541 ACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGATGGCACCAGAAGTTATT 600

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
Db        601 GCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTGACTTGTGGTCTTTGGGT 660

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db        661 ATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCACCCCATGAGA 720

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db        721 GCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGTCTAAGAAGTGGTCAAAA 780

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db        781 AAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCACAGCCAGCGACCAGCAACA 840

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db        841 GAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAATGAGCGACAGGTCCGCATT 900

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db        901 CAACTCAAGGACCATATTGATAGAACAAAGAAGAAGCGAGGAGAAAAAGATGAGACAGAG 960

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db        961 TATGAGTACAGTGGAAGTGAGGAAGAAGAGGAGGAGAAT---GACTCAGGAGAGCCCAGC 1017

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db       1018 TCCATCCTGAATCTGCCAGGGGAGTCGACGCTGCGGAGGGACTTTCTGAGGCTGCAGCTG 1077

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db       1078 GCCAACAAGGAGCGTTCTGAGGCCCTA------CGGAGGCAGCAGCTGGAGCAGCAGCAG 1131

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db       1132 CGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTCAGAAGCGCATCGAGGAG 1191

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
Db       1192 CAGAAAGAGCAGAGGCGGCGGCTGGAGGAGCAACAAAGGCGAGAGAAGGAGCTGCGGAAG 1251

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db       1252 CAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGG------AGCAGATGCGCCGGGAGGAG 1305

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCT---GGAGGAGCAG 1383
Db       1306 GAGAGGAGGCGTGCGGAGCATGAACAGGAATACATCAGGCGACAGTTAGAGGAGGAGCAG 1365
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Qy   1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
Db   1366 AGACAGTTAGAGATCTTGCAGCAGCAGCTACTGCATGAACAAGCTCTACTTCTGGAATAT 1425
Qy   1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCA------------------------------ 1472
Db   1426 AAGCGCAAACAATTGGAAGAACAGAGACAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAA 1485
Qy   1473 ----------------------GAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGG 1509
Db   1486 GAAAGAGACTACTTAGTTTCCCTTCAGCATCAGCGGCAGGAGCAGAGGCCTGTGGAGAAG 1545
Qy   1510 AAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGA 1569
Db   1546 AAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTGAGAAGCCAGCATGGGCCAAG 1605
Qy   1570 GAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAG 1629
Db   1606 GAGGTAGAAGAACGGTCAAGGCTCAACCGGCAAAGTTCCCCTGCCATGCCTCA---CAAG 1662
Qy   1630 CCAGGCAGCACGGGGCCTGAGCCCCCATCCCCC---------AGGCCTCCCCAGGGCCC 1680
Db   1663 GTTGCCAACAGGATATCTGACCCCAACCTGCCCCCAAGGTCGGAGTCCTTCAGCATTAGT 1722
Qy   1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAG--------- 1731
Db   1723 GGAGTTCAGCCTGCTCGAACACCCCCCATGCTCAGACCAGTCGATCCCCAGATCCCACAT 1782
Qy   1732 GAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCC 1791
Db   1783 CTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCTCCCAGTCAGTGCACGAGCAG 1842
Qy   1792 TCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCT 1851
Db   1843 CCCACAAAGGGCCTCTCTGGGTTTCAGGAGGCTCTGAACGTGACCTCCCACCGCGTGGAG 1902
Qy   1852 GTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGA-------- 1903
Db   1903 ATGCCACGCCAGAACTCAGATCCCACCTCGGAAAATCCTCCTCTCCCCACTCGCATTGAA 1962
Qy   1904 -------ATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAG 1956
Db   1963 AAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCTCAA 2022
Qy   1957 AGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCC 2016
Db   2023 AGAACAACTTCTATATCCCCAGCATTAGCCAGAAAGAATTCTCCTGGGAATGGTAGTGCT 2082
Qy   2017 CAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAG--GC 2074
Db   2083 CTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGAACT 2142
Qy   2075 GGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCA 2134
Db   2143 GAGCCCATCTTGGAGAGCCCCTTGCAGAGGACCAGCAGTGGCAGTTCCTCCAGCTCCAGC 2202
Qy   2135 ACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGG----GAACGCTCGGAC 2190
Db   2203 ACCCCTAGCTCCCAGCCCAGCTCCCAAGGAGGCTCCCAGCCTGGATCACAAGCAGGATCC 2262
Qy   2191 AGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGC 2250
Db   2263 AGTGAACGCACCAGAGTTCGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTTCCCCAT 2322
Qy   2251 GTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAG 2310
Db   2323 GAGCCTGCCAAGGTGAAACCAGAAGAATCCAGGGACATTACCCGGCCCAGTCGACCAGCT 2382
Qy   2311 CCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGG 2370
Db   2383 AGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAGCCAAAGAACTAAGAGAACTC 2442
Qy   2371 ACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAG 2430
Db   2443 CGGATTGAAGAAACAAACCGCCCAATGAAGAAGGTGACTGATTACTCCTCCTCCAGTGAG 2502
Qy   2431 GAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGA-- 2488
Db   2503 GAGTCAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGGACA 2562
Qy   2489 ------------------------------GCAGAGATACCCCTGGGGGCCGCAGCGAT 2517
Db   2563 GTGGCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAGCAG 2622
Qy   2518 GGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACC 2577
Db   2623 TACAATGTGGGAATGGTGGGGACGCATGGGCTGGAGACCTCTCATGCGGACAGTTTCAGC 2682
Qy   2578 CAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAAC 2637
Db   2683 GGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAGAGAAGAAGCGA 2742
Qy   2638 CTGCTGCATGCTGACAGCAATGGGT---------ACACAAACCTGCCTGACGTGGTCCAG 2688
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Qy   2689 CCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAA------AGCCCACCCTCGAAGGAT 2742
Db   2803 CAGAGCCATTCTCCAGCTGGAACCCCGACTGAGGGACTGGGGCGCGTCTCAACCCATTCC 2862
Qy   2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
Db   2863 CAGGAGATGGACTCTGGGACTGAATATGGCATGGGGAGCAGCACCAAAGCCTCCTTCACC 2922
Qy   2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGT--------------GGGGAC 2847
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Qy   2848 AGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAG---CTGCAG 2904
Db   2983 GAATCATCAGCCGCAGCTCTGTTTACTAGCGAACTTCTTAGGCAAGAACAGGCCAAACTC 3042
Qy   2905 TACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGT 2964
Db   3043 AATGAAGCAAGAAAGATTTCGGTGGTAAATGTAAACCCAACCAACATTCGGCCTCATAGC 3102
Qy   2965 GAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCC 3024
Db   3103 GACACACCAGAAATCAGAAAATACAAGAAACGATTCAACTCAGAAATACTTTGTGCAGCT 3162
Qy   3025 CTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGT 3084
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Qy   3085 GGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTG 3144
Db   3223 GGGCAAGGCAAAGTCTATAATCTGATCAACCGGAGGCGATTTCAGCAGATGGATGTGCTA 3282
Qy   3145 GAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTAC 3204
Db   3283 GAGGGACTGAATGTCCTTGTGACAATTTCAGGAAAGAAGAATAAGCTACGAGTTTACTAT 3342
Qy   3205 CTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGC 3264
Db   3343 CTTTCATGGTTAAGAAACAGAATACTACATAATGACCCAGAAGTAGAAAAGAAACAAGGC 3402
Qy   3265 TGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGG 3324
Db   3403 TGGATCACTGTTGGGGACTTGGAAGGCTGTATACATTATAAAGTTGTTAAATATGAAAGG 3462
Qy   3325 ATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAA 3384
Db   3463 ATCAAATTTTTGGTGATTGCCTTAAAGAATGCTGTGGAAATATATGCTTGGGCTCCTAAA 3522
Qy   3385 CCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTG 3444
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Db     3523 CCGTATCATAAATTCATGGCATTTAAGTCTTTTGCAGATCTCCAGCACAAGCCTCTGCTA 3582

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Qy     3565 CAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATG 3624
Db     3703 CAGGGCAATATCACTCCTCATGCTATTGTCATCTTGCCTAAAACAGATGGAATGGAAATG 3762

Qy     3625 CTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGAT 3684
Db     3763 CTTGTTTGCTATGAGGATGAGGGGGTGTATGTAAACACCTATGGCCGGATAACTAAGGAT 3822

Qy     3685 GTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATA 3744
Db     3823 GTGGTGCTCCAATGGGGAGAAATGCCCACGTCTGTGGCCTACATTCATTCCAATCAGATA 3882

Qy     3745 ATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGG 3804
Db     3883 ATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTTGGATGGA 3942

Qy     3805 GTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTG 3864
Db     3943 GTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAGGTA 4002

Qy     3865 TTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGT 3924
Db     4003 TTTTTTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTTTTTCATGACCCTCAACAGA 4062

Qy     3925 AACTGCATCATGAACTGGTGA 3945
Db     4063 AATTCCATGATGAACTGGTAA 4083
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RESULT 12
US-09-645-791-1
; Sequence 1, Application US/09645791
; Patent No. 6569658
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AN
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68344-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/645,791
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 09/425,324
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4083
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-645-791-1

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  Query Match            34.4%;  Score 1358.6;  DB 4;  Length 4083;
  Best Local Similarity  61.7%;  Pred. No. 9.2e-275;
  Matches 2532;  Conservative    0;  Mismatches 1389;  Indels  180;  Gaps   16;

Qy        7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
Db        1 ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGAC 60

Qy       67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
Db       61 CCTGCAGGGATCTTTGAATTGGTGGAACTTGTTGGAAATGGAACATACGGGCAAGTTTAT 120

Qy      127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
Db      121 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGGTTATGGATGTCACAGGG 180

Qy      187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
Db      181 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACCGG 240

Qy      247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
Db      241 AATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCACCAGGCATGGATGACCAA 300

Qy      307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db      301 CTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCGACCTGATCAAGAACACA 360

Qy      367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db      361 AAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGCAGGGAAATCTTACGGGGG 420

Qy      427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db      421 CTGAGTCACCTGCACCAGCATAAAGTGATTCATCGAGATATTAAAGGGCAAAATGTCTTG 480

Qy      487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db      481 CTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCAGTGCTCAGCTTGATCGA 540

Qy      547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db      541 ACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGATGGCACCAGAAGTTATT 600

Qy      607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
Db      601 GCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTGACTTGTGGTCTTTGGGT 660

Qy      667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db      661 ATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCACCCCATGAGA 720

Qy      727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db      721 GCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGTCTAAGAAGTGGTCAAAA 780

Qy      787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
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Qy      847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db      841 GAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAATGAGCGACAGGTCCGCATT 900

Qy      907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db      901 CAACTCAAGGACCATATTGATAGAACAAAGAAGAAGCGAGGAGAAAAAGATGAGACAGAG 960

Qy      967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db      961 TATGAGTACAGTGGAAGTGAGGAAGAAGAGGAGGAGAAT---GACTCAGGAGAGCCCAGC 1017

Qy     1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db     1018 TCCATCCTGAATCTGCCAGGGGAGTCGACGCTGCGGAGGGACTTTCTGAGGCTGCAGCTG 1077

Qy     1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db     1078 GCCAACAAGGAGCGTTCTGAGGCCCTA------CGGAGGCAGCAGCTGGAGCAGCAGCAG 1131

Qy     1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
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Db   1132 CGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTCAGAAGCGCATCGAGGAG 1191

Qy   1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
Db   1192 CAGAAAGAGCAGAGGCGGCGGCTGGAGGAGCAACAAAGGCGAGAGAAGGAGCTGCGGAAG 1251

Qy   1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db   1252 CAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGG------AGCAGATGCGCCGGGAGGAG 1305

Qy   1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCT---GGAGGAGCAG 1383
Db   1306 GAGAGGAGGCGTGCGGAGCATGAACAGGAATACATCAGGCGACAGTTAGAGGAGGAGCAG 1365

Qy   1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
Db   1366 AGACAGTTAGAGATCTTGCAGCAGCAGCTACTGCATGAACAAGCTCTACTTCTGGAATAT 1425

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Db   1426 AAGCGCAAACAATTGGAAGAACAGAGACAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAA 1485

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Db   1546 AAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTGAGAAGCCAGCATGGGCCAAG 1605

Qy   1570 GAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAG 1629
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Qy   1630 CCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCC---------AGGCCTCCCCAGGGCCC 1680
Db   1663 GTTGCCAACAGGATATCTGACCCCAACCTGCCCCCAAGGTCGGAGTCCTTCAGCATTAGT 1722

Qy   1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAG--------- 1731
Db   1723 GGAGTTCAGCCTGCTCGAACACCCCCATGCTCAGACCAGTCGATCCCCAGATCCCACAT 1782

Qy   1732 GAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCC 1791
Db   1783 CTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCTCCCAGTCAGTGCACGAGCAG 1842

Qy   1792 TCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCT 1851
Db   1843 CCCACAAAGGGCCTCTCTGGGTTTCAGGAGGCTCTGAACGTGACCTCCCACCGCGTGGAG 1902

Qy   1852 GTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCAGCCCGA-------- 1903
Db   1903 ATGCCACGCCAGAACTCAGATCCCACCTCGGAAAATCCTCCTCTCCCCACTCGCATTGAA 1962

Qy   1904 -------ATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAG 1956
Db   1963 AAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCTCAA 2022

Qy   1957 AGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCC 2016
Db   2023 AGAACAACTTCTATATCCCCAGCATTAGCCAGAAAGAATTCTCCTGGGAATGGTAGTGCT 2082

Qy   2017 CAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAG--GC 2074
Db   2083 CTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGAACT 2142

Qy   2075 GGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCA 2134
Db   2143 GAGCCCATCTTGGAGAGCCCCTTGCAGAGGACCAGCAGTGGCAGTTCCTCCAGCTCCAGC 2202

Qy   2135 ACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGG----GAACGCTCGGAC 2190
Db   2203 ACCCCTAGCTCCCAGCCCAGCTCCCAAGGAGGCTCCCAGCCTGGATCACAAGCAGGATCC 2262

Qy   2191 AGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGC 2250
Db   2263 AGTGAACGCACCAGAGTTCGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTTCCCCAT 2322

Qy   2251 GTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAG 2310
Db   2323 GAGCCTGCCAAGGTGAAACCAGAAGAATCCAGGGACATTACCCGGCCCAGTCGACCAGCT 2382

Qy   2311 CCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGG 2370
Db   2383 AGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAGCCAAAGAACTAAGAGAACTC 2442

Qy   2371 ACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAG 2430
Db   2443 CGGATTGAAGAAACAAACCGCCCAATGAAGAAGGTGACTGATTACTCCTCCTCCAGTGAG 2502

Qy   2431 GAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGA-- 2488
Db   2503 GAGTCAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGGACA 2562

Qy   2489 ------------------------------GCAGAGATACCCCTGGGGGCCGCAGCGAT 2517
Db   2563 GTGGCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAGCAG 2622

Qy   2518 GGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACC 2577
Db   2623 TACAATGTGGGAATGGTGGGGACGCATGGGCTGGAGACCTCTCATGCGGACAGTTTCAGC 2682

Qy   2578 CAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAAC 2637
Db   2683 GGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAGAGAAGAAGCGA 2742

Qy   2638 CTGCTGCATGCTGACAGCAATGGGT---------ACACAAACCTGCCTGACGTGGTCCAG 2688
Db   2743 TCTGGCCACAGTGACAGCAATGGCTTTGCTGGCCACATCAACCTCCCTGACCTGGTGCAG 2802

Qy   2689 CCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAA------AGCCCACCCTCGAAGGAT 2742
Db   2803 CAGAGCCATTCTCCAGCTGGAACCCCGACTGAGGGACTGGGGCGCGTCTCAACCCATTCC 2862

Qy   2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
Db   2863 CAGGAGATGGACTCTGGGACTGAATATGGCATGGGGAGCAGCACCAAAGCCTCCTTCACC 2922

Qy   2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGT--------------GGGGAC 2847
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Qy   2848 AGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAG---CTGCAG 2904
Db   2983 GAATCATCAGCCGCAGCTCTGTTTACTAGCGAACTTCTTAGGCAAGAACAGGCCAAACTC 3042

Qy   2905 TACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGT 2964
Db   3043 AATGAAGCAAGAAAGATTTCGGTGGTAAATGTAAACCCAACCAACATTCGGCCTCATAGC 3102

Qy   2965 GAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCC 3024
Db   3103 GACACACCAGAAATCAGAAAATACAAGAAACGATTCAACTCAGAAATACTTTGTGCAGCT 3162

Qy   3025 CTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGT 3084
Db   3163 CTGTGGGGTGTAAACCTTCTGGTGGGGACTGAAAATGGCCTGATGCTTTTGGACCGAAGT 3222

Qy   3085 GGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTG 3144
Db   3223 GGGCAAGGCAAAGTCTATAATCTGATCAACCGGAGGCGATTTCAGCAGATGGATGTGCTA 3282

Qy   3145 GAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTAC 3204
Db   3283 GAGGGACTGAATGTCCTTGTGACAATTTCAGGAAAGAAGAATAAGCTACGAGTTTACTAT 3342
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Qy       3205 CTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGC 3264
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Qy       3265 TGGACCACCGTGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGG 3324
Db       3403 TGGATCACTGTTGGGGACTTGGAAGGCTGTATACATTATAAAGTTGTTAAATATGAAAGG 3462

Qy       3325 ATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAA 3384
Db       3463 ATCAAATTTTTGGTGATTGCCTTAAAGAATGCTGTGGAAATATATGCTTGGGCTCCTAAA 3522

Qy       3385 CCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTG 3444
Db       3523 CCGTATCATAAATTCATGGCATTTAAGTCTTTTGCAGATCTCCAGCACAAGCCTCTGCTA 3582

Qy       3445 GTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGC 3504
Db       3583 GTTGATCTCACGGTAGAAGAAGGTCAAAGATTAAAGGTTATTTTTGGTTCACACACTGGT 3642

Qy       3505 TTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATC 3564
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Qy       3565 CAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATG 3624
Db       3703 CAGGGCAATATCACTCCTCATGCTATTGTCATCTTGCCTAAAACAGATGGAATGGAAATG 3762

Qy       3625 CTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGAT 3684
Db       3763 CTTGTTTGCTATGAGGATGAGGGGGTGTATGTAAACACCTATGGCCGGATAACTAAGGAT 3822

Qy       3685 GTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATA 3744
Db       3823 GTGGTGCTCCAATGGGGAGAAATGCCCACGTCTGTGGCCTACATTCATTCCAATCAGATA 3882

Qy       3745 ATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGG 3804
Db       3883 ATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTTGGATGGA 3942

Qy       3805 GTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTG 3864
Db       3943 GTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAGGTA 4002

Qy       3865 TTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGT 3924
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Qy       3925 AACTGCATCATGAACTGGTGA 3945
Db       4063 AATTCCATGATGAACTGGTAA 4083
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RESULT 13
US-09-393-569-1
; Sequence 1, Application US/09393569
; Patent No. 6277979
; GENERAL INFORMATION:
; APPLICANT: BINGHAM, SHARON
; APPLICANT: CASE, PATRICK
; APPLICANT: LAWSON, SALLY NEALE
; APPLICANT: NEWTON, RICHARD ANTHONY
; APPLICANT: PIERCY, VALERIE
; APPLICANT: RAUSCH, OLIVER LARS
; APPLICANT: RAVAL, PRAVIN
; APPLICANT: REITH, ALASTAIR DAVID
; APPLICANT: SANGER, GARETH JOHN
; TITLE OF INVENTION: NEW USE
; FILE REFERENCE: P32261
; CURRENT APPLICATION NUMBER: US/09/393,569
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: GB 9907261.3
; EARLIER FILING DATE: 1999-03-29
; EARLIER APPLICATION NUMBER: GB 9819779.1
; EARLIER FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 4181
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-393-569-1

  Query Match   34.4%; Score 1358.6; DB 3; Length 4181;
  Best Local Similarity   61.7%; Pred. No. 9.3e-275;
  Matches 2532; Conservative   0; Mismatches 1389; Indels 180; Gaps   16;

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Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
Db         99 ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGAC 158

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
Db        159 CCTGCAGGGATCTTTGAATTGGTGGAACTTGTTGGAAATGGAACATACGGGCAAGTTTAT 218

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
Db        219 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGGTTATGGATGTCACAGGG 278

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
Db        279 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACCGG 338

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
Db        339 AATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCACCAGGCATGGATGACCAA 398

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db        399 CTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCGACCTGATCAAGAACACA 458

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
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Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db        639 ACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGATGGCACCAGAAGTTATT 698

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
Db        699 GCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTGACTTGTGGTCTTTGGGT 758

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db        759 ATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCACCCCATGAGA 818

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
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Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
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Qy    907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
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Qy    967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
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Qy   1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db   1116 TCCATCCTGAATCTGCCAGGGGAGTCGACGCTGCGGAGGACTTTCTGAGGCTGCAGCTG 1175

Qy   1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db   1176 GCCAACAAGGAGCGTTCTGAGGCCCTA------CGGAGGCAGCAGCTGGAGCAGCAGCAG 1229

Qy   1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
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Qy   1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db   1350 CAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGG------AGCAGATGCGCCGGGAGGAG 1403

Qy   1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCT---GGAGGAGCAG 1383
Db   1404 GAGAGGAGGCGTGCGGAGCATGAACAGGAATACATCAGGCGACAGTTAGAGGAGGAGCAG 1463

Qy   1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
Db   1464 AGACAGTTAGAGATCTTGCAGCAGCAGCTACTGCATGAACAAGCTCTACTTCTGGAATAT 1523

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Db   1524 AAGCGCAAACAATTGGAAGAACAGAGACAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAA 1583

Qy   1473 ------------------------GAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGG 1509
Db   1584 GAAAGAGACTACTTAGTTTCCCTTCAGCATCAGCGGCAGGAGCAGAGGCCTGTGGAGAAG 1643

Qy   1510 AAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGA 1569
Db   1644 AAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTGAGAAGCCAGCATGGGCCAAG 1703

Qy   1570 GAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAG 1629
Db   1704 GAGGTAGAAGAACGGTCAAGGCTCAACCGGCAAAGTTCCCCTGCCATGCCTCA---CAAG 1760

Qy   1630 CCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCC---------AGGCCTCCCCAGGGCCC 1680
Db   1761 GTTGCCAACAGGATATCTGACCCCAACCTGCCCCCAAGGTCGGAGTCCTTCAGCATTAGT 1820

Qy   1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAG--------- 1731
Db   1821 GGAGTTCAGCCTGCTCGAACACCCCCCATGCTCAGACCAGTCGATCCCCAGATCCCACAT 1880

Qy   1732 GAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCC 1791
Db   1881 CTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCTCCCAGTCAGTGCACGAGCAG 1940

Qy   1792 TCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCT 1851
Db   1941 CCCACAAAGGGCCTCTCTGGGTTTCAGGAGGCTCTGAACGTGACCTCCCACCGCGTGGAG 2000

Qy   1852 GTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGA-------- 1903
Db   2001 ATGCCACGCCAGAACTCAGATCCCACCTCGGAAAATCCTCCTCTCCCCACTCGCATTGAA 2060

Qy   1904 -------ATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAG 1956
Db   2061 AAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCTCAA 2120

Qy   1957 AGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGCCGGAGGGTCCCGGCCAGCC 2016
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Qy   2017 CAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAG--GC 2074
Db   2181 CTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGAACT 2240

Qy   2075 GGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCA 2134
Db   2241 GAGCCCATCTTGGAGAGCCCCTTGCAGAGGACCAGCAGTGGCAGTTCCTCCAGCTCCAGC 2300

Qy   2135 ACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGG----GAACGCTCGGAC 2190
Db   2301 ACCCCTAGCTCCCAGCCCAGCTCCCAAGGAGGCTCCCAGCCTGGATCACAAGCAGGATCC 2360

Qy   2191 AGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGC 2250
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Qy   2251 GTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAG 2310
Db   2421 GAGCCTGCCAAGGTGAAACCAGAAGAATCCAGGGACATTACCCGGCCCAGTCGACCAGCT 2480

Qy   2311 CCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGG 2370
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Qy   2371 ACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAG 2430
Db   2541 CGGATTGAAGAAACAAACCGCCCAATGAAGAAGGTGACTGATTACTCCTCCTCCAGTGAG 2600

Qy   2431 GAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGA-- 2488
Db   2601 GAGTCAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGGACA 2660

Qy   2489 ------------------------------GCAGAGATACCCCTGGGGGCCGCAGCGAT 2517
Db   2661 GTGGCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAGCAG 2720

Qy   2518 GGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACC 2577
Db   2721 TACAATGTGGGAATGGTGGGGACGCATGGGCTGGAGACCTCTCATGCGGACAGTTTCAGC 2780

Qy   2578 CAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAAC 2637
Db   2781 GGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAGAGAAGAAGCGA 2840

Qy   2638 CTGCTGCATGCTGACAGCAATGGGT---------ACACAAACCTGCCTGACGTGGTCCAG 2688
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Qy   2689 CCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAA------AGCCCACCCTCGAAGGAT 2742
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Db   2961 CAGGAGATGGACTCTGGGACTGAATATGGCATGGGGAGCAGCACCAAAGCCTCCTTCACC 3020

Qy   2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGT--------------GGGGAC 2847
Db   3021 CCCTTTGTGGACCCCAGAGTATACCAGACGTCTCCCACTGATGAAGATGAAGAGGATGAG 3080

Qy   2848 AGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAG---CTGCAG 2904
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Qy   2905 TACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGT 2964
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Qy     3025 CTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGT 3084
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Qy     3205 CTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGC 3264
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Db     3561 ATCAAATTTTTGGTGATTGCCTTAAAGAATGCTGTGGAAATATATGCTTGGGCTCCTAAA 3620

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Db     3621 CCGTATCATAAATTCATGGCATTTAAGTCTTTTGCAGATCTCCAGCACAAGCCTCTGCTA 3680

Qy     3445 GTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGC 3504
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Qy     3505 TTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATC 3564
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Qy     3565 CAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATG 3624
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Qy     3625 CTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGAT 3684
Db     3861 CTTGTTTGCTATGAGGATGAGGGGGTGTATGTAAACACCTATGGCCGGATAACTAAGGAT 3920

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Db     3981 ATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTTGGATGGA 4040

Qy     3805 GTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTG 3864
Db     4041 GTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAGGTA 4100

Qy     3865 TTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGT 3924
Db     4101 TTTTTTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTTTTCATGACCCTCAACAGA 4160

Qy     3925 AACTGCATCATGAACTGGTGA 3945
Db     4161 AATTCCATGATGAACTGGTAA 4181
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RESULT 14

US-09-688-188B-10
; Sequence 10, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 4055
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-688-188B-10

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  Query Match             34.1%;  Score 1345.6;  DB 4;  Length 4055;
  Best Local Similarity   62.2%;  Pred. No. 4.8e-272;
  Matches 2452;  Conservative    0;  Mismatches 1339;  Indels  153;  Gaps   15;

Qy      110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
Db        2 CTTTCGGGGAGGTCTATGAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGG 61

Qy      170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
Db       62 TTATGGATGTCACAGGGGATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGA 121

Qy      230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
Db      122 AATATTCTCATCACCGGAATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCAC 181

Qy      290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
Db      182 CAGGCATGGATGACCAACTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCG 241

Qy      350 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 409
Db      242 ACCTGATCAAGAACACAAAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGCA 301

Qy      410 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 469
Db      302 GGGAAATCTTACGGGGGCTGAGTCACCTGCACCAGCATAAAGTGATTCATCGAGATATTA 361

Qy      470 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 529
Db      362 AAGGGCAAAATGTCTTGCTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCA 421

Qy      530 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 589
Db      422 GTGCTCAGCTTGATCGAACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGA 481

Qy      590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
Db      482 TGGCACCAGAAGTTATTGCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTG 541

Qy      650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
Db      542 ACTTGTGGTCTTTGGGTATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTG 601

Qy      710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
Db      602 ACATGCACCCCATGAGAGCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGT 661

Qy      770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
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Db    782 AGCGACAGGTCCGCATTCAACTCAAGGACCATATTGATAGAACAAAGAAGAAGCGAGGAG 841

Qy    950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
Db    842 AAAAAGATGAGACAGAGTATGAGTACAGTGGAAGTGAGGAAGAAGAGGAGGAGAAT---G 898

Qy   1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
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Qy   1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
Db    959 TTCTGAGGCTGCAGCTGGCCAACAAGGAGCGTTCTGAGGCCCTA------CGGAGGCAGC 1012

Qy   1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
Db   1013 AGCTGGAGCAGCAGCAGCGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTC 1072

Qy   1190 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1249
Db   1073 AGAAGCGCATCGAGGAGCAGAAAGAGCAGAGGCGGCGGCTGGAGGAGCAACAAAGGCGAG 1132

Qy   1250 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1309
Db   1133 AGAAGGAGCTGCGGAAGCAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGG------AGC 1186

Qy   1310 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGC 1369
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Qy   1370 AGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCT 1429
Db   1247 AATTGGAAGAACAGAGACAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAAGAAAGAGACT 1306

Qy   1430 ACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGC 1489
Db   1307 ACTTAGTTTCCCTTCAGCATCAGCGGCAGGAGCAGAG---------------------- 1343

Qy   1490 AGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTG 1549
Db   1344 -------GCCTGTGGAGAAGAAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTG 1396

Qy   1550 ACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACT 1609
Db   1397 AGAAGCCAGCATGGGCCAAGGAGGTAGAAGAACGGTCAAGGCTCAACCGGCAAAGTTCCC 1456

Qy   1610 CTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCC------ 1663
Db   1457 CTGCCATGCCTCA---CAAGGTTGCCAACAGGATATCTGACCCCAACCTGCCCCCAAGGT 1513

Qy   1664 ---AGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGG 1720
Db   1514 CGGAGTCCTTCAGCATTAGTGGAGTTCAGCCTGCTCGAACACCCCCCATGCTCAGACCAG 1573

Qy   1721 TGGAGCCCCAGGAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTG 1780
Db   1574 TCGATCCCCAGATCCCACATCTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCT 1633

Qy   1781 CCTTCCCAGCCTCCCATGACCCCG---------ACCCTGCCATCCCCGCACCCACTGCCA 1831
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Qy   1832 CGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTG 1891
Db   1694 TGACCTCCCACCGCGTGGAGATGCCACGCCAGAACTCAGATCCCACCTCGGAAAATCCTC 1753

Qy   1892 GCCCCAGCCC---------------GAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGG 1936
Db   1754 CTCTCCCCACTCGCATTGAAAAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACA 1813

Qy   1937 CCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGG 1996
Db   1814 TTCCACCAAAGGTGCCTCAAAGAACAACTTCTATATCCCCAGCATTAGCCAGAAAGAATT 1873

Qy   1997 CCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGC 2056
Db   1874 CTCCTGGGAATGGTAGTGCTCTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCA 1933

Qy   2057 AAATCTATCTGC----AAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCT 2112
Db   1934 ACCCTGATCTCCGGAGAACTGAGCCCATCTTGGAGAGCCCCTTGCAGAGGACCAGCAGTG 1993

Qy   2113 GCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAG--CGACC 2170
Db   1994 GCAGTTCCTCCAGCTCCAGCACCCCTAGCTCCCAGCCCAGCTCCCAAGGAGGCTCCCAGC 2053

Qy   2171 CTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTG 2230
Db   2054 CTGGATCACAAGCAGGATCCAGTGAACGCACCAGAGTTCGAGCCAACAGTAAGTCAGAAG 2113

Qy   2231 GCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCT 2290
Db   2114 GATCACCTGTGCTCCCCCATGAGCCTGCCAAGGTGAAACCAGAAGAATCCAGGGACATTA 2173

Qy   2291 CCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACT 2350
Db   2174 CCCGGCCCAGTCGACCAGCTAGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAG 2233

Qy   2351 TTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGG 2410
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Qy   2411 ACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAG 2470
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Qy   2471 GCGGGCCAGCAGAGGGGAGC---------------------------------AGAGATA 2497
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Qy       3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
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Qy       3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
Db       3194 AAGTAGAAAAGAAACAAGGCTGGATCACTGTTGGGGACTTGGAAGGCTGTATACATTATA 3253

Qy       3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
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Qy       3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
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Db       3794 GTGAAAGAAATGATAAGGTATTTTTTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGT 3853

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US-09-291-417D-10
; Sequence 10, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0329
;  CURRENT APPLICATION NUMBER: US/09/291,417D
;  CURRENT FILING DATE:  1999-04-13
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 4055
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-291-417D-10

  Query Match             34.1%;  Score 1345.6;  DB 4;  Length 4055;
  Best Local Similarity   62.2%;  Pred. No. 4.8e-272;
  Matches 2452;  Conservative    0;  Mismatches 1339;  Indels  153;  Gaps   15;

Qy        110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
Db          2 CTTTCGGGGAGGTCTATGAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGG 61

Qy        170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
Db         62 TTATGGATGTCACAGGGGATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGA 121

Qy        230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
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Qy        290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
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Db        362 AAGGGCAAAATGTCTTGCTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCA 421

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Db        422 GTGCTCAGCTTGATCGAACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGA 481

Qy        590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
Db        482 TGGCACCAGAAGTTATTGCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTG 541

Qy        650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
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Qy        710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
Db        602 ACATGCACCCCATGAGAGCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGT 661

Qy        770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
Db        662 CTAAGAAGTGGTCAAAAAAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCACA 721
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Db    722 GCCAGCGACCAGCAACAGAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAATG 781

Qy    890 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 949
Db    782 AGCGACAGGTCCGCATTCAACTCAAGGACCATATTGATAGAACAAAGAAGAAGCGAGGAG 841

Qy    950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
Db    842 AAAAAGATGAGACAGAGTATGAGTACAGTGGAAGTGAGGAAGAAGAGGAGGAGAAT---G 898

Qy   1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
Db    899 ACTCAGGAGAGCCCAGCTCCATCCTGAATCTGCCAAGGGAGTCGACGCTGCGGAGGGACT 958

Qy   1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
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Qy   1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
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Qy   1430 ACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGC 1489
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Qy   1721 TGGAGCCCCAGGAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTG 1780
Db   1574 TCGATCCCCAGATCCCACATCTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCT 1633

Qy   1781 CCTTCCCAGCCTCCCATGACCCCG---------ACCCTGCCATCCCCGCACCCACTGCCA 1831
Db   1634 CCCAGTCAGTGCACGAGCAGCCCACAAAGGGCCTCTCTGGGTTTCAGGAGGCTCTGAACG 1693

Qy   1832 CGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTG 1891
Db   1694 TGACCTCCCACCGCGTGGAGATGCCACGCCAGAACTCAGATCCCACCTCGGAAAATCCTC 1753

Qy   1892 GCCCCAGCCC---------------GAATCCCCAGCCTGGGTCCGCCCAGATAACGAGG 1936
Db   1754 CTCTCCCCACTCGCATTGAAAAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACA 1813

Qy   1937 CCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGG 1996
Db   1814 TTCCACCAAAGGTGCCTCAAAGAACAACTTCTATATCCCCAGCATTAGCCAGAAAGAATT 1873

Qy   1997 CCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGC 2056
Db   1874 CTCCTGGGAATGGTAGTGCTCTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCA 1933

Qy   2057 AAATCTATCTGC----AAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCT 2112
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Qy   2113 GCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAG--CGACC 2170
Db   1994 GCAGTTCCTCCAGCTCCAGCACCCCTAGCTCCCAGCCCAGCTCCCAAGGAGGCTCCCAGC 2053

Qy   2171 CTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTG 2230
Db   2054 CTGGATCACAAGCAGGATCCAGTGAACGCACCAGAGTTCGAGCCAACAGTAAGTCAGAAG 2113

Qy   2231 GCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCT 2290
Db   2114 GATCACCTGTGCTCCCCCATGAGCCTGCCAAGGTGAAACCAGAAGAATCCAGGGACATTA 2173

Qy   2291 CCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACT 2350
Db   2174 CCCGGCCCAGTCGACCAGCTAGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAG 2233

Qy   2351 TTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGG 2410
Db   2234 CCAAAGAACTAAGAGAACTCCGGATTGAAGAAACAAACCGCCCAATGAAGAAGGTGACTG 2293

Qy   2411 ACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAG 2470
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Qy   2471 GCGGGCCAGCAGAGGGGAGC--------------------------------AGAGATA 2497
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Search completed: March 2, 2004, 14:48:30

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Total number of hits satisfying chosen parameters:      4707466

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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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SUMMARIES

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2		3792.8	96.0	4033	14	US-10-029-115-5	Sequence 5, Appli
3		3635	92.0	4133	10	US-09-291-417-11	Sequence 11, Appl
4		3601	91.1	4863	15	US-10-441-281-30	Sequence 30, Appl
5		3583.8	90.7	3912	10	US-09-789-390-8	Sequence 8, Appli
6		3501.2	88.6	3999	10	US-09-789-390-6	Sequence 6, Appli
7		3437.2	87.0	4414	14	US-10-029-115-3	Sequence 3, Appli
8		3358.2	85.0	3735	10	US-09-789-390-12	Sequence 12, Appl
9		3275.6	82.9	3822	10	US-09-789-390-10	Sequence 10, Appl
10		1551	39.3	1717	10	US-09-789-390-69	Sequence 69, Appl
11		1502.6	38.0	2345	9	US-09-925-297-137	Sequence 137, App
12		1468.4	37.2	1787	10	US-09-789-390-66	Sequence 66, Appl
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17		1345.6	34.1	4055	10	US-09-291-417-10	Sequence 10, Appl
18		1257.4	31.8	3807	15	US-10-353-690-121	Sequence 121, App
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24		786.4	19.9	1657	10	US-09-789-390-29	Sequence 29, Appl
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ALIGNMENTS

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; Publication No. US20030077597A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Ying
;  APPLICANT:  Fu, Alan C
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION: No. US20030077597A1el Germinal Center Kinase Cell Cycle Protiens,
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: A-70229/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/10/029,115
;  CURRENT FILING DATE:  2001-10-19
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 3951
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-1

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Qy       2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100
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Db       2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100

Qy       2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160

Qy       2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220

Qy       2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280

Qy       2281 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGG 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGG 2340

Qy       2341 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAG 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAG 2400
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Qy       2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460

Qy       2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520

Qy       2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580

Qy       2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640

Qy       2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700

Qy       2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760

Qy       2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820
              ||·|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820

Qy       2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880
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Db       2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880

Qy       2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940

Qy       2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000

Qy       3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060

Qy       3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120

Qy       3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180

Qy       3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240

Qy       3241 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC 3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC 3300

Qy       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360

Qy       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420

Qy       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480

Qy       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540

Qy       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600

Qy       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660

Qy       3661 ACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTG 3720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 ACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTG 3720

Qy       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780

Qy       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840

Qy       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA 3900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA 3900

Qy       3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951

RESULT 2
US-10-029-115-5
; Sequence 5, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Ying
;  APPLICANT:  Fu, Alan C
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION: No. US20030077597Alel Germinal Center Kinase Cell Cycle Protiens,
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: A-70229/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/10/029,115
;  CURRENT FILING DATE:  2001-10-19
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 4033
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-5

  Query Match             96.0%;  Score 3792.8;  DB 14;  Length 4033;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 3877;  Conservative    0;  Mismatches    2;  Indels   63;  Gaps    2;

Qy         64 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 123
              |||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db         95 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 154

Qy        124 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 214

Qy        184 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 243
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Db        215 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 274

Qy        244 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 334
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Qy    304 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 363
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Db    335 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 394

Qy    364 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    395 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 454

Qy    424 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    455 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 514

Qy    484 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    515 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 574

Qy    544 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    575 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 634

Qy    604 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    635 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 694

Qy    664 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    695 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 754

Qy    724 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    755 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 814

Qy    784 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    815 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 874

Qy    844 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    875 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 934

Qy    904 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 963
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Db    935 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 994

Qy    964 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    995 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1054

Qy   1024 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1055 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1114

Qy   1084 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1115 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1174

Qy   1144 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1175 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1234

Qy   1204 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGAGCGGGAGCAGCGG 1263
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   1235 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGGGCGGGAGCAGCGG 1294

Qy   1264 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1295 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1354

Qy   1324 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1355 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1414

Qy   1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1415 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1474

Qy   1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1475 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1534

Qy   1504 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1563
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Db   1535 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1594

Qy   1564 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1595 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1654

Qy   1624 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1655 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1714

Qy   1684 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1715 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1774

Qy   1744 A----------------------------------------------------------- 1744
          |
Db   1775 AAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCC 1834

Qy   1745 -AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1803
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1835 CAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1894

Qy   1804 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1895 GACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAG 1954

Qy   1864 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1955 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 2014

Qy   1924 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2015 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 2074

Qy   1984 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2075 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2134

Qy   2044 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2135 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2194

Qy   2104 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2195 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2254

Qy   2164 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2223
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Db   2255 AGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCC 2314

Qy   2224 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2315 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2374

Qy   2284 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2375 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2434

Qy   2344 GCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAG 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2435 GCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAG 2494

Qy   2404 GCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAA 2463
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2495 GCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAA 2554

Qy         2464 GGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGAT 2523
                ||||||||||||||||||||||||||||||||||||||||||||   |||||||||||
Db         2555 GGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGAT 2611

Qy         2524 ACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCC 2583
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2612 ACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCC 2671

Qy         2584 CCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTG 2643
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2672 CCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTG 2731

Qy         2644 CATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCC 2703
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2732 CATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCC 2791

Qy         2704 ACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCT 2763
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2792 ACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCT 2851

Qy         2764 CGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATC 2823
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2852 CGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATC 2911

Qy         2824 TACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGC 2883
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2912 TACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGC 2971

Qy         2884 ACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCC 2943
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2972 ACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCC 3031

Qy         2944 ACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAAC 3003
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3032 ACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAAC 3091

Qy         3004 TCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGG 3063
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3092 TCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGG 3151

Qy         3064 CTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGC 3123
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3152 CTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGC 3211

Qy         3124 TTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGG 3183
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3212 TTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGG 3271

Qy         3184 AACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCA 3243
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3272 AACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCA 3331

Qy         3244 GAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTAC 3303
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3332 GAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTAC 3391

Qy         3304 CGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAG 3363
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3392 CGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAG 3451

Qy         3364 GTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGAC 3423
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3452 GTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGAC 3511

Qy         3424 CTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTC 3483
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3512 CTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTC 3571

Qy         3484 ATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGAC 3543
                |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db         3572 ATCTATGGCTCCAGTGCTGGCTTCCATGCTGCGGATGTCGACTCGGGGAACAGCTATGAC 3631

Qy         3544 ATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCC 3603
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3632 ATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCC 3691

Qy         3604 AACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACG 3663
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3692 AACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACG 3751

Qy         3664 TACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCC 3723
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3752 TACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCC 3811

Qy         3724 TACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTG 3783
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3812 TACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTG 3871

Qy         3784 GAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTG 3843
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Db         3872 GAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTG 3931

Qy         3844 TGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTT 3903
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Db         3932 TGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTT 3991

Qy         3904 TACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
                ||||||||||||||||||||||||||||||||||||||||||
Db         3992 TACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4033
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RESULT 3
US-09-291-417-11
; Sequence 11, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT: MARTINEZ, RICARDO
;  APPLICANT: WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 240/300
;  CURRENT APPLICATION NUMBER: US/09/291,417A
;  CURRENT FILING DATE: 1999-04-13
;  EARLIER APPLICATION NUMBER: US 60/081,784
;  EARLIER FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Mammalian (Human) ZC3
US-09-291-417-11

  Query Match             92.0%;  Score 3635;  DB 10;  Length 4133;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 3824;  Conservative    0;  Mismatches   15;  Indels  150;  Gaps    3;

Qy          110 CCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 169
                | |  ||  |||||||  ||||||||||||||||||||||||||||||||||||||||||
Db            2 CATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGG 61

Qy          170 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 229
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           62 TCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAA 121

Qy          230 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 289
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          122 AGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCC 181

Qy          290 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 349
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          182 CGGGAAACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTG 241
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Qy        350 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCA 301

Qy        410 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCA 361

Qy        470 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGA 421

Qy        530 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 589
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Db        422 GTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGA 481

Qy        590 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTG 541

Qy        650 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 709
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Db        542 ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTG 601

Qy        710 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACATGCACCCCATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGT 661

Qy        770 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACC 721

Qy        830 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 TGAGCCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGG 781

Qy        890 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 AGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTG 841

Qy        950 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 AGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAG 901

Qy       1010 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 AGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGT 961

Qy       1070 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGC 1021

Qy       1130 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGC 1081

Qy       1190 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGG 1141

Qy       1250 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGG 1201

Qy       1310 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCA----------------- 1352
              ||||||||||||||||||||||||||||||||||||| |||||
Db       1202 CTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACA 1261

Qy       1353 ------------------------------------------------------------ 1352

Db       1262 GGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGG 1321

Qy       1353 ----------GGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1402
                        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 CCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1381

Qy       1403 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1441

Qy       1463 AGCAGCTTCAGAAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1522
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 AGCAGCTTCAGAAACAACAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1501

Qy       1523 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1582
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Db       1502 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1561

Qy       1583 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1621

Qy       1643 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTC 1681

Qy       1703 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA------------------ 1744
              ||||||||||||||||||||||||||||||||||||||||||
Db       1682 CTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAGAGCCTGGTGGCACACC 1741

Qy       1745 ------------------------------------------AGTCCCTGCAGGACCAGC 1762
                                                        ||||||||||||||||||
Db       1742 GGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAGC 1801

Qy       1763 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 CCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCAC 1861

Qy       1823 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 CCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTG 1921

Qy       1883 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 AAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCAC 1981

Qy       1943 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 CCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAG 2041

Qy       2003 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 GGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCT 2101

Qy       2063 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 ATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCC 2161

Qy       2123 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2182
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Db       2162 CTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAAC 2221

Qy       2183 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2222 GCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGC 2281

Qy       2243 GGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2302
              ||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||
Db       2282 GGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATA 2341

Qy       2303 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2342 AAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGA 2401

Qy       2363 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        2402 AAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGT 2461

Qy        2423 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2482
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Db        2462 CCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAG 2521

Qy        2483 AGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCA 2542
               |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        2522 AGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATACAGACAGCGTCAGCACCA 2578

Qy        2543 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2602
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Db        2579 TGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCA 2638

Qy        2603 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2662
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Db        2639 TGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGT 2698

Qy        2663 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2722
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Db        2699 ACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCC 2758

Qy        2723 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2782
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Db        2759 AAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCC 2818

Qy        2783 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2842
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Db        2819 CTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTG 2878

Qy        2843 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2902
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Db        2879 GGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGC 2938

Qy        2903 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2962
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Db        2939 AGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACA 2998

Qy        2963 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3022
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Db        2999 GTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAG 3058

Qy        3023 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3082
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Db        3059 CCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3118

Qy        3083 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3142
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3119 GTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGC 3178

Qy        3143 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3202
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3179 TGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATT 3238

Qy        3203 ACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3262
               || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3239 ACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGG 3298

Qy        3263 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3322
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3299 GCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGC 3358

Qy        3323 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3382
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Db        3359 GGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCA 3418

Qy        3383 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3442
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3419 AACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGC 3478

Qy        3443 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3502
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3479 TGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTG 3538

Qy        3503 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3562
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3539 GCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3598

Qy        3563 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3622
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3599 TCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGA 3658

Qy        3623 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3682
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3659 TGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGG 3718

Qy        3683 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3742
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3719 ATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGA 3778

Qy        3743 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3802
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Db        3779 TAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3838

Qy        3803 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3862
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3839 GGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3898

Qy        3863 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3922
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3899 TGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACC 3958

Qy        3923 GTAACTGCATCATGAACTGGTGAAAGGGC 3951
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Db        3959 GTAACCGCATCATGAACTGGTGACGGGGC 3987
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RESULT 4
US-10-441-281-30
; Sequence 30, Application US/10441281
; Publication No. US20030228618A1
; GENERAL INFORMATION:
;  APPLICANT: Levanon Erez, et al.
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING NATURALLY OCCURRING ANTISENSE
;  TITLE OF INVENTION:  TRANSCRIPTS AND METHODS AND KITS UTILIZING SAME
;  FILE REFERENCE: 02/26133
;  CURRENT APPLICATION NUMBER: US/10/441,281
;  CURRENT FILING DATE:  2003-05-20
;  PRIOR APPLICATION NUMBER: US 09/718,407
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: US 09/732,938
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/785,439
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: US 09/907,923
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 009/993,398
;  PRIOR FILING DATE: 2001-11-06
;  PRIOR APPLICATION NUMBER: US 10/201,605
;  PRIOR FILING DATE: 2002-07-24
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 4863
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-441-281-30

  Query Match             91.1%;  Score 3601;  DB 15;  Length 4863;
  Best Local Similarity   95.0%;  Pred. No. 0;
  Matches 3829;  Conservative    0;  Mismatches    5;  Indels  195;  Gaps    3;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 244
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Qy        67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 304

Qy       127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 364

Qy       187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       365 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 424

Qy       247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       425 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 484

Qy       307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       485 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 544

Qy       367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       545 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 604

Qy       427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       605 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 664

Qy       487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Db       665 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 724

Qy       547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       725 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 784

Qy       607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy       667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy       727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy       787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy       847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy       907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1085 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1144

Qy       967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy      1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy      1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy      1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1325 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1384

Qy      1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy      1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy      1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db      1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy      1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy      1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

Qy      1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1685 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1744

Qy      1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy      1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy      1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924

Qy      1745 ----------------------------------------------------------AG 1746
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Db      1925 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1984

Qy      1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1985 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 2044

Qy      1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2045 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 2104

Qy      1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2105 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 2164

Qy      1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2165 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2224

Qy      1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
             |||||||||||||||||||||||||||||||||||||||||||||
Db      2225 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2269

Qy      2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db      2270 ------------------------------------------------------------ 2269

Qy      2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
                                                 ||||||||||||||||||||||||
Db      2270 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 2293

Qy      2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2294 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2353

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
              ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Db       2354 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTG 2413

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2414 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2473

Qy       2347 ------------------------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
                                      ||||||||||||||||||||||||||||||||||||
Db       2474 AGCTATAAGCGAGCAATTGGTGAGGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2533

Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2534 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2593

Qy       2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
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Db       2594 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2653

Qy       2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
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Db       2654 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2713

Qy       2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2714 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2773

Qy       2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
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Db       2774 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2833

Qy       2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
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Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
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Db       2894 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2953

Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
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Db       2954 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 3013

Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
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Db       3014 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 3073

Qy       2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
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Db       3074 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 3133

Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
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Db       3134 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3193

Qy       3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
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Db       3194 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3253

Qy       3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
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Db       3254 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3313

Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3314 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3373

Qy       3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3374 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3433

Qy       3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3434 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3493

Qy       3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3402
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Db       3494 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3553

Qy       3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
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Db       3554 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3613

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3614 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3673

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3734 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3793

Qy       3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3794 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3853

Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3854 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3913

Qy       3763 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3914 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3973

Qy       3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3882
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Db       3974 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 4033

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4034 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 4093

Qy       3943 TGAAAGGGC 3951
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Db       4094 TGACGGGGC 4102
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RESULT 5
US-09-789-390-8
; Sequence 8, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
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;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 3912
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3909)
US-09-789-390-8

  Query Match             90.7%;  Score 3583.8;  DB 10;  Length 3912;
  Best Local Similarity   94.9%;  Pred. No. 0;
  Matches 3816;  Conservative    0;  Mismatches   12;  Indels  195;  Gaps    3;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
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Db          1 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 60

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 300

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 480

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Db        481 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 540

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 660

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 720

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Db        721 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 780

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 840

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 960

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1080

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1140

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1200

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1260

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1320

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||| ||||||||||  |  ||  |   ||| |||||||||||
Db       1321 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGCAGCGG 1380

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
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Db       1381 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1440

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
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Db       1441 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1500

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
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Db       1501 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1560

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1620

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1680

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACA-- 1744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1740

Qy       1745 ----------------------------------------------------------AG 1746
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Db       1741 AGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAG 1800

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1860

Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
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Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
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Db       1921 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1980

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
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Db       1981 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 2040

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
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Db       2041 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 2085

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106

Db       2086 ------------------------------------------------------------ 2085

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
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Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
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Db       2110 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2169

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
              ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Db       2170 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTG 2229

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
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Db       2230 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2289

Qy       2347 ------------------------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
                                      ||||||||||||||||||||||||||||||||||||
Db       2290 AGCTATAAGCGAGCAATTGGTGAGGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2349

Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2409

Qy       2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2469

Qy       2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
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Db       2470 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2529

Qy       2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
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Db       2530 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2589

Qy       2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2649

Qy       2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
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Db       2650 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2709

Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
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Db       2710 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2769

Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
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Db       2770 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2829

Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
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Db       2830 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2889

Qy       2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
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Db       2890 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2949

Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
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Db       2950 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3009

Qy       3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
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Db       3010 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3069

Qy       3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
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Db       3070 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3129

Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
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Db       3130 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3189

Qy       3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
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Db       3190 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3249

Qy       3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
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Db       3250 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3309

Qy       3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3402
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Db       3310 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3369

Qy       3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
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Db       3370 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3429

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
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Db       3430 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3489

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
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Db       3490 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3549

Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3550 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3609

Qy       3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3669

Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3762
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Db       3670 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3729

Qy       3763 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3730 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3789

Qy       3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3882
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Db       3790 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3849

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
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Db       3850 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3909

Qy       3943 TGA 3945
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Db       3910 TGA 3912

RESULT 6
US-09-789-390-6
; Sequence 6, Application US/09789390
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; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 3999
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3996)
US-09-789-390-6

  Query Match             88.6%;  Score 3501.2;  DB 10;  Length 3999;
  Best Local Similarity   93.1%;  Pred. No. 0;
  Matches 3825;  Conservative    0;  Mismatches    3;  Indels  282;  Gaps    4;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
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Db          1 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 60

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
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Db         61 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
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Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
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Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
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Db        241 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 300

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Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
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Db        661 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 720

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Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
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Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
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Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
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Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
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Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
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Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
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Db       1261 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1320

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCA---------------------------------- 1352
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Db       1321 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGGAGCAG 1380

Qy       1353 -----------------------------------------------------GGAATAC 1359
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Db       1381 CGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGGCCCTGCTGCTGGAATAC 1440

Qy       1360 AAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAG 1419
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Qy       1420 GAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAG 1479
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Qy       1540 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAG 1599
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Db   1621 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAG 1680

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Qy   1660 CCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCG 1719
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Qy   1720 GTGGAGCCCCAGGAGGGACCGCACA----------------------------------- 1744
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Db   2041 CCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGG 2100

Qy   1960 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 2019
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Db   2101 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 2160

Qy   2020 GCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCA 2079
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Db   2161 GCAGTCCGTGCC------------------------------------------------ 2172

Qy   2080 GAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCC 2139

Db   2173 ------------------------------------------------------------ 2172

Qy   2140 TCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTT 2199
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Qy   2200 CCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCC 2259
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Qy   2260 TCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGAC 2319
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Qy   2320 CACCGCTCACGGCCAGGCCGGCCCGCA------------------------GACTTTGTG 2355
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Qy   2356 TTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTAC 2415
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Qy   2476 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2535
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Db   2530 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2589

Qy   2536 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2595
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Db   2590 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2649

Qy   2596 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2655
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Db   2650 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2709

Qy   2656 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2715
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Qy   2716 AAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTA 2775
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Qy   2776 AAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGA 2835
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Qy   2836 GGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGAC 2895
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Qy   3076 GACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATG 3135
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Qy   3256 AAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAA 3315
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Db   3310 AAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAA 3369

Qy   3316 TACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGG 3375
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Db   3550 AGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCT 3609

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Qy       3736 AACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCAC 3795
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RESULT 7
US-10-029-115-3
; Sequence 3, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: No. US20030077597A1el Germinal Center Kinase Cell Cycle Protiens,
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: A-70229/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 4414
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-3

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  Query Match             87.0%;  Score 3437.2;  DB 14;  Length 4414;
  Best Local Similarity   90.1%;  Pred. No. 0;
  Matches 3885;  Conservative    0;  Mismatches    3;  Indels  426;  Gaps    2;

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Qy        124 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 183
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Db        161 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 220

Qy        184 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 243
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Db        221 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 280

Qy        244 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 303
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Db        341 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 400

Qy        364 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 460

Qy        424 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 520

Qy        484 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 580

Qy        544 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 640

Qy        604 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 700

Qy        664 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 760

Qy        724 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 820

Qy        784 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 880

Qy        844 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 903
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Db        881 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 940

Qy        904 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 963
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Db        941 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 1000

Qy        964 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1001 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1060

Qy       1024 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1083
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Db       1061 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1120

Qy       1084 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1143
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Qy       1144 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1203
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Qy       1204 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1263
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Db       1241 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1300

Qy       1264 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1323
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Db       1301 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1360

Qy       1324 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1383
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Db       1361 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1420

Qy       1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
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Db       1421 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1480

Qy       1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1503
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Db       1481 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1540

Qy       1504 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1563
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Qy     1564 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1623
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Db     1601 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1660

Qy     1624 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1683
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Db     1661 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1720

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Db     1721 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1780

Qy     1744 A----------------------------------------------------------- 1744
            |
Db     1781 AAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCC 1840

Qy     1745 -AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCC 1803
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Qy     1864 AATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGC 1923
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Qy     1924 CCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTT 1983
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Qy     1984 AACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGC 2043
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Qy     2044 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2103
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Db     2141 AACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCA 2200

Qy     2104 GGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGG 2163
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Qy     2224 CAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCT 2283
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Qy     2284 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2343
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Db     2381 GTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCC 2440

Qy     2344 GCA--------------------------------------------------------- 2346
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Qy     2347 ------------------------------------------------------------ 2346

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Qy     2347 ------------------------------------------------------------ 2346

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Qy     2347 ------------------------------------------------------------ 2346

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Qy     2347 ------------------------------------------------------------ 2346

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Qy     2347 ---------GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCC 2397
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Db     2801 TCCCTGCAGGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCC 2860

Qy     2398 AAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAG 2457
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Qy     2458 GAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGAT 2517
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Db     2921 GAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGAT 2980

Qy     2518 GGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACC 2577
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Db     2981 GGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACC 3040

Qy     2578 CAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAAC 2637
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Qy     2638 CTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCAC 2697
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3101 CCGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCAC 3160

Qy     2698 TCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTAC 2757
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Qy     2758 CAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTA 2817
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Db     3221 CAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTA 3280

Qy     2818 GGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGA 2877
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Qy     2878 GAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTG 2937
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Db     3341 GAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTG 3400

Qy     2938 AATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGA 2997
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Qy     2998 TTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAG 3057
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Db     3461 TTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAG 3520

Qy     3058 AACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGG 3117
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Qy     3118 CGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGG 3177
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Qy     3238 GACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGG 3297
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Qy     3298 CACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCC 3357
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Db       3761 CACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCC 3820

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Qy       3418 GCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTC 3477
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Db       3881 GCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTC 3940

Qy       3478 AAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGC 3537
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Qy       3538 TATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTC 3597
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Qy       3598 CTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTC 3657
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Qy       3658 AACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCT 3717
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Qy       3718 GTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGC 3777
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RESULT 8
US-09-789-390-12
; Sequence 12, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 3735
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3732)
US-09-789-390-12

  Query Match             85.0%;  Score 3358.2;  DB 10;  Length 3735;
  Best Local Similarity   92.7%;  Pred. No. 0;
  Matches 3673;  Conservative    0;  Mismatches   38;  Indels  252;  Gaps    4;

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Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

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Db        541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 660

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 720

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 780

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 840

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 900

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 960
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Qy      967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db      961 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1020

Qy     1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db     1021 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1080

Qy     1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db     1081 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1140

Qy     1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db     1141 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1200

Qy     1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
Db     1201 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1260

Qy     1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db     1261 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1320

Qy     1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
Db     1321 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGCAGCGG 1380

Qy     1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
Db     1381 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1440

Qy     1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
Db     1441 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1500

Qy     1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
Db     1501 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1560

Qy     1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
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Qy     1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
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Qy     1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
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Qy     1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
Db     1684 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1743

Qy     1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
Db     1744 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1803

Qy     1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
Db     1804 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1863

Qy     1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
Db     1864 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCC--------------- 1908

Qy     2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106
Db     1909 ------------------------------------------------------------ 1908

Qy     2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
Db     1909 ------------------------------------AGTAACCCCGACCTCAGGAGGAGC 1932

Qy     2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
Db     1933 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 1992

Qy     2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
Db     1993 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTG 2052

Qy     2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
Db     2053 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2112

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Db     2113 AGCTATAAGCGAGCAATTGGTGAGGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2172

Qy     2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
Db     2173 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2232

Qy     2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
Db     2233 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2292

Qy     2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
Db     2293 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2352

Qy     2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
Db     2353 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2412

Qy     2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
Db     2413 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2472

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Db     2473 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2532

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Qy     2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
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Qy     2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
Db     2653 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2712

Qy     2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
Db     2713 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2772

Qy     2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
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Qy     3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
Db     2833 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 2892

Qy     3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
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Db       2893 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 2952

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Db       2953 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3012

Qy       3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
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Db       3013 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3072

Qy       3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
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Qy       3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3402
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Db       3133 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3192

Qy       3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
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Db       3193 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3252

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3253 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3312

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3313 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3372

Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3373 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3432

Qy       3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3433 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3492

Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3762
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Db       3493 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3552

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Db       3613 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGC 3672

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
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Db       3733 TGA 3735
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RESULT 9
US-09-789-390-10
; Sequence 10, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spaderna, Steven K
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 3822
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3819)
US-09-789-390-10

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  Query Match             82.9%;  Score 3275.6;  DB 10;  Length 3822;
  Best Local Similarity   90.9%;  Pred. No. 0;
  Matches 3682;  Conservative    0;  Mismatches   29;  Indels  339;  Gaps    5;

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Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
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Db         61 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 300

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Db        361 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
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Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 600

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
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Qy     787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
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Qy     847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
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Qy    1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db    1141 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1200

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Qy    1327 GAGCGGCGGCAGGCGGAGCGTGAGCA---------------------------------- 1352
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Qy    1353 ----------------------------------------------------GGAATAC 1359
Db    1381 CGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGGCCCTGCTGCTGGAATAC 1440

Qy    1360 AAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAG 1419
Db    1441 AAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAG 1500

Qy    1420 GAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAG 1479
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Qy    1480 CAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG 1539
Db    1561 CAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATG 1620

Qy    1540 AATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAG 1599
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Qy    1600 CAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATC 1659
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Qy    1660 CCCCAGGCCTCCCCAGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCG 1719
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Qy    1720 GTGGAGCCCCAGGAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCT 1779
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Qy    1780 GCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGT 1839
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Qy    1840 GCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGC 1899
Db    1804 GCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGC 1863

Qy    1900 CCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGG 1959
Db    1864 CCGAATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGG 1923

Qy    1960 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 2019
Db    1924 ACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAG 1983

Qy    2020 GCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCA 2079
Db    1984 GCAGTCCGTGCC------------------------------------------------ 1995

Qy    2080 GAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCC 2139
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Qy    2140 TCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTT 2199
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Qy    2200 CCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCC 2259
Db    2053 CCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTC 2112

Qy    2260 TCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGAC 2319
Db    2113 TCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGAC 2172

Qy    2320 CACCGCTCACGGCCAGGCCGGCCCGCA-----------------------GACTTTGTG 2355
Db    2173 CACCGCTCACGGCCAGGCCGGCCCGCAAGCTATAAGCGAGCAATTGGTGAGGACTTTGTG 2232

Qy    2356 TTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTAC 2415
Db    2233 TTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTAC 2292

Qy    2416 TCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGG 2475
Db    2293 TCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGG 2352

Qy    2476 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2535
Db    2353 CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTC 2412

Qy    2536 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2595
Db    2413 AGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGC 2472

Qy    2596 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2655
Db    2473 GGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGC 2532

Qy    2656 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2715
Db    2533 AATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGC 2592

Qy    2716 AAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTA 2775
Db    2593 AAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTA 2652

Qy    2776 AAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGA 2835
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Db      2653 AAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGA 2712

Qy      2836 GGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGAC 2895
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2713 GGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGAC 2772

Qy      2896 CAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGG 2955
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2773 CAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGG 2832

Qy      2956 GCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTC 3015
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2833 GCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTC 2892

Qy      3016 TGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTG 3075
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2893 TGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTG 2952

Qy      3076 GACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATG 3135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2953 GACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATG 3012

Qy      3136 GATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGG 3195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3013 GATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGG 3072

Qy      3196 GTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAG 3255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3073 GTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAG 3132

Qy      3256 AAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAA 3315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3133 AAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAA 3192

Qy      3316 TACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGG 3375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3193 TACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGG 3252

Qy      3376 GCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGC 3435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3253 GCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGC 3312

Qy      3436 CCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCC 3495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3313 CCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCC 3372

Qy      3496 AGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCT 3555
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3373 AGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCT 3432

Qy      3556 GTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGC 3615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3433 GTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGC 3492

Qy      3616 ATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATC 3675
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3493 ATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATC 3552

Qy      3676 ATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCC 3735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3553 ATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCC 3612

Qy      3736 AACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCAC 3795
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3613 AACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCAC 3672

Qy      3796 CTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAAT 3855
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3673 CTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAAT 3732

Qy      3856 GACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACT 3915
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3733 GACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACT 3792

Qy      3916 CTGAACCGTAACTGCATCATGAACTGGTGA 3945
             ||||||||||||||||||||||||||||||
Db      3793 CTGAACCGTAACTGCATCATGAACTGGTGA 3822
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RESULT 10
US-09-789-390-69
; Sequence 69, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
;   LENGTH: 1717
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-789-390-69

  Query Match             39.3%;  Score 1551;  DB 10;  Length 1717;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1557;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy        10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy        70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy       130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy       190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy       250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy       310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy       370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy       430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480
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Qy        490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy       1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy       1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy       1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy       1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy       1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy       1330 CGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAG 1389
              ||||||||||||||||| |||||||||||  |   ||   |    |||  ||||||||||
Db       1321 CGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGCAGCGGCAG 1380

Qy       1390 TCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAG 1449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAG 1440

Qy       1450 CAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGG 1509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGG 1500

Qy       1510 AAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGA 1569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGA 1560

Qy       1570 GAGGTAG 1576
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Db       1561 GAGGTAG 1567
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RESULT 11
US-09-925-297-137
; Sequence 137, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
;   LENGTH: 2345
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (184)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (339)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (1805)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (1887)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (2325)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (2339)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-137

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  Query Match             38.0%;  Score 1502.6;  DB 9;  Length 2345;
  Best Local Similarity   99.2%;  Pred. No. 0;
  Matches 1527;  Conservative    3;  Mismatches    8;  Indels    2;  Gaps    2;

Qy       2413 TACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGC 2472
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TATTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGC 60

Qy       2473 GGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGC 2532
              |||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db         61 GGGCCAGCAGAGGGGAGCAGAGATACCCYTGGGGGCCGCAGCGATGGGGATACAGACAGC 120

Qy       2533 GTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGG 2592
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCA-CACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGG 179

Qy       2593 GGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGAC 2652
              |  | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GCGGNCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGAC 239

Qy       2653 AGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAAC 2712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAAC 299

Qy       2713 AGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGT-GACTACCAGTCTCGTGGGCT 2771
              ||||||||||||||||||||||||||||||||||||||| |||||||||:||||||||||
Db        300 AGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTNGACTACCAGTYTCGTGGGCT 359
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Qy       2772 GGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCC 2831
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        360 GGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATTTACCAGCC 419

Qy       2832 TGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCT 2891
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        420 TGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGTT 479

Qy       2892 CGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACAC 2951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACAC 539

Qy       2952 CCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGAT 3011
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Db        540 CCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGAT 599

Qy       3012 CCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTT 3071
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Db        600 CCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTT 659

Qy       3072 GCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCA 3131
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Db        660 GCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCA 719

Qy       3132 GATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACT 3191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 GATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACT 779

Qy       3192 GCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGA 3251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 GCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGA 839

Qy       3252 GAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGT 3311
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db        840 GAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTKTTGT 899

Qy       3312 GAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGC 3371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 GAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGC 959

Qy       3372 CTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCA 3431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 CTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCA 1019

Qy       3432 CCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGG 3491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 CCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGG 1079

Qy       3492 CTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACAT 3551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1080 CTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACAT 1139

Qy       3552 CCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGA 3611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 CCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGA 1199

Qy       3612 CGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCG 3671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 CGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCG 1259

Qy       3672 CATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTG 3731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 CATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTG 1319

Qy       3732 CTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGG 3791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 CTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGG 1379

Qy       3792 CCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCG 3851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 CCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCG 1439

Qy       3852 GAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCAT 3911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1440 GAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCAT 1499

Qy       3912 GACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              ||||||||||||||||||||||||||||||||||  ||||
Db       1500 GACTCTGAACCGTAACTGCATCATGAACTGGTGACGGGGC 1539
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RESULT 12
US-09-789-390-66
; Sequence 66, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 1787
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-789-390-66

  Query Match             37.2%;  Score 1468.4;  DB 10;  Length 1787;
  Best Local Similarity   94.7%;  Pred. No. 0;
  Matches 1566;  Conservative    0;  Mismatches    1;  Indels   87;  Gaps    1;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy        370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420
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Qy        430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy        490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy       1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy       1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy       1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy       1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy       1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy       1330 CGGCGGCAGGCGGAGCGTGAGCA------------------------------------- 1352
              ||||||||||||||| |||||
Db       1321 CGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGGAGCAGCGA 1380

Qy       1353 --------------------------------------------------GGAATACAAG 1362
                                                                ||||||||||
Db       1381 CAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGGCCCTGCTGCTGGAATACAAG 1440

Qy       1363 CGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAG 1422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAG 1500

Qy       1423 CATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAG 1482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAG 1560

Qy       1483 CAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAAT 1542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAAT 1620

Qy       1543 CCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAG 1576
              ||||||||||||||||||||||||||||||||||
Db       1621 CCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAG 1654
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RESULT 13
US-09-789-390-64
; Sequence 64, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
;   LENGTH: 1482
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-789-390-64

  Query Match             37.1%;  Score 1466;  DB 10;  Length 1482;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 1472;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy        370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy          430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy          490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy          550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy          610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy          670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy          730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy          790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy          850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy          910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy          970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy         1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy         1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy         1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy         1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy         1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy         1330 CGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAG 1389
                ||||||||||||||||| ||||||||||| |  ||  |   ||| |||||||||||||||
Db         1321 CGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGCAGCGGCAG 1380

Qy         1390 TCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAG 1449
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1381 TCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAG 1440

Qy         1450 CAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAG 1491
                ||||||||||||||||||||||||||||||||||||||||||
Db         1441 CAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAG 1482
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RESULT 14
US-09-789-390-62
; Sequence 62, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
;   LENGTH: 1649
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-789-390-62

  Query Match             37.0%;  Score 1463.4;  DB 10;  Length 1649;
  Best Local Similarity   94.7%;  Pred. No. 0;
  Matches 1561;  Conservative    0;  Mismatches    1;  Indels   87;  Gaps    1;

Qy           10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy           70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy          130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy          190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy          250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy          310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy          370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy          430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy          490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy       1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy       1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy       1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy       1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy       1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy       1330 CGGCGGCAGGCGGAGCGTGAGCA------------------------------------- 1352
              ||||||||||||||||| |||||
Db       1321 CGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTCACAGGCTAGAGGAGGAGCAGCGA 1380

Qy       1353 --------------------------------------------------GGAATACAAG 1362
                                                                ||||||||||
Db       1381 CAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAGGCCCTGCTGCTGGAATACAAG 1440

Qy       1363 CGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAG 1422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAG 1500

Qy       1423 CATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAG 1482
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Db       1501 CATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAG 1560

Qy       1483 CAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAAT 1542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAAT 1620

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Db       1621 CCCGCTGACAAACCAGCCTGGGCCCGAGA 1649
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RESULT 15
US-10-355-975-7
; Sequence 7, Application US/10355975
; Publication No. US20030162277A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/10/355,975
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US/09/579,664B
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 4083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-355-975-7

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  Query Match             34.4%;  Score 1358.6;  DB 14;  Length 4083;
  Best Local Similarity   61.7%;  Pred. No. 0;
  Matches 2532;  Conservative    0;  Mismatches 1389;  Indels  180;  Gaps   16;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||    |    |||| || || |||||||| || || || || || || ||| |||||
Db          1 ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGAC 60

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||| |||||||||||  | |||||  | || || |||||||| ||||| || || ||
Db         61 CCTGCAGGGATCTTTGAATTGGTGGAACTTGTTGGAAATGGAACATACGGGCAAGTTTAT 120

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              |||||||| |||||||| ||||| ||||| || ||||||||||| ||||||||||| | |
Db        121 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAGGTTATGGATGTCACAGGG 180

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              || || |||||||| |||||||| ||  | |||||| |||| || || ||||| |||||
Db        181 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACCGG 240

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              || || || || ||||| || || || ||||| |||| ||| || || |  ||||||||
Db        241 AATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCACCAGGCATGGATGACCAA 300

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              || ||| ||||||||||||| ||||||||||| || || || |||||| | |||||||||
Db        301 CTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACCGACCTGATCAAGAACACA 360

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||| ||| |  |||| ||||| || || || || ||||||||||| ||| |  ||||
Db        361 AAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGCAGGGAAATCTTACGGGGG 420

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              |||   || || ||    || || ||||| |||||||| || || ||||| |||||  ||
Db        421 CTGAGTCACCTGCACCAGCATAAAGTGATTCATCGAGATATTAAAGGGCAAAATGTCTTG 480

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||| || ||||| || || || |||||||| ||||| || ||||||||||| || ||
Db        481 CTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTTGGAGTCAGTGCTCAGCTTGATCGA 540

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              || ||||||||  |||| ||||||||||| ||||||||||||||||| ||||| || ||
Db        541 ACAGTGGGCAGGAGGAATACTTTCATTGGAACTCCCTACTGGATGGCACCAGAAGTTATT 600
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Qy     607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTGGTCTCTAGGA 666
Db     601 GCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTGACTTGTGGTCTTTGGGT 660

Qy     667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
Db     661 ATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCACCCCATGAGA 720

Qy     727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db     721 GCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAGTCTAAGAAGTGGTCAAAA 780

Qy     787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db     781 AAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCACAGCCAGCGACCAGCAACA 840

Qy     847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db     841 GAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAATGAGCGACAGGTCCGCATT 900

Qy     907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
Db     901 CAACTCAAGGACCATATTGATAGAACAAAGAAGAAGCGAGGAGAAAAAGATGAGACAGAG 960

Qy     967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db     961 TATGAGTACAGTGGAAGTGAGGAAGAAGAGGAGGAGAAT---GACTCAGGAGAGCCCAGC 1017

Qy    1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db    1018 TCCATCCTGAATCTGCCAGGGGAGTCGACGCTGCGGAGGGACTTTCTGAGGCTGCAGCTG 1077

Qy    1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db    1078 GCCAACAAGGAGCGTTCTGAGGCCCTA------CGGAGGCAGCAGCTGGAGCAGCAGCAG 1131

Qy    1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db    1132 CGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTCAGAAGCGCATCGAGGAG 1191

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Db    1192 CAGAAAGAGCAGAGGCGGCGGCTGGAGGAGCAACAAAGGCGAGAGAAGGAGCTGCGGAAG 1251

Qy    1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db    1252 CAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGG------AGCAGATGCGCCGGGAGGAG 1305

Qy    1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCT---GGAGGAGCAG 1383
Db    1306 GAGAGGAGGCGTGCGGAGCATGAACAGGAATACATCAGGCGACAGTTAGAGGAGGAGCAG 1365

Qy    1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
Db    1366 AGACAGTTAGAGATCTTGCAGCAGCAGCTACTGCATGAACAAGCTCTACTTCTGGAATAT 1425

Qy    1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCA------------------------------ 1472
Db    1426 AAGCGCAAACAATTGGAAGAACAGAGACAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAA 1485

Qy    1473 -----------------------GAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGG 1509
Db    1486 GAAAGAGACTACTTAGTTTCCCTTCAGCATCAGCGGCAGGAGCAGAGGCCTGTGGAGAAG 1545

Qy    1510 AAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGA 1569
Db    1546 AAGCCACTGTACCATTACAAAGAAGGAATGAGTCCTAGTGAGAAGCCAGCATGGGCCAAG 1605

Qy    1570 GAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAG 1629
Db    1606 GAGGTAGAAGAACGGTCAAGGCTCAACCGGCAAAGTTCCCCTGCCATGCCTCA---CAAG 1662

Qy    1630 CCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCC---------AGGCCTCCCCAGGGCCC 1680
Db    1663 GTTGCCAACAGGATATCTGACCCCAACCTGCCCCCAAGGTCGGAGTCCTTCAGCATTAGT 1722

Qy    1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAG--------- 1731
Db    1723 GGAGTTCAGCCTGCTCGAACACCCCCCATGCTCAGACCAGTCGATCCCCAGATCCCACAT 1782

Qy    1732 GAGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCC 1791
Db    1783 CTGGTAGCTGTAAAATCCCAGGGACCTGCCTTGACCGCCTCCCAGTCAGTGCACGAGCAG 1842

Qy    1792 TCCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCT 1851
Db    1843 CCCACAAAGGGCCTCTCTGGGTTTCAGGAGGCTCTGAACGTGACCTCCCACCGCGTGGAG 1902

Qy    1852 GTCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGA-------- 1903
Db    1903 ATGCCACGCCAGAACTCAGATCCCACCTCGGAAAATCCTCCTCTCCCCACTCGCATTGAA 1962

Qy    1904 -------ATCCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAG 1956
Db    1963 AAGTTTGACCGAAGCTCTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCTCAA 2022

Qy    1957 AGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCC 2016
Db    2023 AGAACAACTTCTATATCCCCAGCATTAGCCAGAAAGAATTCTCCTGGGAATGGTAGTGCT 2082

Qy    2017 CAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAG--GC 2074
Db    2083 CTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGAACT 2142

Qy    2075 GGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCA 2134
Db    2143 GAGCCCATCTTGGAGAGCCCCTTGCAGAGGACCAGCAGTGGCAGTTCCTCCAGCTCCAGC 2202

Qy    2135 ACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGG----GAACGCTCGGAC 2190
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Qy    2191 AGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGC 2250
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Qy    2251 GTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAG 2310
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Qy    2431 GAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGA-- 2488
Db    2503 GAGTCAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGGACA 2562

Qy    2489 ------------------------------GCAGAGATACCCCTGGGGGCCGCAGCGAT 2517
Db    2563 GTGGCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAGCAG 2622

Qy    2518 GGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACC 2577
Db    2623 TACAATGTGGGAATGGTGGGGACGCATGGGCTGGAGACCTCTCATGCGGACAGTTTCAGC 2682

Qy    2578 CAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAAC 2637
Db    2683 GGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAGAGAAGAAGCGA 2742

Qy    2638 CTGCTGCATGCTGACAGCAATGGGT---------ACACAAACCTGCCTGACGTGGTCCAG 2688
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Db       2743 TCTGGCCACAGTGACAGCAATGGCTTTGCTGGCCACATCAACCTCCCTGACCTGGTGCAG 2802

Qy       2689 CCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAA------AGCCCACCCTCGAAGGAT 2742

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Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802

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Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGT--------------GGGGAC 2847

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Db       2983 GAATCATCAGCCGCAGCTCTGTTTACTAGCGAACTTCTTAGGCAAGAACAGGCCAAACTC 3042

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Db       3103 GACACACCAGAAATCAGAAAATACAAGAAACGATTCAACTCAGAAATACTTTGTGCAGCT 3162

Qy       3025 CTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGT 3084

Db       3163 CTGTGGGGTGTAAACCTTCTGGTGGGGACTGAAAATGGCCTGATGCTTTTGGACCGAAGT 3222

Qy       3085 GGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTG 3144

Db       3223 GGGCAAGGCAAAGTCTATAATCTGATCAACCGGAGGCGATTTCAGCAGATGGATGTGCTA 3282

Qy       3145 GAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTAC 3204

Db       3283 GAGGGACTGAATGTCCTTGTGACAATTTCAGGAAAGAAGAATAAGCTACGAGTTTACTAT 3342

Qy       3205 CTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGC 3264

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Db       3403 TGGATCACTGTTGGGGACTTGGAAGGCTGTATACATTATAAAGTTGTTAAATATGAAAGG 3462

Qy       3325 ATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAA 3384

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Qy       3445 GTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGC 3504

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Qy       3625 CTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGAT 3684

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Qy       3745 ATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGG 3804

Db       3883 ATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTTGGATGGA 3942

Qy       3805 GTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTG 3864

Db       3943 GTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAGGTA 4002

Qy       3865 TTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGT 3924

Db       4003 TTTTTTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTTTTTCATGACCCTCAACAGA 4062

Qy       3925 AACTGCATCATGAACTGGTGA 3945

Db       4063 AATTCCATGATGAACTGGTAA 4083
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Search completed: March 2, 2004, 17:16:13
Job time : 946 secs

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OM nucleic - nucleic search, using sw model

Run on:         March  2, 2004, 09:52:59 ; Search time 6282 Seconds
                                           (without alignments)
                                           18781.515 Million cell updates/sec

Title:          US-10-029-115-1
Perfect score:  3951
Sequence:       1 gcccttatgggcgacccagc..........tcatgaactggtgaaagggc 3951

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:      55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
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                28:  gb_gss1:*
                29:  gb_gss2:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1307.2	33.1	7139	11	BC050866	BC050866 Mus muscu
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3	949	24.0	3585	29	AY400358	AY400358 Mus muscu
4	897	22.7	969	13	BU838349	BU838349 AGENCOURT
5	893.8	22.6	3585	29	AY400356	AY400356 Homo sapi
6	872.4	22.1	908	13	BU542554	BU542554 AGENCOURT
7	848	21.5	951	13	BQ706178	BQ706178 AGENCOURT
8	834.2	21.1	1201	9	AL551911	AL551911 AL551911
9	833.4	21.1	3588	29	AY400357	AY400357 Pan trogl
10	814.4	20.6	1026	12	BM541693	BM541693 AGENCOURT
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24	704	17.8	999	12	BM477724	BM477724 AGENCOURT
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ALIGNMENTS

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DEFINITION  Mus musculus RIKEN cDNA 1500031A17 gene, mRNA (cDNA clone
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ACCESSION   BC050866
VERSION     BC050866.1  GI:30047190
KEYWORDS    HTC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 7139)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 7139)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
            Ph.D.
            cDNA Library Preparation: ResGen, Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 109 Row: c Column: 16
            This clone was selected for full length sequencing because it
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            analysis
            This clone has the following problem: frame shifted.
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                     otocysts"
                     /clone_lib="NIH_MGC_130"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6.1"
ORIGIN

  Query Match             33.1%;  Score 1307.2;  DB 11;  Length 7139;
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  Matches 2536;  Conservative    0;  Mismatches 1343;  Indels  263;  Gaps   16;

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Db        430 ATGGCGAGCGACTCCCCAGCTCGCAGCCTGGATGAAATCGATCTCTCCGCCCTGAGGGAC 489

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126

Db        490 CCTGCAGGGATCTTTGAGTTGGTGGAACTTGTCGGAAATGGCACGTATGGTCAAGTTTAT 549

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186

Db        550 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCTGCCATTAAGGTTATGGATGTCACAGGG 609

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246

Db        610 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACAGG 669

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306

Db        670 AACATTGCTACATACTACGGTGCTTTTATCAAAAAGAACCCTCCTGGCATGGATGACCAA 729

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366

Db        730 CTCTGGTTGGTTATGGAGTTCTGTGGTGCTGGCTCTGTCACTGACCTGATCAAGAACACG 789

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426

Db        790 AAAGGCAACACATTGAAAGAGGAGTGGATTGCATACATCTGCAGGGAGATCTTACGGGGC 849

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486

Db        850 CTGAGTCACCTGCACCAGCACAAAGTGATTCATCGAGATATCAAAGGGCAGAACGTCTTG 909

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546

Db        910 TTGACTGAAAATGCAGAGGTTAAGCTAGTGGATTTTGGAGTGAGTGCCCAGCTTGACCGA 969

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Db       1210 TGGCAGAAGGTGCCCCCCCCCTCTGTGACATGCATCCCATGAGAGCCCTCTTCCTCATCC 1269

Qy        743 CTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAGTTCATTGACTTCA 802

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Qy       1163 ACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGC 1222

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Db        4267 TGCCCACATCTGTGGCCTACATTCATTCCAATCAGATAATGGGCTGGGGCGAGAAAGCTA 4326

Qy        3767 TTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTC 3826

Db        4327 TTGAGATCCGGTCAGTGGAAACAGGACATTTGGATGGAGTGTTTATGCATAAACGAGCTC 4386

Qy        3827 AGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTG 3886

Db        4387 AAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAGGTATTTTTTGCATCCGTGCGATCTG 4446

Qy        3887 GGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAA 3946

Db        4447 GAGGAAGTAGCCAAGTGTTTTTCATGACCCTCAACAGAAATTCCATGATGAACTGGTAAC 4506

Qy        3947 AG 3948

Db        4507 AG 4508


RESULT 2
BC050868
LOCUS       BC050868                7139 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION  Mus musculus RIKEN cDNA 1500031A17 gene, mRNA (cDNA clone
            IMAGE:6334359), containing frame-shift errors.
ACCESSION   BC050868
VERSION     BC050868.1  GI:30047833
KEYWORDS    HTC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 7139)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 7139)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
            Ph.D.
            cDNA Library Preparation: ResGen, Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 109 Row: d Column: 16
            This clone has the following problem: frame shifted.
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                     /db_xref="taxon:10090"
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                     /tissue_type="Embryo, day 9 mouse (C57BL/6 background)
                     otocysts"
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                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6.1"
ORIGIN

  Query Match             33.1%;  Score 1307.2;  DB 11;  Length 7139;
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  Matches 2536;  Conservative    0;  Mismatches 1343;  Indels  263;  Gaps   16;

Qy           7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66

Db         430 ATGGCGAGCGACTCCCCAGCTCGCAGCCTGGATGAAATCGATCTCTCCGCCCTGAGGGAC 489

Qy          67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126

Db         490 CCTGCAGGGATCTTTGAGTTGGTGGAACTTGTCGGAAATGGCACGTATGGTCAAGTTTAT 549

Qy         127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186

Db         550 AAGGGTCGTCATGTCAAAACGGGCCAGCTTGCTGCCATTAAGGTTATGGATGTCACAGGG 609

Qy         187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246

Db         610 GATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAGAAATATTCTCATCACAGG 669
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Qy    247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCGGGAAACGATGACCAG 306
Db    670 AACATTGCTACATACTACGGTGCTTTTATCAAAAAGAACCCTCCTGGCATGGATGACCAA 729

Qy    307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
Db    730 CTCTGGTTGGTTATGGAGTTCTGTGGTGCTGGCTCTGTCACTGACCTGATCAAGAACACG 789

Qy    367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
Db    790 AAAGGCAACACATTGAAAGAGGAGTGGATTGCATACATCTGCAGGGAGATCTTACGGGGC 849

Qy    427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
Db    850 CTGAGTCACCTGCACCAGCACAAAGTGATTCATCGAGATATCAAAGGGCAGAACGTCTTG 909

Qy    487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
Db    910 TTGACTGAAAATGCAGAGGTTAAGCTAGTGGATTTTGGAGTGAGTGCCCAGCTTGACCGA 969

Qy    547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
Db    970 ACTGTGGGCAGGAGGAACACGTTCATCGGGACTCCCTACTGGATGGCACCAGAAGTCATT 1029

Qy    607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGG--------------------- 645
Db   1030 GCCTGTGATGAGAACCCGGATGCCACATATGATTTCAAGGGATGGGCTGTTAGTCATGCT 1089

Qy    646 ------------------------------------------------------------ 645
Db   1090 GCAGGCACGGCAGCCCAGTGCTGAGGAAAGAGTGAATTTCCCACCACCAGTCAGGATGAG 1149

Qy    646 -----------------------AGTGATATTTGGTCTCTAGGAATCACAGCCATCGAGA 682
Db   1150 CCGCACCATGGCCAGGAGGAAACAGTGACTTGTGGTCTTTGGGAATCACCGCCATTGAGA 1209

Qy    683 TGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCCCTCTTCCTCATTC 742
Db   1210 TGGCAGAAGGTGCCCCCCCCCTCTGTGACATGCATCCCATGAGAGCCCTCTTCCTCATCC 1269

Qy    743 CTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAGTTCATTGACTTCA 802
Db   1270 CACGGAACCCTGCACCTCGGCTCAAGTCTAAGAAGTGGTCAAAAAAATTCCAGTCATTTA 1329

Qy    803 TTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAGCAGCTACTGAAGT 862
Db   1330 TCGAGAGCTGCTTGGTAAAGAATCACAGCCAGCGGCCAGCCACGGAGCAGTTGATGAAGC 1389

Qy    863 TTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAGCTTAAGGACCACA 922
Db   1390 ACCCATTCATACGAGACCAACCTAATGAGAGGCAGGTCCGCATCCAGCTGAAGGACCACA 1449

Qy    923 TTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATATGAGTACAGCGGCA 982
Db   1450 TTGATCGAACAAAGAAGAAGCGAGGAGAAAAAGATGAGACTGAGTATGAATACAGCGGAA 1509

Qy    983 GCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCCATCATGAACGTGC 1042
Db   1510 GTGAGGAAGAAGAGGAAGAGAAT---GACTCTGGGGAACCCAGCTCCATTCTGAACCTAC 1566

Qy   1043 CTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAAAATAAGAGCAACT 1102
Db   1567 CAGGGGAGTCAACACTGCGAAGGGACTTCCTGAGACTGCAGCTGGCCAACAAGGAGCGCT 1626

Qy   1103 CAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCGAGACCCCGAGGCAC 1162
Db   1627 CAGAGGC------CCTGCGGCGCCAACAGCTGGAGCAGCAGCAGCGGGAGAATGAAGAAC 1680

Qy   1163 ACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGC 1222
Db   1681 ACAAGCGGCAGCTACTGGCTGAGCGCCAGAAGCGCATCGAAGAGCAGAAGGAGCAAAGGC 1740

Qy   1223 GCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGC 1282
Db   1741 GGAGGCTGGAGGAGCAACAAAGGCGAGAAAAAGAGCTTCGGAAACAGCAGGAGCGGGAAC 1800

Qy   1283 AGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGG 1342
Db   1801 AGCGCCGGCACTACGAAGAACAG------ATGCGTCGGGAGGAGGAGAGGAGGCGTGCCG 1854

Qy   1343 AGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTCC 1402
Db   1855 AACATGAGCAGGAATATAAGCGCAAACAATTGGAAGAACAGAGACAAGCAGAAAGACTGC 1914

Qy   1403 AGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAGC 1462
Db   1915 AGAGGCAGCTAAAGCAAGAGCGGGACTATCTGGTTTCCCTCCAGCATCAGCGGCAGGAGC 1974

Qy   1463 AGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTACC 1522
Db   1975 AG----------------------------AGGCCCCTGGAGAAGAAGCCACTGTACC 2004

Qy   1523 ATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGA 1582
Db   2005 ATTACAAGGAGGGCATGAGTCCTAGTGAGAAGCCGGCCTGGGCCAAGGAGGTAGAAGAAC 2064

Qy   1583 GAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGG 1642
Db   2065 GCTCAAGACTCAACCGACAGAGTTCACCTGCCATGCCTCACAAGGTTGCCAACAGGATCT 2124

Qy   1643 GG------CCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCC 1696
Db   2125 CGGACCCCAACCTGCCCCCAAGATCAGAGTCCTTCAGCATTAGTGGGGTTCAGCCTGCAA 2184

Qy   1697 AGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAGTCCCTGCAGG 1756
Db   2185 GGACACCCCCAATGCTCAGACCTGTTGACCCCCAGATCCCGCAGCTGGTAGCTGTCAAAT 2244

Qy   1757 ACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCC---------CGACC 1807
Db   2245 CCCAGGGACCTGCCTTGACGGCCTCCCAGTCAGTACATGAGCAACCCACAAAGGGCCTGT 2304

Qy   1808 CTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATT 1867
Db   2305 CTGGGTTCCAGGAGGCTCTGAATGTGACCTCTCACCGGGTCGAGATGCCACGCCAGAACT 2364

Qy   1868 CAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGA---------------ATCCCCCAG 1912
Db   2365 CGGATCCCACCTCAGAAAACCCTCCTCTCCCCACGAGAATTGAGAAGTTTGACAGAAGCT 2424

Qy   1913 CCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCG 1972
Db   2425 CTTGGTTACGACAGGAAGAAGACATTCCACCAAAGGTGCCTCAAAGAACAACTTCTATAT 2484

Qy   1973 CCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCA 2032
Db   2485 CCCCAGCACTAGCCAGAAAGAATTCCCCTGGCAATGGCAGTGCTCTGGGCCCCAGACTTG 2544

Qy   2033 GACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCC 2092
Db   2545 GATCTCAGCCCATCAGAGCAAGCAACCCTGATCTGC-------------GCAGGACAGAG 2591

Qy   2093 CAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCG 2152
Db   2592 CCAGTCCTGGAGAGTTCCCTG--CAGCGGACAAGCAGTGGCAGTTCCTCCAGCTCCAGCA 2649

Qy   2153 ACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACG 2212
Db   2650 CTCCCAGCTCCCAGCCCAGCTCCCAAGGAGGCTCTCAACCTGGCTCCCAAGCAGGATCTA 2709

Qy   2213 GGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGG 2272
Db   2710 GTGAGCGGTCCAGAGTGCGGGCCAACAGTAAGTCCGAAGGATCACCCGTGCTCCCCCATG 2769

Qy   2273 ACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGC 2332
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Db    2770 AGCCTTCCAAGGTGAAACCAGAAGAATCCAGAGACATCACACGGCCCAGTCGGCCAGCTG 2829

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Qy    3347 TCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCT 3406

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Qy    3527 CGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATG 3586

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Qy    3947 AG 3948

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ACCESSION   AY400358
VERSION     AY400358.1  GI:39756347
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3585)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3585)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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            Adams,M.D. and Cargill,M.
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  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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ORIGIN

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  Matches 1996;  Conservative    0;  Mismatches 1584;  Indels  237;  Gaps   12;

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Db          1 GGTCGACATGTTAAAACGGGTCAGCTGGCCGCCATCAAGGTTATGGACGTCACCGAGNNN 60

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
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Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
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Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
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Qy        370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
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Qy        430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
Db        301 GCACATCTCCATATTCACCACGTTATTCACCGAGATATCAAGGGCCAAAATGTGCTGCTG 360

Qy        490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
Db        361 ACCGAGAATGCTGAGGTGAAACTTGTTGATTTTGGTGTAAGCGCTCAGCTGGACAGGACG 420

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
Db        421 GTTGGACGGAGAAATACGTTCATAGGCACACCCTACTGGATGGCTCCAGAGGTCATCGCC 480

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
Db        481 TGTGATGAGAACCCAGACGCCACTTACGACTACAGANNNNNNNNNNNNNNNNNNNNNNNN 540

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
Db        541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTCTCTGTGACATGCATCCAATGAGAGCG 600

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
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Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
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Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
Db        721 CAACTTTTAAAACACCCTTTCATAAGGGATCAGCCCAATGAAAGGCAGGTTCGAATCCAG 780

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
Db        781 CTTAAGGATCACATAGACCGGACCAGAAAGAAGAGAGGCGAGAAAGATGAGACGGAGTAC 840

Qy        970 GAGTACAGCGGCAGC---GAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db        841 GAGTACAGCGGGAGCGAGGAGGAGGAGGAGGAAGTGCCTGAGCAGGAGGGAGAGCCAAGT 900

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db        901 TCCATCGTCAATGTGCCTGGAGAGTCAACTCTGCGTCGTGATTTCCTGAGACTGCAGCAG 960

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db        961 GAGAACAAGGAGCGGTCTGAGGCTCTGCGGAGACAGCAGCTTCTGCAGGAACAGCAGCTC 1020

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db       1021 CGGGAGCAGGAGGAGTATAAGAGGCAGCTGCTGGCTGAGAGGCAGAAGCGGATTGAACAG 1080

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
Db       1081 CAGAAAGAACAGAGGAGGCGGCTGGAAGAGCAACAAAGAAGAGAACGGGAAGCCAGGAGG 1140

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db       1141 CAGCAGGAGCGTGAGCAGCGGCGGCGTGAACAAGAGGAGAAGAGGCGTCTCGAGGAACTG 1200

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
Db       1201 GAAAGGCG-------------------------GCGTAAAGAAGAGGAAGAGAGGAGA 1233

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
Db       1234 CGGGCAGAAGAGGAGAAGAGGAGAGTGGAGAGGGAACAGGAGTACATCAGG---CGGCAG 1290

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
Db       1291 CTAGAGGAGGAGCAGCGGCACCTGGAGATCCTGCAGCAGCAGCTGCTCCAGGAGCAGGCC 1350

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
Db       1351 ATGTTACTGCAGCACGACCACAGGAGG----------CCGCACGCACAGCAGCAGCCGCC 1400

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
Db       1401 GCCCCCGCAGCAGCAGGACAGGAGCAAACCGAGCTTTCATGCTC---------------- 1444

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
Db       1445 -------------CAGAGCCCAAGCCTCACTATGACCCTGCTGACAGAGCTCGGGAGGTA 1491

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
Db       1492 CAGTGGTCCCACCTGGCATCTCTCAAGAACAATGTCTCCCCTGTCTCGAGATCCCATTCC 1551

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
Db       1552 TTCAGTGA-----------------------------CCCTTCTCCCAAATTCGCACAC 1581

Qy       1807 CCTGCCATCCCCGCACCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
Db       1582 CACCATCTCCGCTCTCAGGACCCATGTCCACCTTCCCGCAGTGAGGGGCTCAGTCAGAGC 1641

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
Db       1642 TCTGACTCTAAGTCGGAGGTGCCCGAGCCCACCCAAAAGGCTTGGTCTAGATCAGAC--- 1698

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
Db       1699 AGTGACGAGGTGCCTCCAAGGGTTCCCGTGAGAACGACCTCTCGTTCCCCTGTCCTCTCC 1758

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
Db       1759 CGTCGGGATTCCCCACTGCAGGGCGGTGGACAGCAGAATAGCCAAGCAGGACAGAGAAAT 1818
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Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106
Db       1819 TCCACCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1878

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
Db       1879 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1938

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
Db       1939 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCATC---------ATCCAAG 1989

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Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
Db       2089 TTGACTGCGTTGGCCAAAGAGCTTCGAGCAGTGGAAGATGTTCGGCCACCTCACAAAGTA 2148

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
Db       2149 ACAGACTACTCATCCTCCAGTGAGGAGTCTGGGACCACAGATGAGGAGGAGGAGGACGTG 2208

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
Db       2209 GAACAGGAGGGGGCTGATGATTCTACCTCGGGACCAGAAGACACCAGAGCAGCGTCATCT 2268

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
Db       2269 CCGAACCTGAGCAACGGTGAAACAGAATCTGTGAAAACAATGATCGTTCATGATGATGTA 2328

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
Db       2329 GAAAGTGAGCCAGCCATG------------ACCCCGTCCAAGGAGGGCACCC-------- 2368

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
Db       2369 --------------------------------------TCATCGTCCGCCAGACTCAGTCC 2391

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
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Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
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Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
Db       2512 TGTGATGGGCTGAGACCAGAAGCCAT---------------------------------- 2537

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
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Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
Db       2587 AACACTAGGCCACAGAGTGATACCCCCGAGATTCGTAAATACAAGAAGAGATTTAACTCA 2646

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
Db       2647 GAGATCCTGTGTGCTGCCTTATGGGGAGTGAACTTGCTGGTTGGTACAGAGAGCGGTCTG 2706

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
Db       2707 ATGCTCTTGGACAGAAGTGGCCAAGGGAAAGTATACCCTCTGATCAGCCGAAGACGGTTC 2766

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
Db       2767 CAGCAAATGGATGTGCTCGAAGGCCTAAATGTCCTGGTGACAATATCTGGCAAAAAGGAT 2826

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
Db       2827 AAGTTACGTGTCTACTATTTATCCTGGCTAAGAAATAAGATTCTTCATAATGATCCAGAG 2886

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
Db       2887 GTTGAGAAGAAGCAGGGGTGGACCACTGTGGGCGACTTGGAAGGGTGCGTGCACTATAAA 2946

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
Db       2947 GTCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3006

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
Db       3007 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTCATTTGGAGAACTG 3066

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
Db       3067 CTACATAAGCCATTACTGGTGGATCTCACTGTGGAGGAAGGCCAGAGGTTGAAAGTGATC 3126

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
Db       3127 TATGGATCCTGTGCGGGATTCCATGCTGTTGATGTGGATTCAGGCTCAGTCTATGACATT 3186

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
Db       3187 TATCTACCAACACACATTCAGTGTAGCATCAAACCCCATGCAATCATTATCCTCCCCAAC 3246

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
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Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
Db       3307 GGAAGGATCACCAAGGACGTGGTTCTGCAGTGGGGAGAGATGCCGACATCTGTAGCATAT 3366

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
Db       3367 ATCCGGTCGAATCAGACAATGGGCTGGGGAGAGAAGGCAATAGAGATACGATCTGTGGAA 3426

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
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Qy       3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTTAC 3906
Db       3487 GAACGCAATGACAAGGTGTTCTTTGCCTCCGTCCGCTCTGGTGGCAGCAGCCAGGTCTAT 3546

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGT 3943
Db       3547 TTCATGACCTTAGGCAGGACTTCTCTTCTGAGCTGGT 3583
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RESULT 4
BU838349

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LOCUS       BU838349                 969 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_8123283 Lupski_dorsal_root_ganglion Homo sapiens cDNA
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ACCESSION   BU838349
VERSION     BU838349.1  GI:24022744
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
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COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13554  row: a  column: 23
            High quality sequence stop: 626.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match             22.7%;  Score 897;  DB 13;  Length 969;
  Best Local Similarity   97.9%;  Pred. No. 7.1e-143;
  Matches  939;  Conservative    0;  Mismatches   17;  Indels    3;  Gaps    3;

Qy       1553 AACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTC 1612
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Db          9 AACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTC 68

Qy       1613 CCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCC 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 CCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCC 128

Qy       1673 CAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGG 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 CAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGG 188

Qy       1733 AGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCT 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 AGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCT 248

Qy       1793 CCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTG 1852
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Qy       1973 CCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCA 2032
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Db        429 CCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCA 488

Qy       2033 GACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCC 548

Qy       2093 CAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCG 2152
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Db        549 CAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCG 608

Qy       2153 ACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACG 2212
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Db        669 GGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGG 728

Qy       2273 ACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGC 2332
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Db        729 ACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAANGCCGACGACCACCGCTCACGGC 788

Qy       2333 CAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGC 2392
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| 
Db        789 CAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAAGCCCCTCGGN 848

Qy       2393 CTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAG-TGAGGAC 2451
              || |||||||||||||||||||||||||||||||||| || ||||||| | | ||||  |
Db        849 CT-CCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAAGAAGTGGAAAACCGNTGAGACC 907

Qy       2452 GACGAGGAGGAAGGCGAAGGCGGGCCAGCAGA-GGGGAGCAGAGATACCCCTGGGGGCC 2509
                | ||||||||||||||||||||||| |||| ||||| || ||||||||||||||| |
Db        908 ACCCAGGAGGAAGGCGAAGGCGGGCCAACAGAGGGGGACCAAAGATACCCCTGGGGGGC 966


RESULT 5
AY400356
LOCUS       AY400356                3585 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens MAP4K4 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY400356
VERSION     AY400356.1  GI:39756345
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3585)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3585)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /gene="MAP4K4"
                     /locus_tag="HCM0530"
ORIGIN

  Query Match             22.6%;  Score 893.8;  DB 29;  Length 3585;
  Best Local Similarity   51.7%;  Pred. No. 4.7e-142;
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Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
Db          1 GGTCGACATGTTAAAACGGGTCAGTTGGCAGCCATCAAAGTTATGGATGTCACTGAGNNN 60

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
Db         61 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 120

Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
Db        121 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 180

Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
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Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
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Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
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Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
Db        721 CAGCTTTTGAAACATCCTTTTATAAGGGATCAGCCAAATGAAAGGCAAGTTAGAATCCAG 780

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Db        781 CTTAAGGATCATATAGATCGTACCAGGAAGAAGAGAGGCGAGAAAGATGAAACTGAGTAT 840

Qy        970 GAGTACAGCGGCAGCGAGGAGGAA---GATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
Db        841 GAGTACAGTGGGAGTGAGGAAGAAGAGGAGGAAGTGCCTGAACAGGAAGGAGAGCCAAGT 900

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db        901 TCCATTGTGAACGTGCCTGGTGAGTCTACTCTTCGCCGAGATTTCCTGAGACTGCAGCAG 960

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db        961 GAGAACAAGGAACGTTCCGAGGCTCTTCGGAGACAACAGTTACTACAGGAGCAACAGCTC 1020

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db       1021 CGGGAGCAGGAAGAATATAAAAGGCAACTGCTGGCAGAGAGACAGAAGCGGATTGAGCAG 1080

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
Db       1081 CAGAAAGAACAGAGGCGACGGCTAGAAGAGCAACAAAGGAGAGAGCGGGAAGCTAGAAGG 1140

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
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Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
Db       1201 GAGAG--------------------------AAGGCGCAAAGAAGAAGAGGAGAGGAGA 1233

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
Db       1234 CGGGCAGAAGAAGAAAAGAGGAGAGTTGAAAGAGAACAGGAGTATATCAGG---CGACAG 1290

Qy       1447 CAGCAGCAACAGCAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
Db       1291 CTAGAAGAGGAGCAGCGGCACTTGGAAGTCCTTCAGCAGCAGCTGCTCCAGGAGCAGGCC 1350

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
Db       1351 ATGTTACTGCATGACCATAGGAGGCCGCACCCGCAGCACTC------------------- 1391

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
Db       1392 --------------------------GCAGCAGCCGCCACCACCGCAGCAGGAAAGGAGC 1425

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
Db       1426 AAGCCAAGCTTCCATGCTCCCGAGCCCAAAGCCCACTACGAGCCTGCTGACCGAGCGCGA 1485

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
Db       1486 GAGGTACAGTGGTCCCACC-----------------TGGCATCTCTCAAGAACAATGTTT 1528

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
Db       1529 CCCCTGTCTCGCGATCCCATTCCTTCAGTGACCCTTCTCCCAAATTTGCACACCACC--A 1586

Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
Db       1587 TCTTCGTTCTCAGGACCCATGTCCAC-----CTTCCCGCAGTGAGGTGCTCAGTCAGAGC 1641

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
Db       1642 TCTGACTCTAAGTCAGAGGCGCCTGACCCTACCCAAAAGGCTTGGTCTAGATCAGAC--- 1698

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
Db       1699 AGTGACGAGGTGCCTCCAAGGGTTCCTGTGAGAACAACATCTCGCTCCCCTGTTCTGTCC 1758

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
Db       1759 CGTCGAGATTCCCCACTGCAGGGCAGTGGGCAGCAGAATAGCCAGGCAGGACAGAGAAAC 1818

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106
Db       1819 TCCACCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1878

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
Db       1879 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1938

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
Db       1939 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNC-------------------- 1979

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
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Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
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Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
Db       2089 CTGACCGCACTGGCCAAAGAGCTTCGAGCAGTGGAAGATGTACGGCCACCTCACAAAGTA 2148

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Db       2149 ACGGACTACTCCTCATCCAGTGAGGAGTCGGGGACGACGGATGAGGAGGACGACGATGTG 2208

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
Db       2209 GAGCAGGAAGGGGCTGACGAGTCCACCTCAGGACCAGAGGACACCAGAG----------- 2257

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
Db       2258 --CAGCGTCATCTCTGAATTTGAGCAATGGTGAAACGGAATCTGTGAAA----------- 2304

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Db       2305 ------------ACCATGATTGTCCATGATGATGTAGAAAGTGAGCCGGCCAT------- 2345

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
Db       2346 --------------GACCCCATCCAAGGAGGGCACTCTAATCGTCCGCCAGACTCAGTCC 2391

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Db       2392 GCTAGTAGCACACTCCA---------------------------GAAACACAAATCTTC 2423

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
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Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
Db       2587 AACACTAGGCCACAGAGTGACACCCCGGAGATTCGTAAATACAAGAAGAGGTTTAACTCT 2646

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
Db       2647 GAGATTCTGTGTGCTGCCTTATGGGGAGTGAATTTGCTAGTGGGTACAGAGAGTGGCCTG 2706

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
Db       2707 ATGCTGCTGGACAGAAGTGGCCAAGGGAAGGTCTATCCTCTTATCAACCGAAGACGATTT 2766

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
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Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
Db       2827 AAGTTACGTGTCTACTATTTGTCCTGGTTAAGAAATAAAATACTTCACAATGATCCAGAA 2886

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
Db       2887 GTTGAGAAGAAGCAGGGATGGACAACCGTAGGGGATTTGGAAGGATGTGTACATTATAAA 2946

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
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Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
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Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
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Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
Db       3127 TATGGATCCTGTGCTGGATTCCATGCTGTTGATGTGGATTCAGGATCAGTCTATGACATT 3186

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
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Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
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Db       3307 GGAAGGATCACCAAGGATGTAGTTCTACAGTGGGGAGAGATGCCTACATCAGTAGCATAT 3366

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
Db       3367 ATTCGATCCAATCAGACAATGGGCTGGGGAGAGAAGGCCATAGAGATCCGATCTGTGGAA 3426

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
Db       3427 ACTGGTCACTTGGATGGTGTGTTCATGCACAAAAGGGCTCAAAGACTAAAATTCTTGTGT 3486

Qy       3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
Db       3487 GAACGCAATGACAAGGTGTTCTTTGCCTCTGTTCGGTCTGGTGGCAGCAGTCAGGTTTAT 3546

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGT 3943
Db       3547 TTCATGACCTTAGGCAGGACTTCTCTTCTGAGCTGGT 3583
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RESULT 6
BU542554
LOCUS       BU542554                 908 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10322513 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6574439
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ACCESSION   BU542554
VERSION     BU542554.1  GI:22853037
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2769  row: 1  column: 23
            High quality sequence stop: 686.
FEATURES             Location/Qualifiers
     source          1..908
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                     /clone_lib="NIH_MGC_40"
                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California,  Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life  Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             22.1%;  Score 872.4;  DB 13;  Length 908;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-138;
  Matches  899;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    2;

Qy       2679 CGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAA 2738
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Db          1 CGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAA 60

Qy       2739 GGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTT 2798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTT 120

Qy       2799 CACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCAT 2858
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Db        121 CACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCAT 180

Qy       2859 CACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAA 2918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAA 240

Qy       2919 GGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGAT 2978
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Db        241 GGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGAT 300

Qy       2979 CCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAA 3038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAA 360

Qy       3039 CCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGT 3098
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Qy       3099 GTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCT 3158
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Db        421 GTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCT 480

Qy       3159 GCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCG 3218
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Db        481 GCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCG 540

Qy       3219 GAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGG 3278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGG 600

Qy       3279 GGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGT 3338
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Db        601 GGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGT 660

Qy       3339 CATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATT 3398
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Qy       3399 CATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAG- 3457
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Db        721 CATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGG 780

Qy       3458 -TAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCA-TGCTGT 3515
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Db        781 TAGAGGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCANTGCTGT 840

Qy       3516 GGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGAT 3575
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Db        841 GGATGTCGACTTCGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGAT 900

Qy       3576 CACGCCCC 3583
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Db        901 CACGCCCC 908


RESULT 7
BQ706178
LOCUS       BQ706178                 951 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353101 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278193
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VERSION     BQ706178.1  GI:21845077
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2465  row: m  column: 10
            High quality sequence start: 12
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                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             21.5%;  Score 848;  DB 13;  Length 951;
  Best Local Similarity   97.2%;  Pred. No. 1.7e-134;
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Db         24 CATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCAC 83

Qy       2601 CATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGG 2660
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Db         84 CATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGG 143

Qy       2661 GTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGG 2720
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Db        144 GTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGG 203

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Qy        2901 GCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCA 2960
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Qy        2961 CAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGC 3020
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Qy        3021 AGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCG 3080
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Qy        3081 AAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGT 3140
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Qy        3380 CCAAACCCTACCACAAATT-CATGGCCTTCAAGTCC--TTTGCCGACCTCCCCCACCGCC 3436
               ||||||||||||||||||| |||| ||||| |||||  ||  |  || ||||| || |||
Db         864 CCAAACCCTACCACAAATTCCATGCCCTTCCAGTCCCTTTGCCGAACTTCCCCAACGGCC 923

Qy        3437 CTCTGCTGGTCGACCTGACA 3456
               ||||||| |     |||| |
Db         924 CTCTGCTTGGTCGACTGAAA 943
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RESULT 8
AL551911
LOCUS       AL551911               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL551911 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI060YH23 5-PRIME, mRNA sequence.
ACCESSION   AL551911
VERSION     AL551911.2  GI:31273727
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12890305.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8486.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI060CD12QP1&cluster=8486.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI060CD12QP1.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI060YH23"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             21.1%;  Score 834.2;  DB 9;  Length 1201;
  Best Local Similarity   91.7%;  Pred. No. 4.3e-132;
  Matches  857;  Conservative   20;  Mismatches   58;  Indels    0;  Gaps    0;

Qy           7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         258 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 317

Qy          67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         318 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 377

Qy         127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         378 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 437

Qy         187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         438 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 497

Qy         247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         498 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 557

Qy         307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         558 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 617

Qy         367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         618 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 677

Qy         427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         678 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 737

Qy         487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         738 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 797

Qy         547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         798 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 857

Qy         607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         858 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 917

Qy         667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         918 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 977
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Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
Db        978 GCCCTCTTCCTCATTYCTCGGRACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGKCTAAG 1037

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
Db       1038 AAGTTCATTGACTTYATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCMTCCACCG 1097

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
Db       1098 GGAAGCTATKAAGTTTCCTTYATCCGGAGCASCCAMGGRRCGGARGKCCCAWYCASTTWA 1157

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAA 941
Db       1158 GRRMMAAWTKACSRTCCGGAAAARSGGGGAAAAA 1192


RESULT 9
AY400357
LOCUS       AY400357                3588 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Pan troglodytes MAP4K4 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY400357
VERSION     AY400357.1  GI:39756346
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 3588)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3588)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..3588
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1..>3588
                     /gene="MAP4K4"
                     /locus_tag="HCM0530"
ORIGIN

  Query Match             21.1%;  Score 833.4;  DB 29;  Length 3588;
  Best Local Similarity   49.5%;  Pred. No. 9.9e-132;
  Matches 1889;  Conservative    0;  Mismatches 1694;  Indels  234;  Gaps   11;

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
Db          1 GGTCGACATGTTAAAACGGGTCAGTTGGCAGCCATCAAAGTTATGGATGTCACTGAGNNN 60

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
Db         61 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 120

Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
Db        121 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 180

Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
Db        181 NNNCTTGTTATGGAGTTCTGTGGGGCTGGGTCCATTACAGACCTTGTGAAGAACACCAAA 240

Qy        370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
Db        241 GGGAACACACTCAAAGAAGACTGGATCGCTTACATCTCCAGAGAAATCCTGAGGGGACTG 300

Qy        430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
Db        301 GCACATCTTCACATTCATCATGTGATTCACCGGGATATCAAGGGCCAGAATGTGTTGCTG 360

Qy        490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
Db        361 ACTGAGAATGCAGAGGTGAAACTTGTTGACTTTGGTGTGAGTGCTCAGCTGGACAGGACT 420

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
Db        421 GTGGGGCGGAGAAATACGTTCATAGGCACTCCCTACTGGATGGCTCCTGAGGTCATCGCC 480

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
Db        481 TGTGATGAGAACCCAGATGCCACCTATGATTACAGANNNNNNNNNNNNNNNNNNNNNNNN 540

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
Db        541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTCTCTGTGACATGCATCCAATGAGAGCA 600

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
Db        601 CTGTTTCTCATTCCCAGAAACCCTCCTCCCCGGCTGAAGTCAAAAAAATGGTCGAAGAAA 660

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
Db        661 TTTTTAGTTTTATAGAAGGGTGCCTGGTGAAGAATTACATGCAGCGGCCCTCTACAGAG 720

Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
Db        721 CAGCTTTTGAAACATCCTTTTATAAGGGATCAGCCAAATGAAAGGCAAGTTAGAATCCAG 780

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
Db        781 CTTAAGGATCATATAGATCGCACCAGGAANNNGAGAGGCGAGAAAGNNNNNNNNNNNNN 840

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC--- 1026
Db        841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNT 900

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
Db        901 TCCATTGTGAACGTGCCTGGTGAGTCTACTCTTCGTCGAGATTTCCTGAGACTGCAGCAG 960

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
Db        961 GAGAACAAGGAACGTTCCGAGGCTCTTCGGAGACAACAGTTACTACAGGAGCAACAGCTC 1020

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
Db       1021 CGGGAGCAGGAAGAATATAAAAGGCAACTGCTGGCAGAGAGACAGAAGCGGATTGAGCAG 1080

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
Db       1081 CAGAAAGAACAGAGGCGACGGCTAGAAGAGCAACAAAGGAGAGAGCGTGAAGCTAGAAGG 1140

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
Db       1141 CAGCAGGAACGTGAACAGCGAAGGAGAGAACAAGAAGAAAAGAGGCGTCTAGAGGAGTTG 1200

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
Db       1201 GAGAG--------------------------AAGGCGCAAAGAAGAAGAGGAGAGGAGA 1233
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Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
Db       1234 CGGGCAGAAGAAGAAAAGAGGAGAGTTGAAAGAGAACAGGAGTATATCAGG---CGACAG 1290

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
Db       1291 CTAGAAGAGGAGCAGCGGCACTTGGAAGTCCTTCAGCAGCAGCTGCTCCAGGAGCAGGCC 1350

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
Db       1351 ATGTTACTGCATGACCATAGGAGGCCGCACCCGCAGCACTCGCAGCAGCCGCCACCACCG 1410

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
Db       1411 CAGCAGGAAAGGAGCAAGCCAAGCTTCCATGCTC------------------------- 1444

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
Db       1445 -------------CCGAGCCCAAAGCCCACTACGAGCCTGCTGACCGAGCGCGAGAGGTA 1491

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
Db       1492 CAGTGGTCCCACCTGGCATCTCTCAAGA--------------------------ACAAT 1524

Qy       1747 TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGAC 1806
Db       1525 GTTTCCCCTGTCTCGCGATCCCATTCCTTCAGTGACCCTTCTCCTCCCAAATTTGCACAC 1584

Qy       1807 CCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAAT 1866
Db       1585 CACCATCTTCGTTCTCAGGACCCATGTCCACCTTCCCGCAGTGAGGTGCTCAGTCAAAGC 1644

Qy       1867 TCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCCCA 1926
Db       1645 TCTGA---TAAGTCAGAGGCGCCTGACCCTACCCAAAAGACTTGGTTTAGATCAGACAGT 1701

Qy       1927 GATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAAC 1986
Db       1702 GGCGAGGTGCCTCCAAGGAGGGTTCCTGTGAGAACAACATCTCGCTCCCCTGTTCTGTCC 1761

Qy       1987 ACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAAC 2046
Db       1762 CGTCGAGATTCCCCACTGCAGGGCAGTGGGCAGCAGAATAGCCAGGCAGGACAGAGAAAC 1821

Qy       2047 TCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGG 2106
Db       1822 TCCACCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1881

Qy       2107 CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGC 2166
Db       1882 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1941

Qy       2167 GACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAG 2226
Db       1942 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNC------------------- 1982

Qy       2227 GCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTGTG 2286
Db       1983 -----------ATCATCCAAGTCTGAAGGCTCTCCATCTCAGCGCCTGGAAAATGCAGTG 2031

Qy       2287 CTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCA 2346
Db       2032 AAAAAACCTGAAGATAAAAAGGAAGTTTTCAAACCCCTCAAGCCTGCTGTAAGGATTGAT 2091

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
Db       2092 CTGACCGCACTGGCCAAAGAGCTTCGAGCAGTGGAAGATGTACGGCCACCTCACAAAGTA 2151

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
Db       2152 ACGGACTACTCCTCATCCAGTGAGGAGTCGGGGACGACGGATGAGGAGGACGACGATGTG 2211

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
Db       2212 GAGCAGGAAGGGGCTGACGAGTCCACCTCAGGACCAGAGGACACCAGAG----------- 2260

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
Db       2261 --CAGCGTCATCTCTGAATTTGAGCAATGGTGAAACGGAATCTGTGAAA----------- 2307

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
Db       2308 ------------ACCATGATTGTCCATGATGATGTAGAAAGTGAGCCGGCCAT------- 2348

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
Db       2349 --------------GACCCCATCCAAGGAGGGCACTCTAATCGTCCGCCAGACTCAGTCC 2394

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
Db       2395 GCTAGTAGCACACTCCAGAAACACAAATCTTCCTCCTCCTTTACACCTTTTATAGACCCC 2454

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
Db       2455 AGATTACTACAGATTTCTCCATCTAGCGGAACAACAGTGACTTCTGTGGTGGGATTTTCC 2514

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
Db       2515 TGTGATGGGATGAGACCAGAAGCCATA--------------------------------- 2541

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
Db       2542 ------------AGGCAAGATCCTACCCGGAAAGGCTCAGTGGTCAATGTGAATCCTACC 2589

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
Db       2590 AACACTAGGCCACAGAGTGACACCCCGGAGATTCGTAAATACAAGAAGAGGTTTAACTCT 2649

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
Db       2650 GAGATTCTGTGTGCTGCCTTATGGGGAGTGAATTTGCTAGTGGGTACAGAGAGTGGCCTG 2709

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
Db       2710 ATGCTGCTGGACAGAAGTGGCCAAGGGAAGGTCTATCCTCTGATCAACCGAAGACGATTT 2769

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
Db       2770 CAACAAATGGACGTACTTGAGGGCTTGAATGTCTTGGTGACAATATCTGGCAAAAAGGAT 2829

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
Db       2830 AAGTTACGTGTCTACTATTTGTCCTGGTTAAGAAATAAAATACTTCACAATGATCCAGAA 2889

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
Db       2890 GTTGAGAAAAAGCAGGGATGGACAACCGTAGGGGATTTGGAAGGATGTGTACATTATAAA 2949

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
Db       2950 GTTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3009

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
Db       3010 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTCATTTGGAGAATTG 3069

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
Db       3070 GTACATAAGCCATTACTGGTGGATCTCACTGTTGAGGAAGGCCAGAGGTTGAAAGTGATC 3129

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
Db       3130 TATGGATCCTGTGCTGGATTCCATGCTGTTGATGTGGATTCAGGATCAGTCTATGACATT 3189

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
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Db       3190 TATCTACCAACACATATCCAGTGTAGCATCAAACCCCATGCAATCATCATCCTCCCCAAT 3249

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              || || || ||||| | ||| |||||| || || |||| || || || ||||| ||
Db       3250 ACAGATGGAATGGAGCTTCTGGTGTGCTATGAAGATGAGGGGTTTATGTAAACACATAT 3309

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||  | ||||  ||||||| || || |||||||| |||||||||| || || || ||
Db       3310 GGAAGGATCACCAAGGATGTAGTTCTACAGTGGGGAGAGATGCCTACGTCAGTAGCATAT 3369

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||  | |||| |||| ||||||||||| ||||| ||||  ||||||  |||||||
Db       3370 ATTCGATCCAATCAGACAATGGGCTGGGGAGAGAAGGCCATAGAGATCCGATCTGTGGAA 3429

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              || || |||  | || || || ||||||||||| | ||||| || || || ||| |||||
Db       3430 ACTGGTCACTTGGATGGTGTGTTCATGCACAAAAGGGCTCAAAGACTAAAATTCTTGTGT 3489

Qy       3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
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Db       3490 GAACGCAATGACAAGGTGTTCTTTGCCTCTGTTCGGTCTGGTGGCAGCAGTCAGGTTTAT 3549

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGT 3943
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Db       3550 TTCATGACCTTAGGCAGGACTTCTCTTCTGAGCTGGT 3586
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RESULT 10
BM541693

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LOCUS       BM541693                1026 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6448280 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531587
            5', mRNA sequence.
ACCESSION   BM541693
VERSION     BM541693.1  GI:18770559
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12213  row: h  column: 20
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5531587"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_71"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb.  "
ORIGIN

  Query Match             20.6%;  Score 814.4;  DB 12;  Length 1026;
  Best Local Similarity   95.5%;  Pred. No. 9.7e-129;
  Matches  871;  Conservative    0;  Mismatches   36;  Indels    5;  Gaps    3;

Qy       2360 TGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGT 2419
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Db          1 TGGACGCGTGGGCTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGT 60

Qy       2420 CGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAG 2479
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Qy       2480 CAGAGGGGAGCAGAGATACCCCTGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCA 2539
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Qy       2540 CCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCA 2599
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Db        181 CCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCA 240

Qy       2600 CCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATG 2659
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Db        241 CCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATG 300

Qy       2660 GGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAG 2719
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Db        481 GTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGC 540

Qy       2900 TGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCC 2959
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Qy       2960 ACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTG 3019
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Db        840 TATTACCTGGTCCTGGCCTCCCGAAAAAGGATTCTGCCCAATGAACCTCAAAATGGGCAG 899

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RESULT 11
BQ684810

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LOCUS       BQ684810                 907 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8346064 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250774
            5', mRNA sequence.
ACCESSION   BQ684810
VERSION     BQ684810.1  GI:21810126
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 907)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2394  row: f  column: 23
            High quality sequence stop: 665.
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                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of  California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             20.2%;  Score 799.6;  DB 13;  Length 907;
  Best Local Similarity   98.9%;  Pred. No. 3.1e-126;
  Matches  805;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

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Qy       3197 TGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGA 3256
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Db         61 TGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGA 120

Qy       3257 AGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAAT 3316
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Db        361 GTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTG 420

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Db        421 TGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCA 480

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Qy       3917 TGAACCGTAACTGCATCATGAACTGGTGAAAGGG 3950
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RESULT 12
BI756763
LOCUS       BI756763                 866 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603024432F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194998 5',
            mRNA sequence.
ACCESSION   BI756763
VERSION     BI756763.1  GI:15748341
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 866)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11487  row: p  column: 07
            High quality sequence stop: 816.
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                     /clone_lib="NIH_MGC_114"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
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                     upon cloning).  Average insert size 1.5 kb, insert size
                     range 1-3 kb.  Library is normalized and enriched for
                     full-length  clones and was constructed by C. Gruber
                     (Invitrogen).  Research  Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             20.2%;  Score 799;  DB 12;  Length 866;
  Best Local Similarity   98.8%;  Pred. No. 3.8e-126;
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Qy       2979 CCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAA 3038
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Qy       3039 CCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGT 3098
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Db        421 CATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCG-CCTCTGCTGGTCGACCTGACAGT 479

Qy       3459 AGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGA 3518
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Db        480 AGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGA 539

Qy       3519 TGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCAC 3578
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RESULT 13
BU542006
LOCUS       BU542006                881 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10252775 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6573796
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ACCESSION   BU542006
VERSION     BU542006.1  GI:22852489
KEYWORDS    EST.
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2768  row: b  column: 04
            High quality sequence stop: 680.
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                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             19.7%;  Score 779.8;  DB 13;  Length 881;
  Best Local Similarity   98.9%;  Pred. No. 7.4e-123;
  Matches  796;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    1;

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Qy        3339 CATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGCCCCCAAACCCTACCACAAATT 3398
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Qy        3399 CATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGT 3458
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Db         721 CATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGT 780

Qy        3459 A--GAGGAGGGGCAGCGGCTCAAGG 3481
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Db         781 AAGAGGAAGGGGCAGCGGCTTCAAG 805


RESULT 14
BM451246
LOCUS       BM451246                 936 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6392707 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5495254
            5', mRNA sequence.
ACCESSION   BM451246
VERSION     BM451246.1  GI:18500286
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 936)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12121  row: n  column: 23
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                     Technologies."
ORIGIN

  Query Match             19.5%;  Score 772.4;  DB 12;  Length 936;
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Qy        2442 CAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCC 2501
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Qy        2562 GGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCC 2621
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Db         121 GGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCC 180

Qy        2622 TGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGT 2681
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Qy        2682 GGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGA 2741
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Qy        3219 GAACAAGATTCTGCACAATGACCCAGAA--GTGGAGAAGAAGCAGGGCTGGACCACCGTG 3276
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Qy        3277 GGGG 3280
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Db         841 GGGG 844


RESULT 15
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LOCUS       CA454128                 881 bp    mRNA    linear   EST 12-NOV-2002
DEFINITION  AGENCOURT_10738502 MAPcL Homo sapiens cDNA clone IMAGE:6718789 5',
            mRNA sequence.
ACCESSION   CA454128
VERSION     CA454128.1  GI:24903563
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
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  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14275  row: k  column: 13
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                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification:  26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
                     cancer genes encoding  membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN

  Query Match            19.3%;  Score 764.4;  DB 14;  Length 881;
  Best Local Similarity  97.5%;  Pred. No. 3.2e-120;
  Matches  821;  Conservative    0;  Mismatches   11;  Indels   10;  Gaps    4;

Qy       1978 GCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCT 2037
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Qy       2038 CGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAG 2097
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2098 CCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTC 2157
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Db        121 CCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTC 180

Qy       2158 AGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCAC 2217
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Qy       2218 CTCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGC 2277
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Qy       2398 AAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAG 2457
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Qy       2578 CAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAAC 2637
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Qy       2698 TCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGG---ATGGGAGTGGTGAC 2754
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Qy       2755 TACCAGTCTCGTGGG--CTGGTAAAGGCCCCTGGCAAGAGCTCG--TTCACGATGTTTGT 2810
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Qy       2811 GG 2812
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Db        838 GG 839

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Job time : 6322 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 14:44:02 ; Search time 9933 Seconds
(without alignments)
17240.343 Million cell updates/sec

Title: US-10-029-115-1
Perfect score: 3951
Sequence: 1 gcccttatgggcgacccagc..........tcatgaactggtgaaagggc 3951

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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39: em_htgo_hum:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2201	55.7	5014	9	BC034673	BC034673 Homo sapi
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	3	1787	45.2	4133	6	AR435598	AR435598 Sequence
	4	1701	43.1	3888	9	AB035698	AB035698 Homo sapi
	5	1689	42.7	4863	9	AB041926	AB041926 Homo sapi
	6	1599	40.5	3735	6	AX235365	AX235365 Sequence
	7	1599	40.5	3822	6	AX235363	AX235363 Sequence
	8	1599	40.5	3912	6	AX235361	AX235361 Sequence
	9	1599	40.5	3999	6	AX235359	AX235359 Sequence
	10	1599	40.5	4590	9	HSM802420	AL157418 Homo sapi
	11	1337	33.8	1482	6	AX235417	AX235417 Sequence
	12	1337	33.8	1649	6	AX235415	AX235415 Sequence
	13	1337	33.8	1717	6	AX235422	AX235422 Sequence
	14	1337	33.8	1787	6	AX235419	AX235419 Sequence
	15	1078	27.3	3824	6	BD183377	BD183377 Novel gen
	16	970	24.6	1964	9	AF218033	AF218033 Homo sapi
	17	575	14.6	1539	6	AX011641	AX011641 Sequence
	18	575	14.6	1539	6	BD226252	BD226252 Pancreati
	19	555	14.0	3152	6	AX834264	AX834264 Sequence
	20	555	14.0	3152	9	AK096610	AK096610 Homo sapi
	21	225	5.7	129169	2	AC032038	AC032038 Homo sapi
c	22	225	5.7	151999	2	AC005973	AC005973 Homo sapi
	23	225	5.7	181825	9	AC109333	AC109333 Homo sapi
	24	225	5.7	184595	2	AC015913	AC015913 Homo sapi
c	25	205	5.2	58311	2	AC110596	AC110596 Homo sapi
c	26	177	4.5	129169	2	AC032038	AC032038 Homo sapi
c	27	172	4.4	184595	2	AC015913	AC015913 Homo sapi
	28	128	3.2	151999	2	AC005973	AC005973 Homo sapi
	29	92	2.3	57205	2	AC107995	AC107995 Homo sapi
c	30	86	2.2	62919	2	AC107963	AC107963 Homo sapi
	31	77	1.9	146	6	AX139136	AX139136 Sequence
	32	77	1.9	146	6	BD014753	BD014753 Gene and
	33	69	1.7	283	6	AX917332	AX917332 Sequence
	34	69	1.7	283	6	BD052865	BD052865 Sequence
	35	69	1.7	285	6	BD076893	BD076893 5' EST of
	36	62	1.6	295	11	G09516	G09516 human STS C
c	37	62	1.6	1665	9	AB070507	AB070507 Homo sapi
c	38	54	1.4	1628	9	AB070512	AB070512 Callithri
c	39	54	1.4	1632	9	AB070513	AB070513 Lemur cat
c	40	54	1.4	1655	9	AB070509	AB070509 Pongo pyg
c	41	54	1.4	1664	9	AB070508	AB070508 Pan panis
c	42	54	1.4	1669	9	AB070510	AB070510 Hylobates
	43	53	1.3	4381	10	BC011346	BC011346 Mus muscu
	44	53	1.3	4842	10	BC052474	BC052474 Mus muscu
	45	53	1.3	4848	10	AB035697	AB035697 Mus muscu
	46	53	1.3	4873	10	AB041925	AB041925 Mus muscu
c	47	53	1.3	123943	10	AL592547	AL592547 Mouse DNA
c	48	53	1.3	171697	2	AC119116	AC119116 Rattus no
c	49	53	1.3	194609	2	AC013775	AC013775 Mus muscu
	50	53	1.3	228232	2	AC090293	AC090293 Mus muscu
	51	53	1.3	263882	2	AC107344	AC107344 Rattus no
c	52	51	1.3	1666	9	AB070511	AB070511 Macaca ar
	53	47	1.2	896	6	AR279565	AR279565 Sequence
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	55	44	1.1	1371	10	BC056650	BC056650 Mus muscu
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	57	44	1.1	1657	6	AX235382	AX235382 Sequence
	58	44	1.1	1725	6	AX235389	AX235389 Sequence
	59	44	1.1	1788	6	AX235386	AX235386 Sequence
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	61	44	1.1	4301	10	AK129191	AK129191 Mus muscu
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	63	44	1.1	185598	2	AC132909	AC132909 Mus muscu
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c	65	42	1.1	192681	3	AC011905	AC011905 Drosophil

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	70	35	0.9	910	11	G40206	G40206 Z20860 Zebr
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c	72	33	0.8	1657	4	AB070519	AB070519 Equus cab
	73	31	0.8	348	3	AF139022	AF139022 Cepaea ne
c	74	31	0.8	1599	4	AB070520	AB070520 Bos tauru
	75	31	0.8	2906	9	HSU07349	U07349 Human B lym
	76	31	0.8	2913	9	BC039839	BC039839 Homo sapi
	77	31	0.8	2921	9	BC047865	BC047865 Homo sapi
c	78	31	0.8	62576	5	FRNINE1	AF146687 Fugu rubr
c	79	31	0.8	150979	2	AC122073	AC122073 Rattus no
	80	31	0.8	186058	2	AC132176	AC132176 Rattus no
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	83	31	0.8	228804	2	AC134537	AC134537 Mus muscu
	84	31	0.8	237361	2	AC107362	AC107362 Rattus no
	85	31	0.8	240090	2	AC111588	AC111588 Rattus no
	86	31	0.8	247582	2	AC115339	AC115339 Rattus no
	87	30	0.8	507	10	MMU49949	U49949 Mus musculu
c	88	30	0.8	1585	4	AB070517	AB070517 Sus scrof
c	89	30	0.8	1654	4	AB070518	AB070518 Balaenopt
c	90	30	0.8	229799	2	AC097797	AC097797 Rattus no
	91	30	0.8	242203	2	AC099230	AC099230 Rattus no
	92	30	0.8	256867	2	AC109662	AC109662 Rattus no
c	93	30	0.8	260347	2	AC127872	AC127872 Rattus no
	94	29	0.7	1103	5	LFL308121	AJ308121 Lampetra
	95	29	0.7	1252	10	BC051478	BC051478 Mus muscu
	96	29	0.7	1881	3	AY136274	AY136274 Antheraea
c	97	29	0.7	2214	6	AR093957	AR093957 Sequence
c	98	29	0.7	2214	6	E15639	E15639 Pinctada fu
	99	29	0.7	2697	8	AK110487	AK110487 Oryza sat
c	100	29	0.7	3331	3	D86074	D86074 Pinctada fu
c	101	29	0.7	3331	6	AR093958	AR093958 Sequence
c	102	29	0.7	3331	6	AR093959	AR093959 Sequence
c	103	29	0.7	3331	6	E15640	E15640 Pinctada fu
c	104	29	0.7	3331	6	BD129567	BD129567 Polynucle
	105	29	0.7	4483	5	BC055134	BC055134 Danio rer
	106	29	0.7	40653	2	AC011906	AC011906 Drosophil
c	107	29	0.7	72562	2	AC019575	AC019575 Drosophil
c	108	29	0.7	83253	3	AY186999	AY186999 Drosophil
c	109	29	0.7	160957	9	AC114487	AC114487 Homo sapi
c	110	29	0.7	172372	3	AC010110	AC010110 Drosophil
	111	29	0.7	180259	2	AC147222	AC147222 Mus muscu
c	112	29	0.7	202374	10	AC122868	AC122868 Mus muscu
	113	29	0.7	227853	2	AC114204	AC114204 Rattus no
c	114	29	0.7	228232	2	AC090293	AC090293 Mus muscu
	115	29	0.7	243260	2	AC131739	AC131739 Mus muscu
c	116	29	0.7	304419	3	AE003476	AE003476 Drosophil
c	117	29	0.7	325898	2	AC122990	AC122990 Rattus no
	118	28	0.7	741	5	AY235187	AY235187 Meleagris
	119	28	0.7	1216	9	AK130198	AK130198 Homo sapi
c	120	28	0.7	3736	8	AF114235	AF114235 Scenedesm
	121	28	0.7	3885	3	DMABDBP3	X16134 Drosophila
	122	28	0.7	4106	3	AY128421	AY128421 Drosophil
	123	28	0.7	4771	3	DMABDBCLA	X51663 D.melanogas
	124	28	0.7	6670	9	HSM805725	BX537423 Homo sapi
	125	28	0.7	6690	9	HSM804919	AL833606 Homo sapi
	126	28	0.7	60471	2	AC015173	AC015173 Drosophil
	127	28	0.7	63940	2	AC017795	AC017795 Drosophil
c	128	28	0.7	72165	10	AL844574	AL844574 Mouse DNA
	129	28	0.7	80423	3	DROABDB	L07835 Drosophila
c	130	28	0.7	96824	2	AC020384	AC020384 Drosophil
	131	28	0.7	103034	2	AC067978	AC067978 Homo sapi
c	132	28	0.7	105791	2	AC095467_3	Continuation (4 of
	133	28	0.7	111934	9	AF281074	AF281074 Homo sapi
	134	28	0.7	116039	9	AC007362	AC007362 Homo sapi
c	135	28	0.7	163979	3	AC099310	AC099310 Drosophil
	136	28	0.7	164038	3	AC009846	AC009846 Drosophil
	137	28	0.7	165165	3	AC095018	AC095018 Drosophil
c	138	28	0.7	165855	3	AC009342	AC009342 Drosophil
	139	28	0.7	174751	3	AC008288	AC008288 Drosophil
c	140	28	0.7	175335	3	AC091636	AC091636 Drosophil
	141	28	0.7	194535	2	AC139950	AC139950 Rattus no
	142	28	0.7	196784	2	AC113006	AC113006 Mus muscu
	143	28	0.7	200734	2	AC109272	AC109272 Mus muscu
c	144	28	0.7	206858	2	AC115733	AC115733 Mus muscu
c	145	28	0.7	216825	2	AC108908	AC108908 Mus muscu
c	146	28	0.7	228544	3	AE003715	AE003715 Drosophil
	147	28	0.7	234378	3	AE003740	AE003740 Drosophil
	148	28	0.7	237066	2	AC134080	AC134080 Rattus no
	149	28	0.7	338234	3	DMU31961	U31961 Drosophila
c	150	28	0.7	348873	3	AE003790	AE003790 Drosophil
c	151	27	0.7	289	11	G09716	G09716 human STS C
	152	27	0.7	1053	10	BC027560	BC027560 Mus muscu
c	153	27	0.7	1834	5	DRE245963	AJ245963 Danio rer
c	154	27	0.7	2045	5	DRE245962	AJ245962 Danio rer
	155	27	0.7	2142	9	AF512948	AF512948 Gorilla g
	156	27	0.7	2142	9	AF512949	AF512949 Pongo pyg
	157	27	0.7	2142	9	AY143180	AY143180 Gorilla g
	158	27	0.7	2145	9	AF512950	AF512950 Macaca mu
	159	27	0.7	2145	9	AY143181	AY143181 Pongo pyg
	160	27	0.7	2657	9	AB055311	AB055311 Homo sapi
	161	27	0.7	2661	5	AY466101	AY466101 Melopsitt
	162	27	0.7	2692	10	BC058960	BC058960 Mus muscu
	163	27	0.7	2857	3	BT003275	BT003275 Drosophil
	164	27	0.7	2955	10	BC053388	BC053388 Mus muscu
	165	27	0.7	3084	3	DMU36477	U36477 Drosophila
	166	27	0.7	3084	6	AX664483	AX664483 Sequence
	167	27	0.7	3135	9	HSU90336	U90336 Human PEG3
	168	27	0.7	3639	3	AF145627	AF145627 Drosophil
	169	27	0.7	3707	3	AY060702	AY060702 Drosophil
	170	27	0.7	4657	10	BC058658	BC058658 Mus muscu
	171	27	0.7	4738	9	AF208969	AF208969 Homo sapi
	172	27	0.7	4947	10	BC059270	BC059270 Mus muscu
	173	27	0.7	5052	9	AF208968	AF208968 Homo sapi
	174	27	0.7	5116	9	AF208970	AF208970 Homo sapi
	175	27	0.7	5245	9	F208971S10	AF208980 Homo sapi
	176	27	0.7	5994	6	AX683162	AX683162 Sequence
	177	27	0.7	5994	9	AB006625	AB006625 Homo sapi
	178	27	0.7	6371	9	AF208967	AF208967 Homo sapi
	179	27	0.7	6754	6	AX821998	AX821998 Sequence
	180	27	0.7	6754	9	AF036892	AF036892 Homo sapi
	181	27	0.7	8019	3	AF289034	AF289034 Drosophil
	182	27	0.7	8328	3	AF293971	AF293971 Drosophil
	183	27	0.7	14297	9	AF515053	AF515053 Pongo pyg
c	184	27	0.7	28133	2	AC012975	AC012975 Drosophil
c	185	27	0.7	28486	6	AX695350	AX695350 Sequence
	186	27	0.7	43155	3	AY190954	AY190954 Drosophil
	187	27	0.7	44352	2	AC019972	AC019972 Drosophil
	188	27	0.7	45258	2	AC015395	AC015395 Drosophil
c	189	27	0.7	46375	2	AC015181	AC015181 Drosophil
c	190	27	0.7	87822	2	AC013928	AC013928 Drosophil
c	191	27	0.7	110000	2	AC101727_0	AC101727 Mus muscu
	192	27	0.7	110000	2	AC126741_3	Continuation (4 of
c	193	27	0.7	113907	10	AL646002	AL646002 Mouse DNA
	194	27	0.7	125686	9	HS503G16	Z93020 Human DNA s
	195	27	0.7	140475	2	AC120081	AC120081 Rattus no
c	196	27	0.7	143322	10	AC115440	AC115440 Rattus no
c	197	27	0.7	152537	2	AC111054	AC111054 Mus muscu
	198	27	0.7	154480	10	AF384675	AF384675 Mus muscu
c	199	27	0.7	163403	3	AC007765	AC007765 Drosophil
c	200	27	0.7	163741	3	AC007821	AC007821 Drosophil
c	201	27	0.7	164920	3	AC092187	AC092187 Drosophil
c	202	27	0.7	166616	2	AC147124	AC147124 Mus muscu
	203	27	0.7	169604	10	AC107775	AC107775 Mus muscu
c	204	27	0.7	173302	2	AC008137	AC008137 Drosophil
c	205	27	0.7	178367	9	AC006115	AC006115 Homo sapi
	206	27	0.7	180425	3	AC008229	AC008229 Drosophil
c	207	27	0.7	182426	2	AC123443	AC123443 Rattus no
	208	27	0.7	186218	3	AC023680	AC023680 Drosophil
c	209	27	0.7	189596	3	AC008313	AC008313 Drosophil
	210	27	0.7	192628	10	AC091533	AC091533 Mus muscu
	211	27	0.7	193458	2	AC147175	AC147175 Silurana

c	212	27	0.7	199071	10	AL669938	AL669938 Mouse DNA
	213	27	0.7	200202	10	AC112154	AC112154 Mus muscu
c	214	27	0.7	204954	2	AC128028	AC128028 Rattus no
c	215	27	0.7	211343	10	AC122630	AC122630 Rattus no
	216	27	0.7	229684	3	AE003815	AE003815 Drosophil
c	217	27	0.7	236096	3	AE003775	AE003775 Drosophil
	218	27	0.7	238466	2	AC097567	AC097567 Rattus no
	219	27	0.7	239986	2	AC107150	AC107150 Rattus no
	220	27	0.7	243210	2	AC136831	AC136831 Rattus no
c	221	27	0.7	243530	2	AC130913	AC130913 Rattus no
c	222	27	0.7	267603	3	AE003676	AE003676 Drosophil
c	223	27	0.7	290773	2	AC129162	AC129162 Rattus no
	224	27	0.7	295883	2	AC138459	AC138459 Mus muscu
	225	27	0.7	309958	3	AE003479	AE003479 Drosophil
	226	27	0.7	314957	3	AE003581	AE003581 Drosophil
	227	27	0.7	320010	2	AC122275	AC122275 Mus muscu
	228	27	0.7	338399	2	AC131975	AC131975 Mus muscu
	229	26	0.7	36	6	A62704	A62704 Sequence 5
	230	26	0.7	54	6	A62703	A62703 Sequence 4
	231	26	0.7	57	6	AR159554	AR159554 Sequence
	232	26	0.7	66	6	A62702	A62702 Sequence 3
	233	26	0.7	69	6	AR159553	AR159553 Sequence
	234	26	0.7	75	6	AR159550	AR159550 Sequence
	235	26	0.7	78	6	AR159551	AR159551 Sequence
	236	26	0.7	78	6	AR159552	AR159552 Sequence
	237	26	0.7	87	6	AX384806	AX384806 Sequence
	238	26	0.7	107	6	BD274846	BD274846 CANCER CE
	239	26	0.7	107	6	AR205312	AR205312 Sequence
	240	26	0.7	112	11	G64274	G64274 20 Human Ho
	241	26	0.7	119	11	G64277	G64277 24 Human Ho
	242	26	0.7	156	11	G10850	G10850 umc52 R mai
	243	26	0.7	163	4	BOVTBPR	L47974 Bos taurus
	244	26	0.7	169	6	BD274843	BD274843 CANCER CE
	245	26	0.7	169	6	AR205309	AR205309 Sequence
c	246	26	0.7	175	3	AF418589	AF418589 Anopheles
	247	26	0.7	183	6	AR401376	AR401376 Sequence
	248	26	0.7	184	4	PIGTBBP	L47972 Sus scrofa
	249	26	0.7	190	4	HRSTBPRA	L47975 Equus cabal
	250	26	0.7	190	6	BD274848	BD274848 CANCER CE
	251	26	0.7	190	6	AR205314	AR205314 Sequence
	252	26	0.7	218	11	G64270	G64270 13 Human Ho
	253	26	0.7	234	9	AY368204	AY368204 Homo sapi
	254	26	0.7	237	3	AY333193	AY333193 Anopheles
	255	26	0.7	238	3	AY333194	AY333194 Anopheles
c	256	26	0.7	239	9	HSA279566	AJ279566 Homo sapi
	257	26	0.7	240	3	AY333191	AY333191 Anopheles
	258	26	0.7	240	3	AY333195	AY333195 Anopheles
	259	26	0.7	243	3	AY333196	AY333196 Anopheles
c	260	26	0.7	250	3	AY029717	AY029717 Anopheles
	261	26	0.7	252	10	MMIIR	X07129 Mouse mIi m
	262	26	0.7	256	11	G64278	G64278 25 Human Ho
	263	26	0.7	264	9	AF330032	AF330032 Papio ham
	264	26	0.7	270	3	AY333192	AY333192 Anopheles
c	265	26	0.7	271	11	G16013	G16013 human STS C
	266	26	0.7	281	3	AY333200	AY333200 Anopheles
	267	26	0.7	282	3	AY333198	AY333198 Anopheles
	268	26	0.7	285	5	GGRE16E1	X78609 G.gallus ge
c	269	26	0.7	292	11	G16008	G16008 human STS C
	270	26	0.7	303	9	AF330031	AF330031 Macaca mu
	271	26	0.7	305	6	BD129589	BD129589 Polynucle
	272	26	0.7	336	3	AY333190	AY333190 Anopheles
	273	26	0.7	339	3	AY333202	AY333202 Anopheles
c	274	26	0.7	354	11	G09937	G09937 human STS C
	275	26	0.7	390	9	AF330028	AF330028 Pan trogl
	276	26	0.7	393	3	AY333203	AY333203 Anopheles
c	277	26	0.7	397	9	HSJ002193	AJ002193 Homo sapi
	278	26	0.7	398	3	SGABDBG	X69161 S.gregaria
	279	26	0.7	398	6	BD129604	BD129604 Polynucle
	280	26	0.7	409	9	AF330029	AF330029 Gorilla g
	281	26	0.7	423	3	AY333206	AY333206 Anopheles
c	282	26	0.7	441	3	HAR504785	AJ504785 Helicover
	283	26	0.7	458	3	AF229981	AF229981 Varroa ja
	284	26	0.7	459	6	AR401373	AR401373 Sequence
	285	26	0.7	463	6	AX210423	AX210423 Sequence
	286	26	0.7	471	9	HSCAG40	X85325 H.sapiens m
	287	26	0.7	476	6	BD129613	BD129613 Polynucle
	288	26	0.7	476	9	HSCBFA1S2	AF001444 Homo sapi
c	289	26	0.7	478	11	AF021127	AF021127 Homo sapi
	290	26	0.7	496	11	G09491	G09491 human STS C
	291	26	0.7	508	10	MUSIFNRES	M35872 Mouse MHC c
	292	26	0.7	520	9	HSA279564	AJ279564 Homo sapi
	293	26	0.7	532	8	AY158017	AY158017 Fucaceae
	294	26	0.7	533	9	HSU80756	U80756 Homo sapien
	295	26	0.7	536	11	G64267	G64267 10 Human Ho
	296	26	0.7	567	8	AF442381	AF442381 Pinus tae
	297	26	0.7	575	9	HSDAN15	Y08266 H.sapiens m
c	298	26	0.7	575	11	BV037017	BV037017 S212P6034
	299	26	0.7	585	10	MMIIGA	X05428 Mouse Ii ge
c	300	26	0.7	588	11	G97681	G97681 S208P6381RG
	301	26	0.7	594	10	MUSOPA	M16362 Mouse opa r
	302	26	0.7	606	11	G16005	G16005 human STS C
	303	26	0.7	623	6	AR159546	AR159546 Sequence
	304	26	0.7	700	8	AF483857	AF483857 Phaseolus
	305	26	0.7	716	9	HSAAD10	Y08267 H.sapiens m
	306	26	0.7	766	9	AF467252	AF467252 Homo sapi
	307	26	0.7	780	9	HSA324720	AJ324720 Homo sapi
c	308	26	0.7	788	10	AF083656	AF083656 Mus muscu
	309	26	0.7	792	6	BD124983	BD124983 Primer fo
	310	26	0.7	792	6	BD126651	BD126651 Primer fo
	311	26	0.7	793	6	BD079422	BD079422 Cancer-as
	312	26	0.7	800	6	A92446	A92446 Sequence 7
	313	26	0.7	800	6	AR018062	AR018062 Sequence
	314	26	0.7	800	6	AR020961	AR020961 Sequence
	315	26	0.7	800	6	AR022342	AR022342 Sequence
	316	26	0.7	800	6	EACDSB	A22653 E.acervulin
	317	26	0.7	800	6	I66468	I66468 Sequence 7
	318	26	0.7	800	6	BD131291	BD131291 Coccidios
	319	26	0.7	818	11	BV036574	BV036574 S212P6452
	320	26	0.7	837	10	MMU53564	U53564 Mus musculu
	321	26	0.7	849	9	HUMMRNAD	L10375 Human (clon
	322	26	0.7	850	9	HSU80758	U80758 Homo sapien
	323	26	0.7	877	9	PPY133272	AJ133272 Pongo pyg
	324	26	0.7	900	3	AY339956	AY339956 Drosophil
	325	26	0.7	912	9	HSU80741	U80741 Homo sapien
	326	26	0.7	925	3	AY339971	AY339971 Drosophil
	327	26	0.7	926	3	AY339948	AY339948 Drosophil
	328	26	0.7	936	3	AY339958	AY339958 Drosophil
	329	26	0.7	942	6	AX794681	AX794681 Sequence
	330	26	0.7	945	6	AX794594	AX794594 Sequence
	331	26	0.7	967	8	AK058253	AK058253 Oryza sat
	332	26	0.7	1049	9	HSU92983	U92983 Homo sapien
	333	26	0.7	1065	6	E09296	E09296 cDNA encodi
	334	26	0.7	1065	10	HAMTBP	D30051 Mesocricetu
c	335	26	0.7	1114	9	AF322859	AF322859 Macaca mu
	336	26	0.7	1124	9	AF284423	AF284423 Homo sapi
	337	26	0.7	1156	10	MMU80889	U80889 Mus musculu
	338	26	0.7	1181	3	AY089280	AY089280 Drosophil
	339	26	0.7	1257	9	AF467253	AF467253 Homo sapi
	340	26	0.7	1293	9	AF467258	AF467258 Homo sapi
	341	26	0.7	1350	3	D83241	D83241 Antheraea p
	342	26	0.7	1368	9	AF467259	AF467259 Homo sapi
	343	26	0.7	1374	10	S74520	S74520 Cdx-2=tissu
	344	26	0.7	1375	10	BC003476	BC003476 Mus muscu
	345	26	0.7	1389	9	AF329264	AF329264 Homo sapi
c	346	26	0.7	1403	4	AB070516	AB070516 Canis fam
	347	26	0.7	1411	9	HUMCBFA	L40992 Homo sapien
	348	26	0.7	1412	9	HSPQPROT	Z50194 H.sapiens m
	349	26	0.7	1413	3	AF364332	AF364332 Antheraea
	350	26	0.7	1492	6	BD190352	BD190352 Prophylac
	351	26	0.7	1509	9	AF454830	AF454830 Homo sapi
	352	26	0.7	1524	3	AY119111	AY119111 Drosophil
	353	26	0.7	1533	6	AX260069	AX260069 Sequence
c	354	26	0.7	1547	6	AX401992	AX401992 Sequence
c	355	26	0.7	1547	10	RNU94710	U94710 Rattus norv
	356	26	0.7	1562	3	DMU33015	U33015 Drosophila
	357	26	0.7	1628	5	AB012300	AB012300 Lampetra

	358	26	0.7	1630	3	AY118785	AY118785 Drosophil
	359	26	0.7	1631	6	BD190351	BD190351 Prophylac
	360	26	0.7	1641	10	BC009120	BC009120 Mus muscu
	361	26	0.7	1659	9	BC018929	BC018929 Homo sapi
	362	26	0.7	1680	6	E09295	E09295 cDNA encodi
	363	26	0.7	1694	6	BD190350	BD190350 Prophylac
	364	26	0.7	1709	5	AB001868	AB001868 Anolis ca
	365	26	0.7	1710	3	AF027123	AF027123 Drosophil
	366	26	0.7	1719	9	HSU80746	U80746 Homo sapien
	367	26	0.7	1722	4	AB048335	AB048335 Equus cab
	368	26	0.7	1725	9	HUMRNAG	L10378 Human (clon
	369	26	0.7	1725	9	HUMRNAH	L10379 Human (clon
	370	26	0.7	1726	9	HSU80759	U80759 Homo sapien
	371	26	0.7	1791	10	AF010284	AF010284 Mus muscu
	372	26	0.7	1802	6	AX440493	AX440493 Sequence
	373	26	0.7	1852	9	HSDAN26	Y08265 H.sapiens m
	374	26	0.7	1862	9	BC012182	BC012182 Homo sapi
	375	26	0.7	1889	8	AK101253	AK101253 Oryza sat
c	376	26	0.7	1922	9	MMU242441	AJ242441 Macaca mu
c	377	26	0.7	1922	9	MMU291498	AJ291498 Macaca mu
c	378	26	0.7	1922	9	MMU291499	AJ291499 Macaca mu
	379	26	0.7	1926	10	AF339104	AF339104 Mus muscu
	380	26	0.7	1956	9	HSAAD14	Y08263 H.sapiens m
	381	26	0.7	2021	3	AY119100	AY119100 Drosophil
	382	26	0.7	2024	6	AX701640	AX701640 Sequence
	383	26	0.7	2024	10	AF349723	AF349723 Rattus no
	384	26	0.7	2066	10	MMAJ5159	AJ005159 Mus muscu
	385	26	0.7	2092	3	AY060224	AY060224 Drosophil
	386	26	0.7	2118	10	AF339103	AF339103 Mus muscu
	387	26	0.7	2145	10	AF339106	AF339106 Mus muscu
	388	26	0.7	2151	9	AF512947	AF512947 Pan trogl
	389	26	0.7	2151	9	AY143178	AY143178 Pan trogl
	390	26	0.7	2151	9	AY143179	AY143179 Pan panis
	391	26	0.7	2156	6	AR280336	AR280336 Sequence
	392	26	0.7	2156	6	BD128682	BD128682 OSF2/CBFA
	393	26	0.7	2176	10	MUSPEBP2A2	D14637 Mouse mRNA
	394	26	0.7	2187	9	AF467257	AF467257 Homo sapi
	395	26	0.7	2201	6	AR141679	AR141679 Sequence
	396	26	0.7	2201	6	AX058278	AX058278 Sequence
	397	26	0.7	2215	3	DMCF1AMRN	X58435 D.melanogas
	398	26	0.7	2294	6	AR280334	AR280334 Sequence
	399	26	0.7	2294	6	BD128680	BD128680 OSF2/CBFA
	400	26	0.7	2315	10	AF005936	AF005936 Mus muscu
	401	26	0.7	2361	9	BC041088	BC041088 Homo sapi
	402	26	0.7	2393	9	AY049734	AY049734 Homo sapi
	403	26	0.7	2415	6	A59887	A59887 Sequence 5
	404	26	0.7	2424	6	AX686703	AX686703 Sequence
c	405	26	0.7	2427	2	AC019751	AC019751 Drosophil
	406	26	0.7	2427	3	DMRNAMSH	X85331 D.melanogas
	407	26	0.7	2439	8	AY237405	AY237405 Phytophth
	408	26	0.7	2444	3	AF395904	AF395904 Drosophil
	409	26	0.7	2453	6	A59888	A59888 Sequence 6
	410	26	0.7	2453	10	MMNTTP1GN	X95518 M.musculus
	411	26	0.7	2472	9	AF337817	AF337817 Homo sapi
	412	26	0.7	2499	10	AB019259	AB019259 Rattus no
	413	26	0.7	2521	6	AR122323	AR122323 Sequence
	414	26	0.7	2521	6	AR431867	AR431867 Sequence
	415	26	0.7	2521	9	AF031815	AF031815 Homo sapi
	416	26	0.7	2526	6	AR122326	AR122326 Sequence
	417	26	0.7	2526	6	AR431870	AR431870 Sequence
	418	26	0.7	2543	3	AY095077	AY095077 Drosophil
	419	26	0.7	2546	4	AY038049	AY038049 Sus scrof
	420	26	0.7	2585	10	AF437877	AF437877 Mus muscu
	421	26	0.7	2589	10	AB019258	AB019258 Rattus no
	422	26	0.7	2594	9	AY144615	AY144615 Homo sapi
	423	26	0.7	2598	3	AY061260	AY061260 Drosophil
	424	26	0.7	2600	10	BC052705	BC052705 Mus muscu
	425	26	0.7	2607	10	AY079003	AY079003 Mus muscu
	426	26	0.7	2647	3	AY070708	AY070708 Drosophil
	427	26	0.7	2649	6	AX763684	AX763684 Sequence
	428	26	0.7	2669	3	AY058313	AY058313 Drosophil
	429	26	0.7	2733	6	AR307660	AR307660 Sequence
	430	26	0.7	2733	6	BD139754	BD139754 Ion chann
	431	26	0.7	2774	3	AF053079	AF053079 Drosophil
	432	26	0.7	2782	3	S79891	S79891 sr=stripe {
	433	26	0.7	2811	3	AB087582	AB087582 Aplysia k
	434	26	0.7	2813	10	BC011132	BC011132 Mus muscu
	435	26	0.7	2814	3	DMARA	X95179 D.melanogas
	436	26	0.7	2824	3	AY061493	AY061493 Drosophil
	437	26	0.7	2830	3	AF009676	AF009676 Drosophil
	438	26	0.7	2833	8	AK110285	AK110285 Oryza sat
	439	26	0.7	2834	3	DROPOUC	M81959 D.melanogas
	440	26	0.7	2868	3	AF084525	AF084525 Drosophil
c	441	26	0.7	2896	10	AY129963	AY129963 Mus muscu
	442	26	0.7	2901	3	DME252124	AJ252124 Drosophil
	443	26	0.7	2922	10	MMU05252	U05252 Mus musculu
c	444	26	0.7	2943	10	BC052726	BC052726 Mus muscu
	445	26	0.7	2954	5	AB001869	AB001869 Anolis ca
	446	26	0.7	2957	3	BT004853	BT004853 Drosophil
	447	26	0.7	2960	3	DMTRACDEF	AJ001615 Drosophil
	448	26	0.7	2969	8	AF321465	AF321465 Yarrowia
c	449	26	0.7	2993	10	BC050858	BC050858 Mus muscu
	450	26	0.7	2994	3	AF461101	AF461101 Drosophil
	451	26	0.7	3009	3	AY070882	AY070882 Drosophil
	452	26	0.7	3054	10	RNIP3	X74227 R.norvegicu
	453	26	0.7	3095	6	AX800484	AX800484 Sequence
	454	26	0.7	3095	9	HSA251016	AJ251016 Homo sapi
	455	26	0.7	3207	3	BT001514	BT001514 Drosophil
	456	26	0.7	3215	3	AGRNAG1	X95912 A.gambiae m
	457	26	0.7	3237	9	AY165003	AY165003 Homo sapi
	458	26	0.7	3251	10	AF532598	AF532598 Mus muscu
	459	26	0.7	3254	3	AF039842	AF039842 Drosophil
	460	26	0.7	3254	6	BD124516	BD124516 Sprouty p
	461	26	0.7	3263	10	MMJ225123	AJ225123 Mus muscu
	462	26	0.7	3280	10	RNO242781	AJ242781 Rattus no
	463	26	0.7	3302	9	AY186997	AY186997 Homo sapi
	464	26	0.7	3305	10	AF028737	AF028737 Mus muscu
	465	26	0.7	3314	3	AY122076	AY122076 Drosophil
	466	26	0.7	3315	3	DMBIBGENE	X53275 D.melanogas
	467	26	0.7	3321	10	BC057085	BC057085 Mus muscu
	468	26	0.7	3327	6	BD183248	BD183248 Marker fo
	469	26	0.7	3334	6	AR280270	AR280270 Sequence
	470	26	0.7	3334	6	BD128616	BD128616 OSF2/CBFA
	471	26	0.7	3335	9	HSU80743	U80743 Homo sapien
	472	26	0.7	3336	6	AR141680	AR141680 Sequence
	473	26	0.7	3336	6	AX058280	AX058280 Sequence
	474	26	0.7	3399	6	BD183250	BD183250 Marker fo
	475	26	0.7	3433	3	AY060442	AY060442 Drosophil
	476	26	0.7	3459	6	BD183247	BD183247 Marker fo
	477	26	0.7	3515	9	AK123604	AK123604 Homo sapi
	478	26	0.7	3520	6	AX780441	AX780441 Sequence
	479	26	0.7	3560	3	AF421370	AF421370 Drosophil
	480	26	0.7	3597	6	BD127355	BD127355 Primer fo
	481	26	0.7	3597	9	AK074900	AK074900 Homo sapi
	482	26	0.7	3604	3	BT010072	BT010072 Drosophil
	483	26	0.7	3641	6	BD183416	BD183416 Novel gen
	484	26	0.7	3641	9	AB058768	AB058768 Homo sapi
	485	26	0.7	3645	6	AX505167	AX505167 Sequence
	486	26	0.7	3655	10	BC020488	BC020488 Mus muscu
	487	26	0.7	3658	3	AF395905	AF395905 Drosophil
	488	26	0.7	3708	3	DVBIGB5	AF023138 Drosophil
	489	26	0.7	3722	10	BC032191	BC032191 Mus muscu
	490	26	0.7	3732	6	AX505243	AX505243 Sequence
	491	26	0.7	3738	8	AK110335	AK110335 Oryza sat
	492	26	0.7	3763	9	AY040324	AY040324 Homo sapi
	493	26	0.7	3786	6	BD251818	BD251818 Phosphory
	494	26	0.7	3792	9	AY212247	AY212247 Homo sapi
	495	26	0.7	3798	6	BD243843	BD243843 STE20-rel
	496	26	0.7	3798	6	AR435596	AR435596 Sequence
	497	26	0.7	3810	3	BT003479	BT003479 Drosophil
	498	26	0.7	3819	6	I13749	I13749 Sequence 3
	499	26	0.7	3864	9	AF096300	AF096300 Homo sapi
	500	26	0.7	3882	10	AF104261	AF104261 Mus muscu
	501	26	0.7	3925	6	AX179648	AX179648 Sequence
	502	26	0.7	3990	9	HSU94836	U94836 Homo sapien
	503	26	0.7	4061	9	AF536542	AF536542 Homo sapi

	504	26	0.7	4077	10	BC040256	BC040256 Mus muscu
	505	26	0.7	4105	9	BC021294	BC021294 Homo sapi
	506	26	0.7	4163	9	HSDANSCA2	Y08262 H.sapiens m
	507	26	0.7	4197	6	AX828638	AX828638 Sequence
	508	26	0.7	4200	6	A62706	A62706 Sequence 7
	509	26	0.7	4262	9	AF239986	AF239986 Homo sapi
	510	26	0.7	4266	6	AR193118	AR193118 Sequence
	511	26	0.7	4266	6	AX828363	AX828363 Sequence
	512	26	0.7	4266	9	AB014587	AB014587 Homo sapi
	513	26	0.7	4368	3	DRODPTP	M81795 Drosophila
	514	26	0.7	4393	3	BT003517	BT003517 Drosophil
	515	26	0.7	4458	3	DMU42402	U42402 Drosophila
	516	26	0.7	4481	6	AR153580	AR153580 Sequence
	517	26	0.7	4481	6	AR401379	AR401379 Sequence
	518	26	0.7	4481	6	AX392465	AX392465 Sequence
	519	26	0.7	4481	9	HSU70323	U70323 Human ataxi
	520	26	0.7	4495	9	AF010227	AF010227 Homo sapi
	521	26	0.7	4568	10	BC062926	BC062926 Mus muscu
	522	26	0.7	4578	10	AF104410	AF104410 Mus muscu
	523	26	0.7	4599	9	HSU46023	U46023 Human Xq28
c	524	26	0.7	4622	10	AY185125	AY185125 Mus muscu
	525	26	0.7	4627	10	AF162853	AF162853 Mus muscu
	526	26	0.7	4653	10	AF200687	AF200687 Mus muscu
	527	26	0.7	4668	9	AF016031	AF016031 Homo sapi
	528	26	0.7	4734	10	AF369980	AF369980 Mus muscu
	529	26	0.7	4959	6	AX686679	AX686679 Sequence
	530	26	0.7	4959	9	HSA277365	AJ277365 Homo sapi
	531	26	0.7	4960	6	AX686708	AX686708 Sequence
	532	26	0.7	4960	10	AF384055	AF384055 Mus muscu
	533	26	0.7	5012	10	BC022153	BC022153 Mus muscu
	534	26	0.7	5082	3	DMU67935	U67935 Drosophila
	535	26	0.7	5129	10	AY303755	AY303755 Mus muscu
	536	26	0.7	5164	9	AB058719	AB058719 Homo sapi
	537	26	0.7	5419	9	AB058722	AB058722 Homo sapi
	538	26	0.7	5419	9	AY040322	AY040322 Homo sapi
	539	26	0.7	5481	10	AK122381	AK122381 Mus muscu
	540	26	0.7	5650	3	DROMASTM	M92914 Drosophila
	541	26	0.7	5729	3	AY069076	AY069076 Drosophil
c	542	26	0.7	5734	3	DROSHSA	L42512 Drosophila
	543	26	0.7	5754	3	DMU42403	U42403 Drosophila
	544	26	0.7	5811	10	BC043125	BC043125 Mus muscu
c	545	26	0.7	5895	6	AX686475	AX686475 Sequence
	546	26	0.7	5970	6	E22895	E22895 Carcinogene
	547	26	0.7	5972	9	AB003039	AB003039 Homo sapi
	548	26	0.7	5992	10	AY050663	AY050663 Mus muscu
	549	26	0.7	6087	9	AB102670	AB102670 Pongo pyg
c	550	26	0.7	6147	6	AX704766	AX704766 Sequence
c	551	26	0.7	6170	9	HSCGGE7	AJ001216 Homo sapi
	552	26	0.7	6200	10	AK129272	AK129272 Mus muscu
	553	26	0.7	6212	10	AY007594	AY007594 Mus muscu
	554	26	0.7	6267	9	AB058721	AB058721 Homo sapi
	555	26	0.7	6282	3	DME75B	X51549 Drosophila
	556	26	0.7	6380	10	AK122517	AK122517 Mus muscu
	557	26	0.7	6463	6	BD211793	BD211793 Angiostat
	558	26	0.7	6478	10	AF071310	AF071310 Mus muscu
	559	26	0.7	6518	10	MUSPEBP2A1	D14636 Mouse mRNA
	560	26	0.7	6558	6	AR322158	AR322158 Sequence
	561	26	0.7	6642	10	BC057119	BC057119 Mus muscu
	562	26	0.7	6733	3	MSQRT2RET	M93691 Anopheles g
	563	26	0.7	6832	6	AX384818	AX384818 Sequence
	564	26	0.7	6835	6	AR316837	AR316837 Sequence
	565	26	0.7	6835	6	BD192354	BD192354 AIB1, a s
	566	26	0.7	6835	9	AF012108	AF012108 Homo sapi
	567	26	0.7	6888	9	AF286598	AF286598 Homo sapi
	568	26	0.7	7072	3	AB090813	AB090813 Anopheles
	569	26	0.7	7164	4	AF225897	AF225897 Bos tauru
	570	26	0.7	7200	10	U00454	U00454 Mus musculu
	571	26	0.7	7288	10	AY079443	AY079443 Mus muscu
	572	26	0.7	7288	10	AY079444	AY079444 Mus muscu
	573	26	0.7	7326	6	AR006845	AR006845 Sequence
	574	26	0.7	7326	6	E36595	E36595 Antisense n
	575	26	0.7	7326	6	AR203333	AR203333 Sequence
	576	26	0.7	7326	6	AR430182	AR430182 Sequence
	577	26	0.7	7326	10	S66385	S66385 CREB-bindin
	578	26	0.7	7568	9	HSMN1	X82209 H.sapiens M
	579	26	0.7	7568	11	G28534	G28534 human STS S
	580	26	0.7	7757	9	AF521671	AF521671 Homo sapi
	581	26	0.7	8207	6	AX780089	AX780089 Sequence
	582	26	0.7	8207	6	AX780090	AX780090 Sequence
	583	26	0.7	8680	2	AC020188	AC020188 Drosophil
c	584	26	0.7	8772	6	AX224128	AX224128 Sequence
c	585	26	0.7	8871	6	AX224126	AX224126 Sequence
	586	26	0.7	9282	3	AF083334	AF083334 Antheraea
c	587	26	0.7	9321	6	AX367102	AX367102 Sequence
	588	26	0.7	9658	10	MMIIG	X13414 Murine I ge
	589	26	0.7	10017	9	AY044869	AY044869 Homo sapi
	590	26	0.7	10515	10	AB092695	AB092695 Mus muscu
c	591	26	0.7	10531	6	AX549238	AX549238 Sequence
c	592	26	0.7	10531	9	AF234887	AF234887 Homo sapi
	593	26	0.7	10623	10	AB092694	AB092694 Mus muscu
	594	26	0.7	10810	2	AC015172	AC015172 Drosophil
	595	26	0.7	11296	3	AF175223	AF175223 Drosophil
	596	26	0.7	11948	2	AC020253	AC020253 Drosophil
c	597	26	0.7	12091	2	AC015048	AC015048 Drosophil
	598	26	0.7	12749	4	AB016793	AB016793 Sus scrof
	599	26	0.7	12749	6	E26529	E26529 Miniswine h
	600	26	0.7	13040	10	AF453571	AF453571 Mus muscu
	601	26	0.7	14009	9	AF515051	AF515051 Pan trogl
	602	26	0.7	14009	9	AF515052	AF515052 Pan trogl
	603	26	0.7	14063	9	AF515031	AF515031 Homo sapi
	604	26	0.7	14063	9	AF515032	AF515032 Homo sapi
	605	26	0.7	14063	9	AF515033	AF515033 Homo sapi
	606	26	0.7	14063	9	AF515034	AF515034 Homo sapi
	607	26	0.7	14063	9	AF515035	AF515035 Homo sapi
	608	26	0.7	14063	9	AF515036	AF515036 Homo sapi
	609	26	0.7	14063	9	AF515037	AF515037 Homo sapi
	610	26	0.7	14063	9	AF515038	AF515038 Homo sapi
	611	26	0.7	14063	9	AF515039	AF515039 Homo sapi
	612	26	0.7	14063	9	AF515040	AF515040 Homo sapi
	613	26	0.7	14063	9	AF515041	AF515041 Homo sapi
	614	26	0.7	14063	9	AF515042	AF515042 Homo sapi
	615	26	0.7	14063	9	AF515043	AF515043 Homo sapi
	616	26	0.7	14063	9	AF515044	AF515044 Homo sapi
	617	26	0.7	14063	9	AF515045	AF515045 Homo sapi
	618	26	0.7	14063	9	AF515046	AF515046 Homo sapi
	619	26	0.7	14063	9	AF515047	AF515047 Homo sapi
	620	26	0.7	14063	9	AF515048	AF515048 Homo sapi
	621	26	0.7	14063	9	AF515049	AF515049 Homo sapi
	622	26	0.7	14063	9	AF515050	AF515050 Homo sapi
	623	26	0.7	14440	3	AB047034	AB047034 Apis mell
	624	26	0.7	14859	6	AX823282	AX823282 Sequence
	625	26	0.7	14874	9	AF010404	AF010404 Homo sapi
	626	26	0.7	14912	10	AF512563	AF512563 Mus muscu
c	627	26	0.7	15029	2	AC015150	AC015150 Drosophil
	628	26	0.7	15362	2	AC019547	AC019547 Drosophil
c	629	26	0.7	15578	2	AC015029	AC015029 Drosophil
	630	26	0.7	15645	6	AX921118	AX921118 Sequence
	631	26	0.7	15750	6	AX821965	AX821965 Sequence
	632	26	0.7	15789	9	AF010403	AF010403 Homo sapi
	633	26	0.7	19631	2	AC017798	AC017798 Drosophil
c	634	26	<0.7	20113	2	AC015413	AC015413 Drosophil
c	635	26	0.7	21972	2	AC013238	AC013238 Drosophil
	636	26	0.7	22307	2	AC015297	AC015297 Drosophil
c	637	26	0.7	24194	2	AC018183	AC018183 Drosophil
c	638	26	0.7	24370	6	AX646739	AX646739 Sequence
c	639	26	0.7	24370	9	AB065955	AB065955 Homo sapi
c	640	26	0.7	24487	2	AC019452	AC019452 Drosophil
	641	26	0.7	25598	2	AC015404	AC015404 Drosophil
	642	26	0.7	29358	3	DMBH61I5	AL035245 Drosophil
c	643	26	0.7	31202	2	AC013022	AC013022 Drosophil
c	644	26	0.7	31311	2	AC017192	AC017192 Drosophil
	645	26	0.7	35722	2	AC015427	AC015427 Drosophil
	646	26	0.7	37388	2	AC017823	AC017823 Drosophil
c	647	26	0.7	37389	2	AC087161	AC087161 Leishmani
	648	26	0.7	37569	2	AC019771	AC019771 Drosophil
c	649	26	0.7	37888	2	AC017571	AC017571 Drosophil

c	650	26	0.7	38230	8	AC067939	AC067939 Neurospor
c	651	26	0.7	39619	2	AC017644	AC017644 Drosophil
	652	26	0.7	40621	3	AC087836	AC087836 Leishmani
	653	26	0.7	40933	3	DMC140G11	AL035395 Drosophil
	654	26	0.7	41818	2	AC018239	AC018239 Drosophil
	655	26	0.7	42248	2	AC020375	AC020375 Drosophil
c	656	26	0.7	44671	2	AC019872	AC019872 Drosophil
	657	26	0.7	45046	2	AC013093	AC013093 Drosophil
c	658	26	0.7	45449	2	AC012817	AC012817 Drosophil
c	659	26	0.7	45912	2	AC091265	AC091265 Mus muscu
c	660	26	0.7	46427	3	AY190956	AY190956 Drosophil
	661	26	0.7	47636	2	AC014385	AC014385 Drosophil
	662	26	0.7	47872	2	AC106844	AC106844 Mus muscu
c	663	26	0.7	47872	2	AC106844	AC106844 Mus muscu
c	664	26	0.7	49999	6	AX015907	AX015907 Sequence
c	665	26	0.7	50185	2	AC020507	AC020507 Drosophil
c	666	26	0.7	50714	3	AC005471	AC005471 Drosophil
c	667	26	0.7	53124	2	AC012698	AC012698 Drosophil
	668	26	0.7	54043	2	AC139419	AC139419 Homo sapi
c	669	26	0.7	54667	2	AC014816	AC014816 Drosophil
c	670	26	0.7	54987	2	AC131499	AC131499 Lytechinu
c	671	26	0.7	56088	2	AC146714	AC146714 Mus muscu
c	672	26	0.7	57336	3	AC005416	AC005416 Drosophil
c	673	26	0.7	59498	3	AC004252	AC004252 Drosophil
	674	26	0.7	61107	2	AC017941	AC017941 Drosophil
	675	26	0.7	63024	2	AC129476	AC129476 Mus muscu
	676	26	0.7	63341	2	AC018047	AC018047 Drosophil
c	677	26	0.7	64294	2	AC016133	AC016133 Drosophil
	678	26	0.7	65031	2	AC114338	AC114338 Mus muscu
c	679	26	0.7	65351	10	AY129964	AY129964 Mus muscu
c	680	26	0.7	65725	8	NCB2J23	AL442164 Neurospor
c	681	26	0.7	67436	2	AC014142	AC014142 Drosophil
c	682	26	0.7	68457	2	AC010702	AC010702 Drosophil
	683	26	0.7	68997	2	DMBN6F4	AL133486 Drosophil
	684	26	0.7	69692	2	AC114446_5	Continuation (6 of
	685	26	0.7	72187	2	AC013433	AC013433 Drosophil
	686	26	0.7	73638	2	AC015613	AC015613 Homo sapi
	687	26	0.7	73889	2	AC009983	AC009983 Drosophil
	688	26	0.7	74759	2	AC100661	AC100661 Mus muscu
	689	26	0.7	77409	3	AC004248	AC004248 Drosophil
c	690	26	0.7	77656	2	AC017522	AC017522 Drosophil
c	691	26	0.7	78874	2	AL355521	AL355521 Homo sapi
	692	26	0.7	81210	2	AC019242	AC019242 Homo sapi
c	693	26	0.7	83607	2	AC019889	AC019889 Drosophil
c	694	26	0.7	83824	2	AC017221	AC017221 Drosophil
	695	26	0.7	85740	2	AC014942	AC014942 Drosophil
	696	26	0.7	86453	9	HS1049G16	AL034418 Human DNA
c	697	26	0.7	87525	2	DMBR41A22	AL133490 Drosophil
c	698	26	0.7	89376	2	AC139073	AC139073 Homo sapi
c	699	26	0.7	89566	9	AL390204	AL390204 Human DNA
c	700	26	0.7	90223	9	AC000105	AC000105 Homo sapi
	701	26	0.7	90696	2	AC017624	AC017624 Drosophil
c	702	26	0.7	91170	2	AC014779	AC014779 Drosophil
c	703	26	0.7	91240	9	AC130566	AC130566 Homo sapi
c	704	26	0.7	91318	2	AC015391	AC015391 Drosophil
	705	26	0.7	91809	2	AC012832	AC012832 Drosophil
	706	26	0.7	92586	2	AC005978	AC005978 Drosophil
	707	26	0.7	92785	10	CNS07YOV	AL713841 Mus muscu
c	708	26	0.7	92958	2	DMBR11J17	AL121811 Drosophil
c	709	26	0.7	94045	2	AC010039	AC010039 Drosophil
	710	26	0.7	95856	2	AC020304	AC020304 Drosophil
	711	26	0.7	96426	2	AC014908	AC014908 Drosophil
c	712	26	0.7	97033	2	AC015146	AC015146 Drosophil
	713	26	0.7	99745	2	AC017305	AC017305 Drosophil
c	714	26	0.7	100984	10	AL929138	AL929138 Mouse DNA
c	715	26	0.7	103196	3	AC023738	AC023738 Drosophil
	716	26	0.7	107514	2	AC026404	AC026404 Homo sapi
	717	26	0.7	107642	10	AF125313	AF125313 Mus muscu
	718	26	0.7	107717	9	AC137055	AC137055 Homo sapi
c	719	26	0.7	108139	2	AC004085_3	Continuation (4 of
c	720	26	0.7	110000	2	AC074221_0	AC074221 Mus muscu
c	721	26	0.7	110000	2	AC106698_5	Continuation (6 of
	722	26	0.7	110000	2	AC112083_2	Continuation (3 of

	723	26	0.7	110000	2	AC114446_4	Continuation (5 of
c	724	26	0.7	110000	2	AC020884_2	Continuation (3 of
	725	26	0.7	110000	2	AC128384_0	AC128384 Rattus no
	726	26	0.7	110000	2	AL672265_2	Continuation (3 of
	727	26	0.7	111073	10	AL928567	AL928567 Mouse DNA
c	728	26	0.7	111893	2	AC120419	AC120419 Mus muscu
	729	26	0.7	112010	2	AC010302	AC010302 Homo sapi
	730	26	0.7	113816	2	AC004358	AC004358 Drosophil
c	731	26	0.7	114181	2	AC110875	AC110875 Gallus ga
	732	26	0.7	114532	9	AL389883	AL389883 Human DNA
	733	26	0.7	116603	2	AL157901	AL157901 Homo sapi
c	734	26	0.7	117037	2	AC023269	AC023269 Homo sapi
	735	26	0.7	117812	2	AC020493	AC020493 Drosophil
	736	26	0.7	118036	2	AC008198	AC008198 Drosophil
c	737	26	0.7	119844	2	AC010044	AC010044 Drosophil
c	738	26	0.7	120637	10	CNS07YP1	AL713884 Mus muscu
	739	26	0.7	120864	2	AC079884	AC079884 Rattus no
	740	26	0.7	121310	2	AC141831	AC141831 Apis mell
c	741	26	0.7	121474	2	AC007150	AC007150 Drosophil
c	742	26	0.7	122163	8	AC125783	AC125783 Oryza sat
	743	26	0.7	122871	2	AC144617	AC144617 Medicago
c	744	26	0.7	123290	2	AC016020	AC016020 Drosophil
c	745	26	0.7	125303	10	AC121578	AC121578 Mus muscu
c	746	26	0.7	125479	9	HSJ244F24	AL096865 Human DNA
c	747	26	0.7	128729	9	AC137590	AC137590 Homo sapi
c	748	26	0.7	128747	10	AL669846	AL669846 Mouse DNA
	749	26	0.7	129690	9	AC004827	AC004827 Homo sapi
c	750	26	0.7	131135	2	AC147551	AC147551 Mus muscu
	751	26	0.7	132444	9	AC019226	AC019226 Homo sapi
	752	26	0.7	133918	9	AL512290	AL512290 Human DNA
c	753	26	0.7	134804	8	AP004888	AP004888 Oryza sat
	754	26	0.7	136809	10	AL683892	AL683892 Mouse DNA
	755	26	0.7	137334	10	AC121952	AC121952 Mus muscu
	756	26	0.7	137960	2	AC103889	AC103889 Homo sapi
	757	26	0.7	138091	2	AC113583	AC113583 Tetraodon
	758	26	0.7	139074	2	AC131191	AC131191 Mus muscu
c	759	26	0.7	139258	2	AC073673	AC073673 Mus muscu
	760	26	0.7	139480	2	AC012837	AC012837 Drosophil
c	761	26	0.7	139665	2	AP000865	AP000865 Homo sapi
	762	26	0.7	139781	2	AC122437	AC122437 Mus muscu
	763	26	0.7	140244	2	AC119962	AC119962 Mus muscu
	764	26	0.7	142037	10	AL844516	AL844516 Mouse DNA
c	765	26	0.7	146349	10	AL662903	AL662903 Mouse DNA
	766	26	0.7	146936	2	AP005010	AP005010 Oryza sat
	767	26	0.7	149726	2	AC021970	AC021970 Homo sapi
	768	26	0.7	150122	10	BX088567	BX088567 Mouse DNA
	769	26	0.7	151610	3	AC009462	AC009462 Drosophil
	770	26	0.7	151822	9	AC020606	AC020606 Homo sapi
	771	26	0.7	152021	2	AC010923	AC010923 Drosophil
	772	26	0.7	152135	9	AC011199	AC011199 Homo sapi
c	773	26	0.7	152224	2	AC141680	AC141680 Apis mell
	774	26	0.7	152564	10	AC127549	AC127549 Mus muscu
c	775	26	0.7	153291	2	AC117653	AC117653 Mus muscu
c	776	26	0.7	154771	3	AC009214	AC009214 Drosophil
c	777	26	0.7	154895	2	AC020329	AC020329 Drosophil
c	778	26	0.7	156142	3	AC091228	AC091228 Drosophil
c	779	26	0.7	156335	3	AC008219	AC008219 Drosophil
c	780	26	0.7	156705	10	AL929037	AL929037 Mouse DNA
c	781	26	0.7	157057	2	AC127160	AC127160 Rattus no
c	782	26	0.7	157833	9	AC132186	AC132186 Homo sapi
c	783	26	0.7	158169	2	AC141751	AC141751 Apis mell
	784	26	0.7	158191	2	AC124660	AC124660 Mus muscu
	785	26	0.7	158402	3	AC008343	AC008343 Drosophil
	786	26	0.7	158719	3	AC010008	AC010008 Drosophil
c	787	26	0.7	159455	3	AC009460	AC009460 Drosophil
	788	26	0.7	159646	2	AC146930	AC146930 Bos tauru
c	789	26	0.7	160440	3	AC023741	AC023741 Drosophil
	790	26	0.7	160445	3	AC010123	AC010123 Drosophil
	791	26	0.7	160504	3	AC091207	AC091207 Drosophil
	792	26	0.7	160827	3	AC099025	AC099025 Drosophil
	793	26	0.7	161652	6	AR374388	AR374388 Sequence
	794	26	0.7	161652	9	AC004774	AC004774 Homo sapi
	795	26	0.7	161773	2	AC119935	AC119935 Mus muscu

c	796	26	0.7	163087	2	AC139383	AC139383 Rattus no
	797	26	0.7	163162	3	AC006247	AC006247 Drosophil
	798	26	0.7	163217	9	AF336797	AF336797 Homo sapi
	799	26	0.7	163378	2	AC008336	AC008336 Drosophil
c	800	26	0.7	163389	9	AL589765	AL589765 Human DNA
	801	26	0.7	163711	3	AC093436	AC093436 Drosophil
	802	26	0.7	163764	3	AC023740	AC023740 Drosophil
	803	26	0.7	163885	2	AC132012	AC132012 Rattus no
	804	26	0.7	163958	3	AC010705	AC010705 Drosophil
c	805	26	0.7	164201	3	AC010047	AC010047 Drosophil
	806	26	0.7	164507	9	AC012067	AC012067 Homo sapi
c	807	26	0.7	164599	2	AC068971	AC068971 Homo sapi
c	808	26	0.7	164722	2	AC129349	AC129349 Rattus no
	809	26	0.7	164761	3	AC023695	AC023695 Drosophil
c	810	26	0.7	164970	3	AC016792	AC016792 Drosophil
	811	26	0.7	165014	3	AC104609	AC104609 Drosophil
c	812	26	0.7	165928	3	AC023725	AC023725 Drosophil
	813	26	0.7	166352	3	AC010069	AC010069 Drosophil
c	814	26	0.7	166520	3	AC010709	AC010709 Drosophil
	815	26	0.7	166719	9	AC136957	AC136957 Homo sapi
	816	26	0.7	166735	2	AC095126	AC095126 Rattus no
	817	26	0.7	166935	3	AC010920	AC010920 Drosophil
c	818	26	0.7	168379	2	AC128921	AC128921 Rattus no
	819	26	0.7	168542	2	AC058792	AC058792 Homo sapi
	820	26	0.7	168570	2	AC119472	AC119472 Rattus no
	821	26	0.7	169116	2	AC121906	AC121906 Mus muscu
c	822	26	0.7	169124	3	AC023716	AC023716 Drosophil
	823	26	0.7	169218	9	AL355297	AL355297 Human DNA
c	824	26	0.7	169241	9	AL390252	AL390252 Human DNA
	825	26	0.7	169581	3	AC008043	AC008043 Drosophil
	826	26	0.7	169618	3	AC105055	AC105055 Drosophil
	827	26	0.7	169680	3	AC008337	AC008337 Drosophil
c	828	26	0.7	169704	2	AC144932	AC144932 Mus muscu
	829	26	0.7	170053	2	AC133069	AC133069 Macaca mu
c	830	26	0.7	170301	3	AC023694	AC023694 Drosophil
	831	26	0.7	170523	2	AC116717	AC116717 Mus muscu
	832	26	0.7	170885	10	AC126933	AC126933 Mus muscu
	833	26	0.7	170900	3	AC107487	AC107487 Drosophil
c	834	26	0.7	170900	3	AC107487	AC107487 Drosophil
	835	26	0.7	170945	2	AC079911	AC079911 Mus muscu
	836	26	0.7	170988	3	AC091223	AC091223 Drosophil
c	837	26	0.7	171115	9	AC068385	AC068385 Homo sapi
c	838	26	0.7	171201	2	AC115714	AC115714 Mus muscu
	839	26	0.7	171451	3	AC010561	AC010561 Drosophil
	840	26	0.7	171586	2	AC138292	AC138292 Mus muscu
	841	26	0.7	171678	3	AC010059	AC010059 Drosophil
	842	26	0.7	171689	3	AC093435	AC093435 Drosophil
	843	26	0.7	171807	2	BX000463	BX000463 Danio rer
	844	26	0.7	171882	9	AC136932	AC136932 Homo sapi
	845	26	0.7	172037	2	AC119981	AC119981 Mus muscu
c	846	26	0.7	172084	2	AC138595	AC138595 Mus muscu
c	847	26	0.7	172284	3	AC010018	AC010018 Drosophil
c	848	26	0.7	172438	9	AP005269	AP005269 Pan trogl
	849	26	0.7	172493	2	AC146888	AC146888 Bos tauru
c	850	26	0.7	172562	9	AC008764	AC008764 Homo sapi
	851	26	0.7	172695	2	AC102258	AC102258 Mus muscu
c	852	26	0.7	172784	3	AC105352	AC105352 Drosophil
c	853	26	0.7	173069	2	AC129563	AC129563 Mus muscu
c	854	26	0.7	173331	9	AC128639	AC128639 Papio anu
c	855	26	0.7	173386	3	AC010716	AC010716 Drosophil
c	856	26	0.7	173558	3	AC093500	AC093500 Drosophil
	857	26	0.7	174400	9	AC011603	AC011603 Homo sapi
	858	26	0.7	175458	2	AC139978	AC139978 Rattus no
	859	26	0.7	175781	3	AC008091	AC008091 Drosophil
c	860	26	0.7	175827	9	AL358472	AL358472 Human DNA
c	861	26	0.7	176394	3	AC007928	AC007928 Drosophil
	862	26	0.7	176952	2	AC113805	AC113805 Rattus no
c	863	26	0.7	176991	3	AC008029	AC008029 Drosophil
	864	26	0.7	177104	10	AC091237	AC091237 Mus muscu
c	865	26	0.7	177205	2	AC079217	AC079217 Mus muscu
c	866	26	0.7	177255	2	AC145529	AC145529 Callithri
c	867	26	0.7	177471	3	AC008361	AC008361 Drosophil
	868	26	0.7	177516	10	AC138174	AC138174 Mus muscu
	869	26	0.7	178019	3	AC091206	AC091206 Drosophil
c	870	26	0.7	178419	2	AC074040	AC074040 Mus muscu
c	871	26	0.7	178472	2	AC125597	AC125597 Rattus no
c	872	26	0.7	178679	2	AC113946	AC113946 Mus muscu
	873	26	0.7	178931	3	AC008197	AC008197 Drosophil
c	874	26	0.7	179085	9	AC011611	AC011611 Homo sapi
	875	26	0.7	179312	3	AC023745	AC023745 Drosophil
c	876	26	0.7	179335	2	AC147192	AC147192 Papio anu
c	877	26	0.7	179525	9	AC087252	AC087252 Papio anu
	878	26	0.7	179649	3	AC010045	AC010045 Drosophil
c	879	26	0.7	179838	3	AC091220	AC091220 Drosophil
	880	26	0.7	180263	3	AC010671	AC010671 Drosophil
c	881	26	0.7	180823	2	AC128250	AC128250 Rattus no
c	882	26	0.7	180859	2	AC091126	AC091126 Drosophil
	883	26	0.7	180903	2	AC131810	AC131810 Rattus no
c	884	26	0.7	180961	10	AC121838	AC121838 Mus muscu
	885	26	0.7	181037	2	AC116729	AC116729 Mus muscu
c	886	26	0.7	181075	10	CNS07YP2	AL713885 Mus muscu
c	887	26	0.7	181083	10	AC108950	AC108950 Mus muscu
c	888	26	0.7	181238	2	AC116937	AC116937 Bos tauru
c	889	26	0.7	181386	9	AC007686	AC007686 Homo sapi
c	890	26	0.7	181726	3	AC010114	AC010114 Drosophil
	891	26	0.7	181792	2	AC122102	AC122102 Rattus no
	892	26	0.7	181831	3	AC107403	AC107403 Drosophil
c	893	26	0.7	181927	3	AC010573	AC010573 Drosophil
	894	26	0.7	181950	3	AC008093	AC008093 Drosophil
c	895	26	0.7	181955	3	AC008304	AC008304 Drosophil
	896	26	0.7	182039	3	AC099026	AC099026 Drosophil
c	897	26	0.7	182507	9	AC013441	AC013441 Homo sapi
	898	26	0.7	182579	2	AC134985	AC134985 Mus muscu
	899	26	0.7	183051	10	AL844519	AL844519 Mouse DNA
	900	26	0.7	183252	2	AC113907	AC113907 Rattus no
c	901	26	0.7	183719	2	AC139382	AC139382 Mus muscu
	902	26	0.7	183729	2	AC136383	AC136383 Rattus no
	903	26	0.7	184091	2	BX294393	BX294393 Mus muscu
c	904	26	0.7	184681	2	AC084409	AC084409 Mus muscu
c	905	26	0.7	184984	2	AC112056	AC112056 Rattus no
	906	26	0.7	185171	2	AC141817	AC141817 Apis mell
	907	26	0.7	185404	3	AC104703	AC104703 Drosophil
	908	26	0.7	185671	2	AC084376	AC084376 Homo sapi
c	909	26	0.7	185872	2	AC068810	AC068810 Mus muscu
	910	26	0.7	186008	2	AC129123	AC129123 Rattus no
	911	26	0.7	186139	2	AC116540	AC116540 Drosophil
	912	26	0.7	186441	10	AC122258	AC122258 Mus muscu
c	913	26	0.7	186443	3	AC093439	AC093439 Drosophil
c	914	26	0.7	186512	2	AC146612	AC146612 Mus muscu
	915	26	0.7	187000	3	AC091201	AC091201 Drosophil
	916	26	0.7	187605	2	AC141810	AC141810 Apis mell
	917	26	0.7	187654	2	BX324194	BX324194 Danio rer
	918	26	0.7	188272	3	AC005639	AC005639 Drosophil
	919	26	0.7	188379	2	BX322652	BX322652 Mus muscu
	920	26	0.7	188772	10	AL773525	AL773525 Mouse DNA
	921	26	0.7	188794	10	AC127319	AC127319 Mus muscu
	922	26	0.7	188804	10	AC090121	AC090121 Mus muscu
c	923	26	0.7	188989	10	AC132685	AC132685 Mus muscu
c	924	26	0.7	189315	3	AC008319	AC008319 Drosophil
	925	26	0.7	189341	2	AC147190	AC147190 Otolemur
c	926	26	0.7	189400	9	AC146090	AC146090 Pan trogl
c	927	26	0.7	189610	9	AC104301	AC104301 Homo sapi
c	928	26	0.7	189765	9	HS353E16	AL031591 Human DNA
	929	26	0.7	189904	3	AC093045	AC093045 Drosophil
	930	26	0.7	189927	10	AC116588	AC116588 Mus muscu
	931	26	0.7	190153	2	AC109221	AC109221 Mus muscu
	932	26	0.7	190379	2	AC134136	AC134136 Rattus no
	933	26	0.7	190784	10	AL645797	AL645797 Mouse DNA
	934	26	0.7	190944	2	AC147417	AC147417 Papio ham
c	935	26	0.7	191300	2	AC109020	AC109020 Rattus no
	936	26	0.7	191331	10	AC131325	AC131325 Mus muscu
	937	26	0.7	191400	2	AC113899	AC113899 Rattus no
c	938	26	0.7	191457	2	BX469927	BX469927 Homo sapi
	939	26	0.7	191466	3	AC008348	AC008348 Drosophil
c	940	26	0.7	191582	2	AC113036	AC113036 Mus muscu
c	941	26	0.7	191656	2	AC118574	AC118574 Lemur cat

c 942	26	0.7	191699	2	AC126931	AC126931 Mus muscu
c 943	26	0.7	192292	2	AC129068	AC129068 Rattus no
944	26	0.7	192380	2	BX510648	BX510648 Danio rer
945	26	0.7	192520	2	AC129986	AC129986 Rattus no
946	26	0.7	192541	3	AC010846	AC010846 Drosophil
947	26	0.7	192783	2	AC113951	AC113951 Mus muscu
948	26	0.7	193215	2	AC126411	AC126411 Mus muscu
949	26	0.7	193422	2	AC068664	AC068664 Mus muscu
950	26	0.7	193474	10	AC125179	AC125179 Mus muscu
951	26	0.7	193708	9	AC005035	AC005035 Homo sapi
c 952	26	0.7	193915	2	AC113549	AC113549 Mus muscu
953	26	0.7	194135	2	AC121549	AC121549 Mus muscu
c 954	26	0.7	194182	2	AC139960	AC139960 Rattus no
c 955	26	0.7	194520	10	AL691424	AL691424 Mouse DNA
c 956	26	0.7	194712	2	AC145426	AC145426 Homo sapi
957	26	0.7	194732	2	AC127804	AC127804 Rattus no
958	26	0.7	195189	2	AC034149	AC034149 Homo sapi
959	26	0.7	195991	2	AC134487	AC134487 Rattus no
c 960	26	0.7	196606	9	AP000779	AP000779 Homo sapi
961	26	0.7	197271	2	AC102370	AC102370 Mus muscu
c 962	26	0.7	197473	2	AC109740	AC109740 Rattus no
963	26	0.7	197678	2	AC139957	AC139957 Rattus no
964	26	0.7	197891	2	AC109837	AC109837 Rattus no
965	26	0.7	198056	2	AC106280	AC106280 Rattus no
c 966	26	0.7	198159	2	AC123721	AC123721 Mus muscu
c 967	26	0.7	198245	3	AC023701	AC023701 Drosophil
c 968	26	0.7	198254	10	AC140375	AC140375 Mus muscu
969	26	0.7	198434	9	AC109994	AC109994 Homo sapi
970	26	0.7	198494	2	AC119626	AC119626 Rattus no
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974	26	0.7	200006	2	AC116446	AC116446 Mus muscu
c 975	26	0.7	200685	9	AC004032	AC004032 Homo sapi
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ALIGNMENTS

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DEFINITION  Homo sapiens misshapen/NIK-related kinase, transcript variant 3,
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ACCESSION   BC034673
VERSION     BC034673.1  GI:21961594
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 5014)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
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  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
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ORIGIN

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DEFINITION  STE20-related protein kinases.
ACCESSION   BD243845
VERSION     BD243845.1  GI:33053615
KEYWORDS    JP 2002522009-A/7.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4133)
  AUTHORS   Plowman,G., Martinez,R. and Whyte,D.
  TITLE     STE20-related protein kinases
  JOURNAL   Patent: JP 2002522009-A 7 23-JUL-2002;
            SUGEN INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002522009-A/7
            PD   23-JUL-2002
            PF   13-APR-1999 JP 2000543584
            PR   14-APR-1998 US     60/081784
            PI   GREGORY PLOWMAN,RICARDO MARTINEZ,DAVID WHYTE
            PC   C12N15/09,A61K38/55,A61P9/00,A61P9/10,A61P13/12,A61P25/00, PC
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ORIGIN

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Qy         1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1784 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1843

Qy         1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1844 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1903

Qy         1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1904 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1963

Qy         1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1964 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2023

Qy         1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2024 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2083

Qy         2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2084 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2143

Qy         2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2144 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2203

Qy         2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2204 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2263

Qy         2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
                ||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||
Db         2264 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2323

Qy         2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2324 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2383

Qy         2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2384 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2443

Qy         2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
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Db         2444 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2503

Qy         2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
                |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db         2504 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2560

Qy         2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2561 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2620
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Qy       2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
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Db       2621 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2680

Qy       2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
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Db       2681 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2740

Qy       2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
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Db       2741 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2800

Qy       2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
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Db       2801 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2860

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
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Db       2861 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2920

Qy       2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
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Db       2921 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2980

Qy       2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
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Db       2981 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3040

Qy       3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3041 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3100

Qy       3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
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Db       3101 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3160

Qy       3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
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Db       3161 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3220

Qy       3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
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Db       3221 ACAAACTGCGGGTGTATTACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3280

Qy       3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3281 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3340

Qy       3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
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Db       3341 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3400

Qy       3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
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Db       3401 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3460

Qy       3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
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Db       3461 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3520

Qy       3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
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Db       3521 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3580

Qy       3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3581 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3640

Qy       3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
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Db       3641 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3700

Qy       3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
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Db       3701 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3760

Qy       3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
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Db       3761 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3820

Qy       3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
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Db       3821 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3880

Qy       3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
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Db       3881 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3940

Qy       3905 ACTTCATGACTCTGAACCGTAAC 3927
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Db       3941 ACTTCATGACTCTGAACCGTAAC 3963
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RESULT 3
AR435598
LOCUS       AR435598                4133 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 11 from patent US 6656716.
ACCESSION   AR435598
VERSION     AR435598.1  GI:40198579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4133)
  AUTHORS   Plowman,G., Martinez,R. and Whyte,D.
  TITLE     Polypeptide fragments of human PAK5 protein kinase
  JOURNAL   Patent: US 6656716-A 11 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1..4133
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             45.2%;  Score 1787;  DB 6;  Length 4133;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2177;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy       1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1784 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1843

Qy       1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1844 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1903

Qy       1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1904 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1963

Qy       1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1964 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2023

Qy       1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2024 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2083

Qy       2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2084 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2143

Qy       2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2144 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2203

Qy       2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
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Db        2204 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2263

Qy        2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
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Db        2264 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2323

Qy        2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
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Db        2324 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2383

Qy        2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2384 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2443

Qy        2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
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Db        2444 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2503

Qy        2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
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Db        2504 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2560

Qy        2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2561 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2620

Qy        2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2621 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2680

Qy        2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2681 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2740

Qy        2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2741 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2800

Qy        2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
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Db        2801 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2860

Qy        2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2861 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2920

Qy        2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2921 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2980

Qy        2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2981 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3040

Qy        3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
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Db        3041 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3100

Qy        3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3101 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3160

Qy        3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
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Db        3161 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3220

Qy        3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
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Db        3221 ACAAACTGCGGGTGTATTACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3280

Qy        3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
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Db        3281 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3340

Qy        3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
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Db        3341 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3400

Qy        3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
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Qy        3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
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Db        3461 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3520

Qy        3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
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Db        3521 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3580

Qy        3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
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Db        3581 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3640

Qy        3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
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Qy        3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
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Qy        3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
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Qy        3905 ACTTCATGACTCTGAACCGTAAC 3927
               |||||||||||||||||||||||
Db        3941 ACTTCATGACTCTGAACCGTAAC 3963
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RESULT 4
AB035698
LOCUS       AB035698                3888 bp    mRNA    linear   PRI 18-APR-2000
DEFINITION  Homo sapiens mRNA for Misshapen/NIK-related kinase MINK-1, complete
            cds.
ACCESSION   AB035698
VERSION     AB035698.1  GI:6970477
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
            Fukagaya,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
            Matsumoto,K., Ninomiya-Tsuji,J. and Kusumi,A.
  TITLE     Molecular cloning of MINK, a novel member of mammalian GCK family
            kinases, which is up-regulated during postnatal mouse cerebral
            development
  JOURNAL   FEBS Lett. 469 (1), 19-23 (2000)
  MEDLINE   20175403
   PUBMED   10708748
REFERENCE   2  (bases 1 to 3888)
  AUTHORS   Dan,I., Watanabe,N.M. and Kusumi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-1999) Ippeita Dan, ERATO, Kusumi Membrane
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                  Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi
                  460-0012, Japan (E-mail:dang@bio.nagoya-u.ac.jp,
                  Tel:81-52-789-2497, Fax:81-52-789-2968)
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ORIGIN

  Query Match            43.1%;  Score 1701;  DB 9;  Length 3888;
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RESULT 5
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ACCESSION   AB041926
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
            Fukagaya,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
            Matsumoto,K., Ninomiya-Tsuji,J. and Kusumi,A.
  TITLE     Molecular cloning of MINK, a novel member of mammalian GCK family
            kinases, which is up-regulated during postnatal mouse cerebral
            development
  JOURNAL   FEBS Lett. 469 (1), 19-23 (2000)
  MEDLINE   20175403
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REFERENCE   2  (bases 1 to 4863)
  AUTHORS   Watanabe,N.M., Dan,I. and Kusumi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2000) Ippeita Dan, Nagoya University, Dept. of
            Biological Science; Chikusa-ku, Furo-cho, Nagoya, Aichi 464-8602,
            Japan (E-mail:dang@bio.nagoya-u.ac.jp,
            URL:http://www.supra.bio.nagoya-u.ac.jp/DNA/, Tel:81-52-789-2497,
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ORIGIN

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Db       1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
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Db       1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
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Db       1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
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Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
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Db       1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
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Db       1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
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Db       1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
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Db       1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
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Db       1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

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Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
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Db       1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
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Db       1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
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Db       1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924

RESULT 6
AX235365
LOCUS       AX235365                3735 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 12 from Patent WO0162928.
ACCESSION   AX235365
VERSION     AX235365.1  GI:15593897
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 12 30-AUG-2001;
            Curagen Corporation (US)
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ORIGIN

  Query Match             40.5%;  Score 1599;  DB 6;  Length 3735;
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Db       2137 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2196
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Qy   2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
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Db   2197 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2256

Qy   2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
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Db   2257 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2316

Qy   2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
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Db   2317 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2376

Qy   2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
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Db   2377 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2436

Qy   2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
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Db   2437 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2496

Qy   2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
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Db   2497 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2556

Qy   2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
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Db   2557 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2616

Qy   2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
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Db   2617 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2676

Qy   2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
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Qy   2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
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Qy   3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
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Qy   3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
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Qy   3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
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Qy   3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
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Db   3097 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3156

Qy   3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
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Db   3157 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3216

Qy   3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
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Db   3217 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3276

Qy   3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3277 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3336

Qy   3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
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Db   3337 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3396

Qy   3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
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Qy   3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
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RESULT 7
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DEFINITION  Sequence 10 from Patent WO0162928.
ACCESSION   AX235363
VERSION     AX235363.1  GI:15593895
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 10 30-AUG-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db       2224 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2283

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
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Db       2284 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2343

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGCCGCAGCGATGGGGATACA 2526
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Db       2344 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGCCGCAGCGATGGGGATACA 2403

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
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Db       2404 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2463

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
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Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
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Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
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Db       2584 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2643

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
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Db       2644 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2703

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
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Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
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Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
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Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
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Db       2884 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 2943

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
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Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
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Db       3004 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3063

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Db       3064 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3123

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Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
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Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
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Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
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Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
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Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
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Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
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Qy       3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
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Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
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Db       3784 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3822

RESULT 8
AX235361
LOCUS       AX235361                3912 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 8 from Patent WO0162928.
ACCESSION   AX235361
VERSION     AX235361.1  GI:15593893
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 8 30-AUG-2001;
            Curagen Corporation (US)
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ORIGIN

  Query Match             40.5%;  Score 1599;  DB 6;  Length 3912;
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Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
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Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
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Db       2374 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2433

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
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Db       2434 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2493

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
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Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
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Db       2554 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2613

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
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Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
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Db       2674 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2733

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
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Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
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Db       2794 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2853

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
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Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
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Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
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Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
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Db       3514 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3573

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RESULT 9

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AX235359
LOCUS       AX235359                 3999 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 6 from Patent WO0162928.
ACCESSION   AX235359
VERSION     AX235359.1  GI:15593891
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 6 30-AUG-2001;
            Curagen Corporation (US)
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ORIGIN

  Query Match             40.5%;  Score 1599;  DB 6;  Length 3999;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
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Db       2461 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2520

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
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Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
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Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
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Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
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Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
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Db       3181 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3240

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
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Db       3241 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3300

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
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Db       3301 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3360

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
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Db       3361 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3420

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
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Db       3421 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3480

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
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Db       3481 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3540

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
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Db       3541 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3600

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
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Db       3601 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3660

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
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Db       3661 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3720

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
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Db        3721 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGAGATGCCTACTTCTGTGGCCTAC 3780

Qy        3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
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Db        3781 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3840

Qy        3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
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Db        3841 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3900

Qy        3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
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Db        3901 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3960

Qy        3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
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Db        3961 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3999


RESULT 10
HSM802420
LOCUS       HSM802420                4590 bp    mRNA    linear   PRI 18-FEB-2000
DEFINITION  Homo sapiens mRNA; cDNA DKFZp761K18121 (from clone DKFZp761K18121).
ACCESSION   AL157418
VERSION     AL157418.1  GI:7018439
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4590)
  AUTHORS   Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2000) MIPS, Am Klopferspitz 18a, D-82152
            Martinsried, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp761K18121) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://www.mips.biochem.mpg.de/proj/cDNA/.
FEATURES             Location/Qualifiers
     source          1. .4590
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="17"
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                     /tissue_type="amygdala"
                     /clone_lib="761 (synonym: hamy2). Vector pSport1; host
                     DH10B; sites NotI + SalI"
                     /dev_stage="adult"
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ORIGIN

  Query Match             40.5%;  Score 1599;  DB 9;  Length 4590;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
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Db        2197 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2256

Qy        2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2257 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2316

Qy        2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
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Db        2317 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2376

Qy        2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
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Db        2377 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2436

Qy        2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
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Db        2437 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2496

Qy        2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2497 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2556

Qy        2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
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Db        2557 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2616

Qy        2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
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Db        2617 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2676

Qy        2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2677 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2736

Qy        2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2737 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2796

Qy        2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
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Db        2797 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 2856

Qy        3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
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Db        2857 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 2916

Qy        3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
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Db        2917 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 2976

Qy        3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
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Db        2977 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3036

Qy        3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
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Db        3037 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3096

Qy        3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
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Db        3097 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3156

Qy        3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
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Db        3157 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3216

Qy        3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
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Db        3217 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3276

Qy        3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
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Db        3277 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3336

Qy        3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
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Db        3337 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3396

Qy        3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
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Db        3397 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3456

Qy        3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
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Db        3457 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3516

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Db        3517 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3576

Qy        3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
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Qy        3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
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Db        3637 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3696

Qy        3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
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Db        3697 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3756

Qy        3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
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Db        3757 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3795


RESULT 11
AX235417
LOCUS       AX235417               1482 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 64 from Patent WO0162928.
ACCESSION   AX235417
VERSION     AX235417.1  GI:15593928
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 64 30-AUG-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1..1482
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             33.8%;  Score 1337;  DB 6;  Length 1482;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
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Db           1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy          70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
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Db          61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy         130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
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Qy         190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
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Db         181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy         250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
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Db         241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy         310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
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Db         301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy         370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy         430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
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Qy         490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
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Db         481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy         550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
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Qy         670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
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Qy         790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
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Qy         850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
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Qy         910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
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Db         901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy         970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
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Db         961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy        1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
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Qy        1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
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Qy        1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
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Db        1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy        1330 CGGCGGCAGGCGGAGCG 1346
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Db       1321 CGGCGGCAGGCGGAGCG 1337

RESULT 12
AX235415
LOCUS       AX235415                1649 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 62 from Patent WO0162928.
ACCESSION   AX235415
VERSION     AX235415.1  GI:15593927
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 62 30-AUG-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1..1649
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ORIGIN

  Query Match             33.8%;  Score 1337;  DB 6;  Length 1649;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy        370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy        430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy        490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
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Db        721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy       1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
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Db       1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy       1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy       1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy       1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy       1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy       1330 CGGCGGCAGGCGGAGCG 1346
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Db       1321 CGGCGGCAGGCGGAGCG 1337

RESULT 13
AX235422
LOCUS       AX235422                1717 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 69 from Patent WO0162928.
ACCESSION   AX235422
VERSION     AX235422.1  GI:15593930
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 69 30-AUG-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1..1717
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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ORIGIN

  Query Match             33.8%;  Score 1337;  DB 6;  Length 1717;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
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Db          1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
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Db         61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy        370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
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Db        361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy        430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
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Db        421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy        490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
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Db        481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
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Db        541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
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Db        721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy       1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy       1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy       1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
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Db       1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy       1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy       1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy       1330 CGGCGGCAGGCGGAGCG 1346
              |||||||||||||||||
Db       1321 CGGCGGCAGGCGGAGCG 1337


RESULT 14
AX235419
LOCUS       AX235419                1787 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 66 from Patent WO0162928.
ACCESSION   AX235419
VERSION     AX235419.1  GI:15593929
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and
            Spaderna,S.K.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0162928-A 66 30-AUG-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1..1787
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             33.8%;  Score 1337;  DB 6;  Length 1787;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300
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Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
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Db        301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy        370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy        430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
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Db        421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy        490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
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Db        481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
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Db        541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
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Db        601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
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Db        721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
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Db        841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
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Db        901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
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Db        961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy       1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
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Db       1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy       1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

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Db       1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy       1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
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Db       1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy       1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy       1330 CGGCGGCAGGCGGAGCG 1346
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Db       1321 CGGCGGCAGGCGGAGCG 1337
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RESULT 15
BD183377
LOCUS       BD183377                3824 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Novel genes and proteins encoded by the genes.
ACCESSION   BD183377
VERSION     BD183377.1  GI:31875577
KEYWORDS    JP 2002345492-A/90.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3824)
  AUTHORS   Ohara,O., Nagase,T. and Nakajima,D.
  TITLE     Novel genes and proteins encoded by the genes
  JOURNAL   Patent: JP 2002345492-A 90 03-DEC-2002;
            KAZUSA DNA RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002345492-A/90
            PD   03-DEC-2002
            PF   26-FEB-2002 JP 2002049009
            PI   OSAMU OHARA,TAKAHIRO NAGASE,DAISUKE NAKAJIMA
            PC   C12N15/09,C07K14/47//A61K31/711,A61K38/00,A61K48/00,A61P25/00,
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1078;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1977 AGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGT 2036

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Search completed: March 2, 2004, 20:03:40
Job time : 9996 secs

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 14:48:42 ; Search time 974 Seconds
(without alignments)
17232.680 Million cell updates/sec

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Perfect score: 3951
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	1694	42.9	4133	2	AAZ40485	Aaz40485 Human ZC3
	5	1689	42.7	4863	4	AAK52286	Aak52286 Human pol
	6	1689	42.7	4863	6	AAL48626	Aal48626 Human ins
	7	1689	42.7	4863	8	AAL61132	Aal61132 Human MIN
	8	1683	42.6	4414	9	ADE34153	Ade34153 Human DNA
	9	1599	40.5	3735	5	AAD17762	Aad17762 Human nov
	10	1599	40.5	3822	5	AAD17761	Aad17761 Human nov
	11	1599	40.5	3912	5	AAD17760	Aad17760 Human nov
	12	1599	40.5	3999	5	AAD17759	Aad17759 Human nov
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	14	1030	26.1	2345	3	AAC98909	Aac98909 Human pan
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c	23	224	5.7	467	4	ABA51751	Aba51751 Human foe
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c	25	224	5.7	467	4	ABA21580	Aba21580 Probe #46
c	26	224	5.7	467	4	AAK25497	Aak25497 Human bon
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c	36	222	5.6	257	4	AAK38617	Aak38617 Human bon
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	42	205	5.2	500	8	ACH45103	Ach45103 Human foe
	43	194	4.9	403	3	AAA44094	Aaa44094 Human sec
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c	45	172	4.4	12400	6	ABL88268	Abl88268 Human CHR
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c	47	171	4.3	481	4	AAI10122	Aai10122 Probe #55
c	48	171	4.3	481	4	ABA51752	Aba51752 Human foe
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c	50	171	4.3	481	4	ABA21581	Aba21581 Probe #47
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c	58	142	3.6	179	4	ABA64432	Aba64432 Human foe
c	59	142	3.6	179	4	AAI44607	Aai44607 Probe #13
c	60	142	3.6	179	4	ABA46569	Aba46569 Human bre
c	61	142	3.6	179	4	ABA31569	Aba31569 Probe #10
c	62	142	3.6	179	4	AAK38618	Aak38618 Human bon
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c	72	128	3.2	140	4	ABA46567	Aba46567 Human bre
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c	76	128	3.2	140	4	ABS38181	Abs38181 Human liv
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c	78	128	3.2	140	6	ABS12683	Abs12683 Human gen
c	79	128	3.2	465	4	AAI10120	Aai10120 Probe #53
c	80	128	3.2	465	4	ABA51750	Aba51750 Human foe
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c	82	128	3.2	465	4	ABA21579	Aba21579 Probe #45
c	83	128	3.2	465	4	AAK25496	Aak25496 Human bon
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c	86	128	3.2	465	5	AAI00061	Aai00061 Probe #52
c	87	128	3.2	465	6	ABS00062	Abs00062 Human gen
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	95	82	2.1	274	6	ABL71349	Abl71349 Corn tass
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	97	77	1.9	146	4	AAF30493	Aaf30493 Human YSK
	98	69	1.7	283	3	AAC29120	Aac29120 Human sec
	99	69	1.7	285	2	AAX40546	Aax40546 Human sec
	100	68	1.7	387	5	AAS80795	Aas80795 DNA encod
	101	68	1.7	387	9	ADE09489	Ade09489 Novel DNA
	102	68	1.7	756	9	ADE07226	Ade07226 Novel cod
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c	104	58	1.5	449	4	AAI35029	Aai35029 Probe #37
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c	106	58	1.5	449	4	AAK29083	Aak29083 Human bon
c	107	58	1.5	449	4	AAK03622	Aak03622 Human bra
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c	118	54	1.4	96	7	ACD97410	Acd97410 Human col
	119	47	1.2	337	5	AAS88204	Aas88204 DNA encod
	120	47	1.2	896	4	AAC90430	Aac90430 Murine De
	121	42	1.1	4635	4	ABL18571	Abl18571 Drosophil
c	122	31	0.8	62	7	ABZ81743	Abz81743 Huntingto
c	123	31	0.8	74	7	ABZ81744	Abz81744 Huntingto
	124	31	0.8	2480	8	AAL61078	Aal61078 Human MAP
	125	31	0.8	2871	8	AAL61076	Aal61076 Human MAP
	126	31	0.8	2906	8	AAL61075	Aal61075 Human MAP
	127	31	0.8	2906	9	ADE31756	Ade31756 Human 209
	128	31	0.8	2964	8	AAL61077	Aal61077 Human MAP
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c	133	29	0.7	443	7	ABX48099	Abx48099 Bovine ES
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c	135	29	0.7	3331	2	AAV22683	Aav22683 New DNA s
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	138	28	0.7	416	7	ABX53657	Abx53657 Bovine ES
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	141	28	0.7	5824	4	ABL15249	Abl15249 Drosophil
	142	28	0.7	6705	4	AAF32778	Aaf32778 Human sec
	143	28	0.7	8055	4	ABL30126	Abl30126 Drosophil
	144	28	0.7	9276	4	ABL19684	Abl19684 Drosophil
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	146	28	0.7	11743	4	ABL15248	Abl15248 Drosophil
	147	27	0.7	138	4	ABL23985	Abl23985 Drosophil
	148	27	0.7	570	7	AAD50974	Aad50974 Caenorhab
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c	152	27	0.7	1218	4	ABA50502	Aba50502 Human bre
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c	154	27	0.7	1218	4	AAK42594	Aak42594 Human bon
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c	160	27	0.7	1954	4	ABA55860	Aba55860 Human foe
c	161	27	0.7	1954	4	AAI35517	Aai35517 Probe #42
c	162	27	0.7	1954	4	ABA45372	Aba45372 Human bre
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	170	27	0.7	2687	4	ABL02107	Abl02107 Drosophil
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	177	27	0.7	5113	4	ABL14387	Abl14387 Drosophil
	178	27	0.7	5994	9	ADB80558	Adb80558 Ovarian c
	179	27	0.7	5994	9	ADB79896	Adb79896 Human put
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	181	27	0.7	6754	4	AAF26490	Aaf26490 Human SRC
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c	185	27	0.7	28486	8	ADA02458	Ada02458 Mouse Ccn
c	186	27	0.7	28486	9	ADB72197	Adb72197 Mouse Ccn
c	187	27	0.7	28486	9	ADE82929	Ade82929 Mouse Ccn
	188	26	0.7	36	2	AAT78910	Aat78910 Poly-glut
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	194	26	0.7	75	2	AAV17230	Aav17230 SCA2 gene
	195	26	0.7	78	2	AAV17231	Aav17231 SCA2 gene
	196	26	0.7	78	2	AAV17232	Aav17232 SCA2 gene
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	200	26	0.7	169	3	AAA63168	Aaa63168 Ii revers
	201	26	0.7	190	3	AAA63173	Aaa63173 Ii revers
	202	26	0.7	223	4	AAI21216	Aai21216 Probe #11
	203	26	0.7	223	4	ABA66296	Aba66296 Human foe
	204	26	0.7	223	4	AAI46487	Aai46487 Probe #15
	205	26	0.7	223	4	ABA48400	Aba48400 Human bre
	206	26	0.7	223	4	ABA33362	Aba33362 Probe #11
	207	26	0.7	223	4	AAK40457	Aak40457 Human bon
	208	26	0.7	223	4	AAK14714	Aak14714 Human bra
	209	26	0.7	223	4	ABS40020	Abs40020 Human liv
	210	26	0.7	223	5	AAI06926	Aai06926 Probe #69
	211	26	0.7	223	6	ABS14449	Abs14449 Human gen
	212	26	0.7	228	4	ABL27225	Abl27225 Drosophil
	213	26	0.7	277	3	ABK10239	Abk10239 Trinucleo
	214	26	0.7	293	4	AAI21460	Aai21460 Probe #11
	215	26	0.7	293	4	ABA66542	Aba66542 Human foe
	216	26	0.7	293	4	AAI46749	Aai46749 Probe #15
	217	26	0.7	293	4	ABA48628	Aba48628 Human bre
	218	26	0.7	293	4	ABA33603	Aba33603 Probe #12
	219	26	0.7	293	4	AAK40695	Aak40695 Human bon
	220	26	0.7	293	4	AAK14962	Aak14962 Human bra
	221	26	0.7	293	4	ABS40263	Abs40263 Human liv
	222	26	0.7	293	5	AAI07156	Aai07156 Probe #71
	223	26	0.7	293	6	ABS14658	Abs14658 Human gen
	224	26	0.7	305	2	AAZ32043	Aaz32043 Human MET
	225	26	0.7	305	5	AAC90100	Aac90100 HTTAQ67R
c	226	26	0.7	346	5	AAS79688	Aas79688 DNA encod
c	227	26	0.7	346	5	AAS91261	Aas91261 DNA encod
c	228	26	0.7	370	5	AAS91972	Aas91972 DNA encod
c	229	26	0.7	370	5	AAS87785	Aas87785 DNA encod
	230	26	0.7	389	3	ABK10248	Abk10248 Tri-nucle
	231	26	0.7	398	2	AAZ32058	Aaz32058 Human MET
	232	26	0.7	398	5	AAC90315	Aac90315 X69161 cD
	233	26	0.7	444	4	AAI12012	Aai12012 Probe #19
	234	26	0.7	444	4	ABA53714	Aba53714 Human foe
	235	26	0.7	444	4	AAI33346	Aai33346 Probe #20
	236	26	0.7	444	4	ABA43283	Aba43283 Human bre
	237	26	0.7	444	4	ABA23467	Aba23467 Probe #19
	238	26	0.7	444	4	AAK27436	Aak27436 Human bon
	239	26	0.7	444	4	AAK01978	Aak01978 Human bra
	240	26	0.7	444	4	ABS27002	Abs27002 Human liv
	241	26	0.7	444	5	AAI01940	Aai01940 Probe #19
	242	26	0.7	444	6	ABS01930	Abs01930 Human gen

c	243	26	0.7	448	5	AAS91969	Aas91969 DNA encod
	244	26	0.7	459	4	AAI12263	Aai12263 Probe #21
	245	26	0.7	459	4	ABA53968	Aba53968 Human foe
	246	26	0.7	459	4	AAI33617	Aai33617 Probe #23
	247	26	0.7	459	4	ABA43516	Aba43516 Human bre
	248	26	0.7	459	4	ABA23716	Aba23716 Probe #21
	249	26	0.7	459	4	AAK27681	Aak27681 Human bon
	250	26	0.7	459	4	AAK02234	Aak02234 Human bra
	251	26	0.7	459	4	ABS27253	Abs27253 Human liv
	252	26	0.7	459	5	AAI02177	Aai02177 Probe #21
	253	26	0.7	459	6	ABS02145	Abs02145 Human gen
	254	26	0.7	462	4	ABL26941	Abl26941 Drosophil
	255	26	0.7	463	5	AAH81556	Aah81556 Human dif
	256	26	0.7	476	2	AAZ32067	Aaz32067 Human MET
	257	26	0.7	476	5	AAC90324	Aac90324 AF001444
	258	26	0.7	516	2	AAV06551	Aav06551 SCA2 gene
	259	26	0.7	561	4	ABL22805	Abl22805 Drosophil
	260	26	0.7	603	3	AAF11492	Aaf11492 Aspergill
	261	26	0.7	623	2	AAV17229	Aav17229 SCA2 gene
	262	26	0.7	625	4	AAI22504	Aai22504 Probe #12
	263	26	0.7	625	4	ABA67580	Aba67580 Human foe
	264	26	0.7	625	4	AAI47796	Aai47796 Probe #16
	265	26	0.7	625	4	ABA49677	Aba49677 Human bre
	266	26	0.7	625	4	ABA34657	Aba34657 Probe #13
	267	26	0.7	625	4	AAK41748	Aak41748 Human bon
	268	26	0.7	625	4	AAK16002	Aak16002 Human bra
	269	26	0.7	625	4	ABS41341	Abs41341 Human liv
	270	26	0.7	625	5	AAI08190	Aai08190 Probe #81
	271	26	0.7	625	6	ABS15757	Abs15757 Human gen
	272	26	0.7	792	4	AAK93622	Aak93622 Human cDN
	273	26	0.7	792	4	AAK91954	Aak91954 Human cDN
	274	26	0.7	793	2	AAX39688	Aax39688 Gastric c
	275	26	0.7	800	2	AAQ32000	Aaq32000 Encodes e
	276	26	0.7	800	2	AAV31333	Aav31333 Eimeria a
	277	26	0.7	801	4	ABL26399	Abl26399 Drosophil
	278	26	0.7	924	4	ABL19283	Abl19283 Drosophil
	279	26	0.7	936	2	AAV22213	Aav22213 Human Cdx
	280	26	0.7	942	9	ADD36449	Add36449 Human THA
	281	26	0.7	945	9	ADD36362	Add36362 Human THA
	282	26	0.7	951	4	ABL11357	Abl11357 Drosophil
	283	26	0.7	990	4	ABL05665	Abl05665 Drosophil
	284	26	0.7	1002	4	AAK51628	Aak51628 Human pol
	285	26	0.7	1010	5	AAS68262	Aas68262 DNA encod
	286	26	0.7	1038	4	ABL27667	Abl27667 Drosophil
	287	26	0.7	1065	2	AAQ74149	Aaq74149 Plasmid p
	288	26	0.7	1068	4	ABL23721	Abl23721 Drosophil
	289	26	0.7	1082	3	AAC78047	Aac78047 Human can
	290	26	0.7	1155	4	ABL13431	Abl13431 Drosophil
	291	26	0.7	1277	4	ABL20961	Abl20961 Drosophil
	292	26	0.7	1311	4	ABL26093	Abl26093 Drosophil
	293	26	0.7	1336	4	ABL24591	Abl24591 Drosophil
	294	26	0.7	1412	6	ABK84787	Abk84787 Human cDN
	295	26	0.7	1492	7	ACC44604	Acc44604 Human CBF
	296	26	0.7	1529	4	ABL16653	Abl16653 Drosophil
	297	26	0.7	1533	6	ABA90388	Aba90388 Drosophil
	298	26	0.7	1545	4	ABL27309	Abl27309 Drosophil
c	299	26	0.7	1547	6	ABK63761	Abk63761 Rat seque
c	300	26	0.7	1547	7	ABT42016	Abt42016 Toxicity
c	301	26	0.7	1547	9	ADB58351	Adb58351 Toxicity-
c	302	26	0.7	1547	9	ADB52915	Adb52915 Primary r
	303	26	0.7	1557	7	ABX94057	Abx94057 Bone and
	304	26	0.7	1631	7	ACC44603	Acc44603 Human CBF
	305	26	0.7	1680	2	AAQ74150	Aaq74150 Plasmid p
	306	26	0.7	1694	7	ACC44602	Acc44602 Human CBF
	307	26	0.7	1725	6	ABK83820	Abk83820 Human cDN
	308	26	0.7	1802	6	ABA99136	Aba99136 HPDE-1 en
	309	26	0.7	1804	7	ABX94058	Abx94058 Bone and
	310	26	0.7	1810	2	AAQ13573	Aaq13573 E75B spec
	311	26	0.7	1833	4	ABL07931	Abl07931 Drosophil
	312	26	0.7	1865	4	ABL03153	Abl03153 Drosophil
	313	26	0.7	1880	6	ABQ60893	Abq60893 Clone MGC
	314	26	0.7	1933	4	ABL19239	Abl19239 Drosophil
	315	26	0.7	1979	4	AAI13269	Aai13269 Probe #32
	316	26	0.7	1979	4	ABA54968	Aba54968 Human foe
	317	26	0.7	1979	4	AAI34622	Aai34622 Probe #33
	318	26	0.7	1979	4	ABA44526	Aba44526 Human bre
	319	26	0.7	1979	4	ABA24732	Aba24732 Probe #31
	320	26	0.7	1979	4	AAK28693	Aak28693 Human bon
	321	26	0.7	1979	4	AAK03239	Aak03239 Human bra
	322	26	0.7	1979	4	ABS28293	Abs28293 Human liv
	323	26	0.7	1979	5	AAI03174	Aai03174 Probe #31
	324	26	0.7	1979	6	ABS03204	Abs03204 Human gen
	325	26	0.7	2024	6	ABZ69920	Abz69920 Rat Tob c
	326	26	0.7	2035	4	ABL19647	Abl19647 Drosophil
	327	26	0.7	2079	4	ABL16037	Abl16037 Drosophil
	328	26	0.7	2094	4	ABL15969	Abl15969 Drosophil
	329	26	0.7	2115	4	ABL26940	Abl26940 Drosophil
	330	26	0.7	2122	4	ABL03707	Abl03707 Drosophil
	331	26	0.7	2124	4	ABL16559	Abl16559 Drosophil
	332	26	0.7	2202	5	AAC87948	Aac87948 Human lon
	333	26	0.7	2228	4	ABL27224	Abl27224 Drosophil
	334	26	0.7	2242	6	ABQ61209	Abq61209 Unidentif
	335	26	0.7	2268	4	ABL08666	Abl08666 Drosophil
	336	26	0.7	2280	5	AAS82146	Aas82146 DNA encod
	337	26	0.7	2294	2	AAV80181	Aav80181 Alternati
	338	26	0.7	2298	4	ABL18481	Abl18481 Drosophil
	339	26	0.7	2311	10	ADE52641	Ade52641 Murine dn
	340	26	0.7	2341	4	ABL07089	Abl07089 Drosophil
	341	26	0.7	2364	4	ABL15947	Abl15947 Drosophil
	342	26	0.7	2415	2	AAT86757	Aat86757 cDNA of t
	343	26	0.7	2424	6	ABS55226	Abs55226 Human N-t
	344	26	0.7	2424	7	ABX11413	Abx11413 DNA encod
	345	26	0.7	2453	2	AAT86758	Aat86758 cDNA of t
	346	26	0.7	2453	6	AAD41236	Aad41236 Murine ne
	347	26	0.7	2454	4	ABL14527	Abl14527 Drosophil
	348	26	0.7	2462	2	AAV35473	Aav35473 Human hSK
	349	26	0.7	2521	2	AAX08414	Aax08414 Human sma
	350	26	0.7	2521	7	ACA64903	Aca64903 Human KCN
	351	26	0.7	2561	4	ABL22804	Abl22804 Drosophil
	352	26	0.7	2571	4	ABL30283	Abl30283 Drosophil
	353	26	0.7	2649	8	ACC70742	Acc70742 Mouse Jun
	354	26	0.7	2733	2	AAX84442	Aax84442 Mouse bra
	355	26	0.7	2776	4	ABL07259	Abl07259 Drosophil
	356	26	0.7	2838	4	ABL09337	Abl09337 Drosophil
c	357	26	0.7	2933	4	ABL26398	Abl26398 Drosophil
	358	26	0.7	2951	4	ABL11356	Abl11356 Drosophil
	359	26	0.7	3095	8	ACF03947	Acf03947 Human SK-
	360	26	0.7	3095	9	ADE31740	Ade31740 Human 122
c	361	26	0.7	3161	4	ABL27666	Abl27666 Drosophil
c	362	26	0.7	3182	4	ABL05664	Abl05664 Drosophil
	363	26	0.7	3207	4	ABL11219	Abl11219 Drosophil
	364	26	0.7	3254	2	AAV32402	Aav32402 Drosphila
	365	26	0.7	3327	9	ADC59311	Adc59311 DNA encod
	366	26	0.7	3334	2	AAV80117	Aav80117 Osf2/Cbfa
	367	26	0.7	3336	5	AAC87949	Aac87949 Human sho
	368	26	0.7	3339	4	ABL01915	Abl01915 Drosophil
	369	26	0.7	3346	5	AAS79689	Aas79689 DNA encod
	370	26	0.7	3399	9	ADC59315	Adc59315 DNA encod
	371	26	0.7	3414	6	ABT07557	Abt07557 Human bre
	372	26	0.7	3441	4	ABL20763	Abl20763 Drosophil
	373	26	0.7	3459	9	ADC59309	Adc59309 DNA encod
	374	26	0.7	3582	4	ABL24590	Abl24590 Drosophil
	375	26	0.7	3591	4	ABL16652	Abl16652 Drosophil
	376	26	0.7	3591	4	ABL20960	Abl20960 Drosophil
	377	26	0.7	3597	4	AAK94326	Aak94326 Human ful
	378	26	0.7	3645	6	ABQ94233	Abq94233 FLO11 gen
	379	26	0.7	3645	6	ABK12769	Abk12769 Mouse cDN
	380	26	0.7	3649	4	ABL08200	Abl08200 Drosophil
	381	26	0.7	3732	6	ABQ94271	Abq94271 Fungal ge
	382	26	0.7	3747	7	ACA03912	Aca03912 cDNA down
	383	26	0.7	3775	5	AAS81656	Aas81656 DNA encod
	384	26	0.7	3786	3	AAZ46153	Aaz46153 cDNA sequ
	385	26	0.7	3798	2	AAZ40483	Aaz40483 Human ZC1
	386	26	0.7	3819	2	AAQ14530	Aaq14530 T cell pr
	387	26	0.7	3819	2	AAQ63617	Aaq63617 T-cell tr
	388	26	0.7	3864	5	AAS81657	Aas81657 DNA encod

	389	26	0.7	3864	6	AAL48628	Aal48628 Human ins
	390	26	0.7	3864	7	ABX08783	Abx08783 Angiogene
	391	26	0.7	3873	4	ABL26092	Abl26092 Drosophil
	392	26	0.7	3881	4	ABL16654	Abl16654 Drosophil
	393	26	0.7	3925	5	AAD08642	Aad08642 Human kin
	394	26	0.7	3925	9	ADE25654	Ade25654 Human cDN
	395	26	0.7	3933	4	ABL19238	Abl19238 Drosophil
	396	26	0.7	3981	4	ABL08679	Abl08679 Drosophil
	397	26	0.7	4083	4	ABL09873	Abl09873 Drosophil
c	398	26	0.7	4121	4	ABL13430	Abl13430 Drosophil
	399	26	0.7	4122	4	ABL03706	Abl03706 Drosophil
	400	26	0.7	4130	4	ABL27308	Abl27308 Drosophil
c	401	26	0.7	4177	4	ABL19282	Abl19282 Drosophil
	402	26	0.7	4200	2	AAT78912	Aat78912 Spinocere
	403	26	0.7	4206	9	ADC30128	Adc30128 Human nov
	404	26	0.7	4266	5	AAS81655	Aas81655 DNA encod
	405	26	0.7	4266	6	ABK11027	Abk11027 DNA encod
c	406	26	0.7	4298	4	ABL18480	Abl18480 Drosophil
	407	26	0.7	4367	2	AAV30270	Aav30270 Gene caus
	408	26	0.7	4481	2	AAV06552	Aav06552 Human SCA
	409	26	0.7	4481	2	AAZ23428	Aaz23428 Human SCA
	410	26	0.7	4481	7	ABV75291	Abv75291 Human SCA
	411	26	0.7	4481	9	ADD18753	Add18753 Human dis
c	412	26	0.7	4569	4	ABL15968	Abl15968 Drosophil
	413	26	0.7	4631	4	ABL23720	Abl23720 Drosophil
	414	26	0.7	4665	4	ABL19646	Abl19646 Drosophil
c	415	26	0.7	4685	5	AAS87783	Aas87783 DNA encod
	416	26	0.7	4777	4	ABL28633	Abl28633 Drosophil
	417	26	0.7	4829	4	ABL13399	Abl13399 Drosophil
	418	26	0.7	4852	4	ABL09963	Abl09963 Drosophil
	419	26	0.7	4920	4	ABL09461	Abl09461 Drosophil
	420	26	0.7	4959	6	ABS55223	Abs55223 Mouse N-t
	421	26	0.7	4959	7	ABX11410	Abx11410 DNA encod
	422	26	0.7	4960	6	ABS55228	Abs55228 Mouse myo
	423	26	0.7	4960	7	ABX11415	Abx11415 DNA encod
	424	26	0.7	4969	5	AAS81653	Aas81653 DNA encod
c	425	26	0.7	4981	4	ABL15946	Abl15946 Drosophil
	426	26	0.7	4989	7	AAD54622	Aad54622 Human Mas
	427	26	0.7	5025	4	ABL09336	Abl09336 Drosophil
	428	26	0.7	5049	4	ABL18499	Abl18499 Drosophil
	429	26	0.7	5106	5	AAS72419	Aas72419 DNA encod
	430	26	0.7	5139	4	ABL09373	Abl09373 Drosophil
c	431	26	0.7	5178	4	ABL03152	Abl03152 Drosophil
	432	26	0.7	5252	4	ABL14526	Abl14526 Drosophil
	433	26	0.7	5377	4	ABL16036	Abl16036 Drosophil
	434	26	0.7	5419	7	ABA00947	Aba00947 MAML2 cod
	435	26	0.7	5556	4	ABL09460	Abl09460 Drosophil
c	436	26	0.7	5568	5	AAS87788	Aas87788 DNA encod
c	437	26	0.7	5895	6	ABT06294	Abt06294 Human NOV
	438	26	0.7	5970	2	AAX26546	Aax26546 Nucleic a
	439	26	0.7	6395	4	ABL09872	Abl09872 Drosophil
	440	26	0.7	6463	3	AAZ45239	Aaz45239 DNA encod
	441	26	0.7	6541	4	ABL04172	Abl04172 Drosophil
	442	26	0.7	6558	3	AAZ45602	Aaz45602 cDNA sequ
	443	26	0.7	6577	4	ABL13777	Abl13777 Drosophil
	444	26	0.7	6832	6	AAD30439	Aad30439 Human amp
	445	26	0.7	6835	2	AAV99915	Aav99915 AIB1 (Amp
	446	26	0.7	6845	9	ADE76189	Ade76189 Human AIB
	447	26	0.7	7162	2	AAV22214	Aav22214 Mouse Cdx
	448	26	0.7	7188	7	AAD55833	Aad55833 Human nuc
	449	26	0.7	7326	2	AAQ99456	Aaq99456 Sequence
	450	26	0.7	7326	2	AAV10093	Aav10093 Cellular
	451	26	0.7	7326	3	AAA15554	Aaa15554 Mouse nuc
	452	26	0.7	7326	3	AAA62948	Aaa62948 CREB bind
c	453	26	0.7	7568	5	AAS87784	Aas87784 DNA encod
	454	26	0.7	7568	5	AAS72421	Aas72421 DNA encod
	455	26	0.7	7572	7	ABX74469	Abx74469 Human cDN
	456	26	0.7	7593	4	ABL07930	Abl07930 Drosophil
	457	26	0.7	7680	4	AAI59276	Aai59276 Human pol
	458	26	0.7	7967	4	ABL18498	Abl18498 Drosophil
	459	26	0.7	8043	8	AAD57227	Aad57227 Human CGD
c	460	26	0.7	8772	4	AAS11678	Aas11678 Human Fla
c	461	26	0.7	8871	4	AAS11677	Aas11677 Human Fla
c	462	26	0.7	9321	6	ABK15177	Abk15177 Human REP
	463	26	0.7	9931	4	ABL07088	Abl07088 Drosophil
c	464	26	0.7	10531	7	ABZ42868	Abz42868 Human GPC
c	465	26	0.7	10882	4	ABL08678	Abl08678 Drosophil
	466	26	0.7	10910	4	ABL03131	Abl03131 Drosophil
c	467	26	0.7	12363	4	ABL11218	Abl11218 Drosophil
	468	26	0.7	12713	4	ABL07608	Abl07608 Drosophil
	469	26	0.7	12749	2	AAX78032	Aax78032 Human Hun
c	470	26	0.7	16975	4	ABL30282	Abl30282 Drosophil
	471	26	0.7	18495	4	AAK65235	Aak65235 Human imm
c	472	26	0.7	18495	7	ABT16920	Abt16920 Human sec
c	473	26	0.7	18495	7	ABZ67561	Abz67561 Human sec
c	474	26	0.7	18495	7	ABZ73980	Abz73980 Secreted
	475	26	0.7	18877	4	ABL28632	Abl28632 Drosophil
c	476	26	0.7	19754	4	ABL07258	Abl07258 Drosophil
	477	26	0.7	20377	4	ABA07231	Aba07231 Human pan
	478	26	0.7	20377	4	AAK89872	Aak89872 Human dig
c	479	26	0.7	24370	9	ADC86478	Adc86478 Human GPC
	480	26	0.7	31214	4	ABL16558	Abl16558 Drosophil
	481	26	0.7	31562	4	ABL03868	Abl03868 Drosophil
c	482	26	0.7	39746	4	ABL13398	Abl13398 Drosophil
	483	26	0.7	44456	4	ABL09962	Abl09962 Drosophil
c	484	26	0.7	49999	2	AAZ23895	Aaz23895 Murine LO
	485	26	0.7	110000	7	ABX16390_4	Continuation (5 of
c	486	26	0.7	268685	6	ABS56563	Abs56563 Human SUL
	487	25	0.6	153	2	AAT78907	Aat78907 Poly-glut
	488	25	0.6	184	4	ABL23505	Abl23505 Drosophil
	489	25	0.6	195	4	ABL27913	Abl27913 Drosophil
	490	25	0.6	379	2	AAQ04602	Aaq04602 Cryptical
	491	25	0.6	402	2	AAT78906	Aat78906 Poly-glut
	492	25	0.6	548	9	ADD34150	Add34150 Mouse mit
	493	25	0.6	657	4	ABL10519	Abl10519 Drosophil
	494	25	0.6	668	3	AAF13154	Aaf13154 Aspergill
c	495	25	0.6	1109	2	AAZ24880	Aaz24880 Human sec
c	496	25	0.6	1245	9	ADE28660	Ade28660 Human NOV
	497	25	0.6	1396	2	AAZ21259	Aaz21259 Human cel
	498	25	0.6	1396	4	AAS11583	Aas11583 Human cDN
	499	25	0.6	1396	6	ABK87047	Abk87047 Human cel
c	500	25	0.6	1418	7	ACC79031	Acc79031 Human sec
	501	25	0.6	1478	4	ABL05963	Abl05963 Drosophil
	502	25	0.6	1509	4	ABL24571	Abl24571 Drosophil
	503	25	0.6	1533	4	ABL27787	Abl27787 Drosophil
	504	25	0.6	1598	4	ABL09793	Abl09793 Drosophil
	505	25	0.6	1738	4	ABL30141	Abl30141 Drosophil
	506	25	0.6	1921	4	ABL05597	Abl05597 Drosophil
	507	25	0.6	1931	4	ABL30163	Abl30163 Drosophil
	508	25	0.6	1984	4	ABL17439	Abl17439 Drosophil
	509	25	0.6	2048	6	ABS76463	Abs76463 cDNA enco
	510	25	0.6	2056	4	AAD18037	Aad18037 Human sia
	511	25	0.6	2075	6	AAD35226	Aad35226 Human TRN
	512	25	0.6	2090	7	ADA53234	Ada53234 Human cod
c	513	25	0.6	2184	4	ABL23504	Abl23504 Drosophil
	514	25	0.6	2223	6	ABK46531	Abk46531 Human PDZ
	515	25	0.6	2277	4	ABL27912	Abl27912 Drosophil
	516	25	0.6	2490	4	ABL26439	Abl26439 Drosophil
	517	25	0.6	2561	4	ABL02359	Abl02359 Drosophil
	518	25	0.6	2623	3	AAA62684	Aaa62684 Human MyT
c	519	25	0.6	2657	4	ABL10518	Abl10518 Drosophil
	520	25	0.6	2669	4	ABL08099	Abl08099 Drosophil
	521	25	0.6	3012	4	ABL23891	Abl23891 Drosophil
	522	25	0.6	3154	6	AAD30406	Aad30406 Drosophil
	523	25	0.6	3237	4	ABL03607	Abl03607 Drosophil
	524	25	0.6	3315	9	ADB78970	Adb78970 Rice tran
	525	25	0.6	3318	9	ADB78942	Adb78942 Rice tran
	526	25	0.6	3402	4	ABL17455	Abl17455 Drosophil
	527	25	0.6	3475	4	ABL03103	Abl03103 Drosophil
	528	25	0.6	3708	7	AAL51458	Aal51458 Rat IRSAL
	529	25	0.6	3795	4	ABL23829	Abl23829 Drosophil
	530	25	0.6	3857	4	AAF85148	Aaf85148 DNA encod
	531	25	0.6	3868	4	ABL04755	Abl04755 Drosophil
	532	25	0.6	3884	4	ABL24570	Abl24570 Drosophil
	533	25	0.6	3973	4	ABL05717	Abl05717 Drosophil
	534	25	0.6	4067	4	ABL05962	Abl05962 Drosophil

c	535	25	0.6	4141	4	ABL05596	Abl05596 Drosophil
	536	25	0.6	4172	4	ABL13509	Abl13509 Drosophil
	537	25	0.6	4341	4	AAH49494	Aah49494 D. melano
	538	25	0.6	4510	4	ABL20209	Abl20209 Drosophil
	539	25	0.6	4621	2	AAV99919	Aav99919 Murine pC
	540	25	0.6	4785	4	ABL13743	Abl13743 Drosophil
	541	25	0.6	4826	4	ABL17497	Abl17497 Drosophil
	542	25	0.6	4949	4	ABL08615	Abl08615 Drosophil
	543	25	0.6	4984	4	ABL10778	Abl10778 Drosophil
	544	25	0.6	5125	2	AAQ29703	Aaq29703 IRS-1. 3/
	545	25	0.6	5138	4	ABL17438	Abl17438 Drosophil
	546	25	0.6	5175	2	AAZ00022	Aaz00022 os1 DNA n
	547	25	0.6	5257	6	ABV94246	Abv94246 Breast ca
	548	25	0.6	5286	4	ABL05391	Abl05391 Drosophil
c	549	25	0.6	5330	4	ABL13318	Abl13318 Drosophil
	550	25	0.6	5508	8	AAD57441	Aad57441 Fruit fly
	551	25	0.6	5618	4	ABL27786	Abl27786 Drosophil
	552	25	0.6	5697	2	AAZ00023	Aaz00023 os1 genom
	553	25	0.6	5718	4	ABL04853	Abl04853 Drosophil
	554	25	0.6	5718	4	AAS57077	Aas57077 cDNA enco
	555	25	0.6	5718	9	ADC35756	Adc35756 Drosophil
	556	25	0.6	5868	4	ABL04754	Abl04754 Drosophil
	557	25	0.6	5959	6	ABL66686	Abl66686 Lung canc
	558	25	0.6	5959	6	ABK84651	Abk84651 Human cDN
c	559	25	0.6	6039	4	ABL07844	Abl07844 Drosophil
	560	25	0.6	6101	4	ABL05716	Abl05716 Drosophil
	561	25	0.6	6110	4	ABL23890	Abl23890 Drosophil
	562	25	0.6	6333	7	AAD54620	Aad54620 Drosophil
	563	25	0.6	6523	3	AAC76548	Aac76548 Human ORF
	564	25	0.6	6545	2	AAZ00020	Aaz00020 os1+ DNA
	565	25	0.6	6912	4	ABL23828	Abl23828 Drosophil
	566	25	0.6	7005	4	ABL15355	Abl15355 Drosophil
c	567	25	0.6	7144	4	ABL08098	Abl08098 Drosophil
	568	25	0.6	7521	4	ABL18831	Abl18831 Drosophil
	569	25	0.6	7737	4	ABL02204	Abl02204 Drosophil
c	570	25	0.6	7766	4	ABL17496	Abl17496 Drosophil
c	571	25	0.6	7807	4	ABL17454	Abl17454 Drosophil
	572	25	0.6	8113	4	ABL06899	Abl06899 Drosophil
	573	25	0.6	8303	4	ABL05390	Abl05390 Drosophil
	574	25	0.6	9330	4	ABL13508	Abl13508 Drosophil
c	575	25	0.6	9400	4	ABL04852	Abl04852 Drosophil
c	576	25	0.6	9400	4	AAS57076	Aas57076 DNA encod
c	577	25	0.6	9400	9	ADC35755	Adc35755 Drosophil
	578	25	0.6	9673	4	ABL26438	Abl26438 Drosophil
	579	25	0.6	10072	4	ABL10828	Abl10828 Drosophil
	580	25	0.6	10620	4	ABL17327	Abl17327 Drosophil
	581	25	0.6	10868	4	ABL02358	Abl02358 Drosophil
	582	25	0.6	11133	4	ABL18830	Abl18830 Drosophil
	583	25	0.6	11961	4	ABL09792	Abl09792 Drosophil
	584	25	0.6	12748	4	ABL17326	Abl17326 Drosophil
c	585	25	0.6	13015	4	AAF75571	Aaf75571 Drosophil
	586	25	0.6	13075	4	ABL15354	Abl15354 Drosophil
	587	25	0.6	16969	4	ABL26778	Abl26778 Drosophil
	588	25	0.6	20990	4	ABL03102	Abl03102 Drosophil
	589	25	0.6	21379	4	ABL30162	Abl30162 Drosophil
	590	25	0.6	21409	4	ABL30140	Abl30140 Drosophil
c	591	25	0.6	21475	4	ABL08614	Abl08614 Drosophil
	592	25	0.6	22788	4	ABL20208	Abl20208 Drosophil
c	593	25	0.6	23306	4	ABL13338	Abl13338 Drosophil
c	594	25	0.6	28660	4	ABL03606	Abl03606 Drosophil
c	595	25	0.6	31449	4	ABL09172	Abl09172 Drosophil
	596	25	0.6	37322	4	ABL06898	Abl06898 Drosophil
	597	25	0.6	44242	4	ABL19930	Abl19930 Drosophil
	598	25	0.6	49431	4	ABL13742	Abl13742 Drosophil
c	599	25	0.6	171936	6	ABS56565	Abs56565 Human SUL
	600	24	0.6	109	4	AAI21491	Aai21491 Probe #11
	601	24	0.6	109	4	ABA66571	Aba66571 Human foe
	602	24	0.6	109	4	AAI46782	Aai46782 Probe #15
	603	24	0.6	109	4	ABA48659	Aba48659 Human bre
	604	24	0.6	109	4	ABA33636	Aba33636 Probe #12
	605	24	0.6	109	4	AAK40728	Aak40728 Human bon
	606	24	0.6	109	4	AAK14995	Aak14995 Human bra
	607	24	0.6	109	4	ABS40299	Abs40299 Human liv

	608	24	0.6	109	5	AAI07188	Aai07188 Probe #71
	609	24	0.6	109	6	ABS14687	Abs14687 Human gen
	610	24	0.6	253	4	AAI21383	Aai21383 Probe #11
	611	24	0.6	253	4	ABA66465	Aba66465 Human foe
	612	24	0.6	253	4	AAI46664	Aai46664 Probe #15
	613	24	0.6	253	4	ABA48552	Aba48552 Human bre
	614	24	0.6	253	4	ABA33525	Aba33525 Probe #11
	615	24	0.6	253	4	AAK40618	Aak40618 Human bon
	616	24	0.6	253	4	AAK14884	Aak14884 Human bra
	617	24	0.6	253	4	ABS40185	Abs40185 Human liv
	618	24	0.6	253	5	AAI07078	Aai07078 Probe #70
	619	24	0.6	253	6	ABS14585	Abs14585 Human gen
	620	24	0.6	414	3	AAA31507	Aaa31507 Plant mic
	621	24	0.6	427	2	AAV89806	Aav89806 EST clone
	622	24	0.6	455	4	AAI12184	Aai12184 Probe #21
	623	24	0.6	455	4	ABA53889	Aba53889 Human foe
	624	24	0.6	455	4	AAI33530	Aai33530 Probe #22
	625	24	0.6	455	4	ABA43438	Aba43438 Human bre
	626	24	0.6	455	4	ABA23636	Aba23636 Probe #21
	627	24	0.6	455	4	AAK27602	Aak27602 Human bon
	628	24	0.6	455	4	AAK02154	Aak02154 Human bra
	629	24	0.6	455	4	ABS27173	Abs27173 Human liv
	630	24	0.6	455	5	AAI02097	Aai02097 Probe #20
	631	24	0.6	455	6	ABS02070	Abs02070 Human gen
	632	24	0.6	472	4	AAI12295	Aai12295 Probe #22
	633	24	0.6	472	4	ABA53998	Aba53998 Human foe
	634	24	0.6	472	4	AAI33651	Aai33651 Probe #23
	635	24	0.6	472	4	ABA43548	Aba43548 Human bre
	636	24	0.6	472	4	ABA23750	Aba23750 Probe #22
	637	24	0.6	472	4	AAK27715	Aak27715 Human bon
	638	24	0.6	472	4	AAK02268	Aak02268 Human bra
	639	24	0.6	472	4	ABS27290	Abs27290 Human liv
	640	24	0.6	472	5	AAI02210	Aai02210 Probe #22
	641	24	0.6	472	6	ABS02175	Abs02175 Human gen
c	642	24	0.6	597	6	ABK33107	Abk33107 DNA encod
	643	24	0.6	970	4	ABL13259	Abl13259 Drosophil
c	644	24	0.6	1018	4	AAI22494	Aai22494 Probe #12
c	645	24	0.6	1018	4	ABA67570	Aba67570 Human foe
c	646	24	0.6	1018	4	AAI47786	Aai47786 Probe #16
c	647	24	0.6	1018	4	ABA49667	Aba49667 Human bre
c	648	24	0.6	1018	4	ABA34647	Aba34647 Probe #13
c	649	24	0.6	1018	4	AAK41738	Aak41738 Human bon
c	650	24	0.6	1018	4	AAK15992	Aak15992 Human bra
c	651	24	0.6	1018	4	ABS41331	Abs41331 Human liv
c	652	24	0.6	1018	5	AAI08180	Aai08180 Probe #81
c	653	24	0.6	1018	6	ABS15747	Abs15747 Human gen
	654	24	0.6	1235	4	ABL08663	Abl08663 Drosophil
	655	24	0.6	1273	7	ABZ36212	Abz36212 Human sec
	656	24	0.6	1329	4	ABL27023	Abl27023 Drosophil
	657	24	0.6	1350	4	ABL06633	Abl06633 Drosophil
	658	24	0.6	1417	3	AAZ33343	Aaz33343 Human sec
	659	24	0.6	1464	5	AAD08651	Aad08651 Mouse can
	660	24	0.6	1578	2	AAX19960	Aax19960 Human Tan
	661	24	0.6	1593	4	ABL30175	Abl30175 Drosophil
	662	24	0.6	1981	3	AAF14618	Aaf14618 Aspergill
	663	24	0.6	2104	4	ABL09709	Abl09709 Drosophil
	664	24	0.6	2138	4	ABL24940	Abl24940 Drosophil
	665	24	0.6	2240	4	ABL07261	Abl07261 Drosophil
	666	24	0.6	2295	5	AAS72219	Aas72219 DNA encod
	667	24	0.6	2295	5	AAS91825	Aas91825 DNA encod
	668	24	0.6	2408	4	ABL14691	Abl14691 Drosophil
c	669	24	0.6	2435	4	ABL24360	Abl24360 Drosophil
c	670	24	0.6	2485	4	ABL06632	Abl06632 Drosophil
	671	24	0.6	2656	4	ABL08375	Abl08375 Drosophil
	672	24	0.6	2706	4	ABL12001	Abl12001 Drosophil
	673	24	0.6	2879	4	ABL02847	Abl02847 Drosophil
	674	24	0.6	2909	5	AAS72220	Aas72220 DNA encod
	675	24	0.6	3042	4	ABL28445	Abl28445 Drosophil
	676	24	0.6	3099	4	ABL23050	Abl23050 Drosophil
	677	24	0.6	3104	4	ABL04869	Abl04869 Drosophil
	678	24	0.6	3216	4	ABL07525	Abl07525 Drosophil
	679	24	0.6	3423	6	AAD46318	Aad46318 Human EGF
	680	24	0.6	3570	4	ABL19381	Abl19381 Drosophil

c	681	24	0.6	3593	4	ABL30174 Abl30174 Drosophil
	682	24	0.6	3679	4	ABL04099 Abl04099 Drosophil
c	683	24	0.6	3820	4	ABL27022 Abl27022 Drosophil
	684	24	0.6	4110	4	ABL06447 Abl06447 Drosophil
	685	24	0.6	4251	4	ABL17365 Abl17365 Drosophil
	686	24	0.6	4443	4	ABL04821 Abl04821 Drosophil
	687	24	0.6	4455	7	ABT17054 Abt17054 Human MP2
	688	24	0.6	4656	4	ABL08374 Abl08374 Drosophil
c	689	24	0.6	4826	4	ABL07260 Abl07260 Drosophil
	690	24	0.6	4835	2	AAT37050 Aat37050 Drosophil
	691	24	0.6	4994	7	ACC44331 Acc44331 Gene enco
	692	24	0.6	5101	4	ABL28057 Abl28057 Drosophil
	693	24	0.6	5109	4	ABL17409 Abl17409 Drosophil
	694	24	0.6	5184	9	ADE25651 Ade25651 Human cDN
c	695	24	0.6	5215	4	ABL28444 Abl28444 Drosophil
	696	24	0.6	5227	4	ABL06175 Abl06175 Drosophil
	697	24	0.6	5337	4	ABL06529 Abl06529 Drosophil
	698	24	0.6	5407	4	ABL08765 Abl08765 Drosophil
	699	24	0.6	5448	4	ABL12000 Abl12000 Drosophil
	700	24	0.6	6033	4	ABL23051 Abl23051 Drosophil
	701	24	0.6	6186	4	ABL29885 Abl29885 Drosophil
	702	24	0.6	6223	4	ABL14690 Abl14690 Drosophil
	703	24	0.6	6307	4	ABL05643 Abl05643 Drosophil
	704	24	0.6	6325	4	AAK80005 Aak80005 Human imm
	705	24	0.6	6359	4	ABL04098 Abl04098 Drosophil
	706	24	0.6	6693	4	ABL02645 Abl02645 Drosophil
c	707	24	0.6	6915	4	ABL07524 Abl07524 Drosophil
	708	24	0.6	7101	4	ABL28056 Abl28056 Drosophil
	709	24	0.6	7243	4	ABL02521 Abl02521 Drosophil
	710	24	0.6	7278	4	ABL09708 Abl09708 Drosophil
c	711	24	0.6	7314	4	ABL17364 Abl17364 Drosophil
	712	24	0.6	7522	9	ADD18689 Add18689 Human dis
	713	24	0.6	7522	9	ADE71243 Ade71243 Novel hum
c	714	24	0.6	7887	4	ABL08662 Abl08662 Drosophil
	715	24	0.6	8100	4	ABL13276 Abl13276 Drosophil
c	716	24	0.6	8141	4	ABL04820 Abl04820 Drosophil
	717	24	0.6	8147	6	ABS73313 Abs73313 DNA encod
	718	24	0.6	8357	4	ABL06174 Abl06174 Drosophil
c	719	24	0.6	9105	4	ABL29884 Abl29884 Drosophil
	720	24	0.6	9165	4	ABL06528 Abl06528 Drosophil
	721	24	0.6	9555	7	ABX34542 Abx34542 Human mdd
c	722	24	0.6	9936	4	ABL13258 Abl13258 Drosophil
c	723	24	0.6	9939	4	ABL06446 Abl06446 Drosophil
	724	24	0.6	10558	4	ABL02846 Abl02846 Drosophil
	725	24	0.6	10979	4	ABL02644 Abl02644 Drosophil
c	726	24	0.6	11439	4	ABL14258 Abl14258 Drosophil
c	727	24	0.6	11613	4	ABL05642 Abl05642 Drosophil
c	728	24	0.6	17841	4	ABL04868 Abl04868 Drosophil
c	729	24	0.6	18977	4	ABL19380 Abl19380 Drosophil
	730	24	0.6	21748	4	ABL02520 Abl02520 Drosophil
	731	24	0.6	26767	4	ABL08654 Abl08654 Drosophil
	732	24	0.6	26960	4	ABL08712 Abl08712 Drosophil
	733	24	0.6	36336	4	ABL08764 Abl08764 Drosophil
c	734	24	0.6	40152	4	ABL17408 Abl17408 Drosophil
c	735	24	0.6	81440	6	ABQ76617 Abq76617 C. albica
c	736	24	0.6	106323	7	ABX14591 Abx14591 Human chl
c	737	24	0.6	106323	9	AAD58821 Aad58821 Human tra
c	738	23	0.6	23	2	AAZ40517 Aaz40517 Human STE
	739	23	0.6	23	2	AAZ40518 Aaz40518 Human STE
	740	23	0.6	23	6	ABL39570 Abl39570 Human can
	741	23	0.6	96	4	AAI27788 Aai27788 Probe #17
	742	23	0.6	96	4	ABA76100 Aba76100 Human foe
	743	23	0.6	96	4	AAI56760 Aai56760 Probe #25
	744	23	0.6	96	4	ABA40655 Aba40655 Probe #19
	745	23	0.6	96	4	AAK50771 Aak50771 Human bon
	746	23	0.6	96	4	AAK24774 Aak24774 Human bra
	747	23	0.6	96	4	ABS50361 Abs50361 Human liv
	748	23	0.6	96	6	ABS24250 Abs24250 Human gen
	749	23	0.6	165	4	AAF75506 Aaf75506 Polygluta
c	750	23	0.6	169	5	AAH82144 Aah82144 Rat diffe
c	751	23	0.6	216	7	ABX90681 Abx90681 Murine ge
	752	23	0.6	309	4	ABL13299 Abl13299 Drosophil
	753	23	0.6	324	4	ABL26619 Abl26619 Drosophil
c	754	23	0.6	351	9	ADB95017 Adb95017 A. thalia
	755	23	0.6	360	4	ABL25081 Abl25081 Drosophil
	756	23	0.6	362	8	ACL18963 Acl18963 DNA clone
c	757	23	0.6	466	3	AAC42435 Aac42435 Arabidops
	758	23	0.6	477	4	ABL07485 Abl07485 Drosophil
	759	23	0.6	486	4	AAF75507 Aaf75507 Polygluta
	760	23	0.6	562	5	AAS05415 Aas05415 Mammalian
	761	23	0.6	569	8	ACL18962 Acl18962 DNA clone
	762	23	0.6	577	4	AAI18861 Aai18861 Probe #87
	763	23	0.6	577	4	ABA63860 Aba63860 Human foe
	764	23	0.6	577	4	AAI43983 Aai43983 Probe #12
	765	23	0.6	577	4	ABA31040 Aba31040 Probe #95
	766	23	0.6	577	4	AAK38087 Aak38087 Human bon
	767	23	0.6	577	4	AAK12370 Aak12370 Human bra
	768	23	0.6	577	4	ABS37704 Abs37704 Human liv
	769	23	0.6	577	6	ABS12099 Abs12099 Human gen
	770	23	0.6	602	8	ACL18964 Acl18964 DNA clone
	771	23	0.6	616	4	AAI93709 Aai93709 Human pol
	772	23	0.6	762	4	ABL28195 Abl28195 Drosophil
c	773	23	0.6	790	6	ABL01400 Abl01400 Murine ap
	774	23	0.6	811	4	ABL10185 Abl10185 Drosophil
	775	23	0.6	921	4	ABL17215 Abl17215 Drosophil
	776	23	0.6	923	4	ABL10189 Abl10189 Drosophil
	777	23	0.6	927	6	ABQ94265 Abq94265 lovF gene
	778	23	0.6	927	6	ABN79906 Abn79906 Fungal ZB
	779	23	0.6	930	4	ABL21657 Abl21657 Drosophil
	780	23	0.6	939	4	ABL28527 Abl28527 Drosophil
	781	23	0.6	996	4	ABL12271 Abl12271 Drosophil
	782	23	0.6	1080	4	ABL22295 Abl22295 Drosophil
	783	23	0.6	1089	4	ABL18089 Abl18089 Drosophil
	784	23	0.6	1144	3	AAC59719 Aac59719 Human sec
	785	23	0.6	1353	7	ABT41973 Abt41973 Toxicity
	786	23	0.6	1353	9	ADB58275 Adb58275 Toxicity-
	787	23	0.6	1686	5	AAS74183 Aas74183 DNA encod
	788	23	0.6	1715	4	ABL27703 Abl27703 Drosophil
	789	23	0.6	1726	4	ABL13809 Abl13809 Drosophil
	790	23	0.6	1745	4	AAI29497 Aai29497 C883P det
	791	23	0.6	1745	6	AAI72629 Aai72629 CDX2 cDNA
	792	23	0.6	1745	7	ABZ33683 Abz33683 Human col
	793	23	0.6	1795	3	AAZ50065 Aaz50065 Soybean a
	794	23	0.6	1875	4	ABL27163 Abl27163 Drosophil
	795	23	0.6	1967	4	ABL07527 Abl07527 Drosophil
c	796	23	0.6	2062	6	ABN85850 Abn85850 Nucleotid
	797	23	0.6	2112	4	ABL13587 Abl13587 Drosophil
	798	23	0.6	2146	4	AAK94825 Aak94825 Human ful
	799	23	0.6	2160	4	AAI66703 Aai66703 A. gossyp
c	800	23	0.6	2210	4	ABL26748 Abl26748 Drosophil
c	801	23	0.6	2309	4	ABL13298 Abl13298 Drosophil
c	802	23	0.6	2324	4	ABL26618 Abl26618 Drosophil
	803	23	0.6	2331	4	ABL24927 Abl24927 Drosophil
	804	23	0.6	2339	4	ABL20445 Abl20445 Drosophil
	805	23	0.6	2405	5	AAS74184 Aas74184 DNA encod
	806	23	0.6	2453	4	ABL02487 Abl02487 Drosophil
	807	23	0.6	2529	4	ABL22299 Abl22299 Drosophil
c	808	23	0.6	2552	4	ABL15638 Abl15638 Drosophil
c	809	23	0.6	2552	4	ABL18372 Abl18372 Drosophil
c	810	23	0.6	2669	4	ABL07484 Abl07484 Drosophil
	811	23	0.6	2682	4	ABL25080 Abl25080 Drosophil
c	812	23	0.6	2756	4	ABL27702 Abl27702 Drosophil
c	813	23	0.6	2847	4	ABL28194 Abl28194 Drosophil
c	814	23	0.6	2860	2	AAX91533 Aax91533 Luteinizi
	815	23	0.6	2988	4	ABL03147 Abl03147 Drosophil
c	816	23	0.6	2997	7	ADA00895 Ada00895 Mouse ost
	817	23	0.6	3048	4	ABL24827 Abl24827 Drosophil
	818	23	0.6	3057	4	AAD08348 Aad08348 Human sec
	819	23	0.6	3125	4	ABL28526 Abl28526 Drosophil
	820	23	0.6	3236	4	ABL15799 Abl15799 Drosophil
	821	23	0.6	3263	4	ABL10403 Abl10403 Drosophil
c	822	23	0.6	3269	4	ABL30322 Abl30322 Drosophil
	823	23	0.6	3282	7	ADA70873 Ada70873 Rice gene
	824	23	0.6	3332	4	ABL20171 Abl20171 Drosophil
	825	23	0.6	3355	4	ABL06009 Abl06009 Drosophil
	826	23	0.6	3373	4	ABL17214 Abl17214 Drosophil

	827	23	0.6	3407	4	ABL18088	Abl18088 Drosophil
	828	23	0.6	3455	3	AAA96703	Aaa96703 Reporter
	829	23	0.6	3462	4	AAF25378	Aaf25378 Nucleotid
	830	23	0.6	3483	4	ABL14095	Abl14095 Drosophil
	831	23	0.6	3584	4	ABL07253	Abl07253 Drosophil
	832	23	0.6	3598	4	ABL27843	Abl27843 Drosophil
	833	23	0.6	3756	4	ABL08875	Abl08875 Drosophil
	834	23	0.6	3762	4	ABL14087	Abl14087 Drosophil
	835	23	0.6	3790	4	ABL14101	Abl14101 Drosophil
c	836	23	0.6	3791	4	ABL04336	Abl04336 Drosophil
	837	23	0.6	3801	4	ABL07597	Abl07597 Drosophil
	838	23	0.6	3951	4	ABL24893	Abl24893 Drosophil
	839	23	0.6	3959	4	ABL08865	Abl08865 Drosophil
c	840	23	0.6	3967	4	ABL07526	Abl07526 Drosophil
c	841	23	0.6	3998	4	ABL27162	Abl27162 Drosophil
c	842	23	0.6	4014	4	ABL21656	Abl21656 Drosophil
	843	23	0.6	4203	6	ABX97119	Abx97119 Human NOV
c	844	23	0.6	4229	6	ABK91051	Abk91051 Genomic D
	845	23	0.6	4233	4	ABL25099	Abl25099 Drosophil
	846	23	0.6	4331	4	ABL24926	Abl24926 Drosophil
	847	23	0.6	4356	2	AAQ37543	Aaq37543 Cardiac a
	848	23	0.6	4356	2	AAQ95540	Aaq95540 Cardiac a
	849	23	0.6	4387	6	ABN59837	Abn59837 Novel hum
	850	23	0.6	4400	4	ABL18665	Abl18665 Drosophil
	851	23	0.6	4409	4	ABL17895	Abl17895 Drosophil
	852	23	0.6	4629	4	ABL29279	Abl29279 Drosophil
c	853	23	0.6	4662	4	ABL13808	Abl13808 Drosophil
c	854	23	0.6	4705	4	ABL10184	Abl10184 Drosophil
	855	23	0.6	4916	4	ABL18373	Abl18373 Drosophil
	856	23	0.6	5021	4	ABL11783	Abl11783 Drosophil
	857	23	0.6	5054	4	ABA09272	Aba09272 Human dJ1
	858	23	0.6	5054	4	AAK52712	Aak52712 Human pol
c	859	23	0.6	5083	3	AAF22393	Aaf22393 Human sec
	860	23	0.6	5123	4	ABL27842	Abl27842 Drosophil
	861	23	0.6	5264	4	ABL22294	Abl22294 Drosophil
	862	23	0.6	5360	8	AAD56168	Aad56168 Drosophil
	863	23	0.6	5418	4	ABL16891	Abl16891 Drosophil
	864	23	0.6	5482	5	AAF63955	Aaf63955 Drosophil
	865	23	0.6	5484	4	ABL08155	Abl08155 Drosophil
	866	23	0.6	5564	4	ABL28214	Abl28214 Drosophil
	867	23	0.6	5710	4	ABL18813	Abl18813 Drosophil
c	868	23	0.6	5718	4	ABL04853	Abl04853 Drosophil
c	869	23	0.6	5718	4	AAS57077	Aas57077 cDNA enco
c	870	23	0.6	5718	9	ADC35756	Adc35756 Drosophil
	871	23	0.6	5720	2	AAT42117	Aat42117 Lats gene
	872	23	0.6	5720	3	AAZ51508	Aaz51508 Drosophil
	873	23	0.6	5720	8	AAD56167	Aad56167 Drosophil
	874	23	0.6	5910	4	AAK51728	Aak51728 Human pol
	875	23	0.6	5975	4	ABL12270	Abl12270 Drosophil
c	876	23	0.6	6034	4	ABL22516	Abl22516 Drosophil
	877	23	0.6	6129	4	ABL22298	Abl22298 Drosophil
c	878	23	0.6	6177	4	ABL14094	Abl14094 Drosophil
c	879	23	0.6	6284	4	ABL15798	Abl15798 Drosophil
c	880	23	0.6	6416	4	ABL13586	Abl13586 Drosophil
c	881	23	0.6	6416	4	ABL20170	Abl20170 Drosophil
	882	23	0.6	6594	4	ABL15639	Abl15639 Drosophil
	883	23	0.6	6693	4	ABL29278	Abl29278 Drosophil
	884	23	0.6	6776	4	ABL04337	Abl04337 Drosophil
c	885	23	0.6	6895	4	ABL10188	Abl10188 Drosophil
c	886	23	0.6	6919	4	ABL05593	Abl05593 Drosophil
	887	23	0.6	7008	4	ABL24826	Abl24826 Drosophil
	888	23	0.6	7179	4	ABL25098	Abl25098 Drosophil
	889	23	0.6	7394	4	ABL17894	Abl17894 Drosophil
	890	23	0.6	7529	4	ABL02486	Abl02486 Drosophil
	891	23	0.6	7614	4	ABL11782	Abl11782 Drosophil
	892	23	0.6	7969	4	ABL07263	Abl07263 Drosophil
c	893	23	0.6	8974	4	ABL14100	Abl14100 Drosophil
	894	23	0.6	8984	4	ABL24892	Abl24892 Drosophil
c	895	23	0.6	9283	4	ABL14086	Abl14086 Drosophil
	896	23	0.6	9400	4	ABL04852	Abl04852 Drosophil
	897	23	0.6	9400	4	AAS57076	Aas57076 DNA encod
	898	23	0.6	9400	9	ADC35755	Adc35755 Drosophil
	899	23	0.6	9907	4	ABL08864	Abl08864 Drosophil

c	900	23	0.6	10194	4	ABL08154	Abl08154 Drosophil
	901	23	0.6	10230	4	ABL15505	Abl15505 Drosophil
	902	23	0.6	11029	4	ABL20444	Abl20444 Drosophil
	903	23	0.6	11693	4	ABL30327	Abl30327 Drosophil
	904	23	0.6	12099	4	ABL16890	Abl16890 Drosophil
c	905	23	0.6	12155	4	ABL06990	Abl06990 Drosophil
c	906	23	0.6	12260	4	ABL08874	Abl08874 Drosophil
	907	23	0.6	13531	4	ABL07252	Abl07252 Drosophil
	908	23	0.6	15405	4	ABL03146	Abl03146 Drosophil
c	909	23	0.6	15648	4	ABL30326	Abl30326 Drosophil
c	910	23	0.6	15923	4	ABL07596	Abl07596 Drosophil
	911	23	0.6	16962	4	ABL10402	Abl10402 Drosophil
c	912	23	0.6	18506	4	ABL05592	Abl05592 Drosophil
	913	23	0.6	18748	4	ABL05146	Abl05146 Drosophil
	914	23	0.6	19399	4	ABL06008	Abl06008 Drosophil
	915	23	0.6	20245	4	ABL15504	Abl15504 Drosophil
	916	23	0.6	20892	4	ABL22310	Abl22310 Drosophil
	917	23	0.6	30143	4	ABL18664	Abl18664 Drosophil
	918	23	0.6	37687	4	ABL29366	Abl29366 Drosophil
	919	23	0.6	44577	8	ADA03038	Ada03038 Human ROR
	920	23	0.6	44577	8	ADA66322	Ada66322 Human ROR
	921	23	0.6	44577	9	ADB72776	Adb72776 Human ROR
c	922	23	0.6	56686	4	ABL18488	Abl18488 Drosophil
	923	22	0.6	25	9	ADC38187	Adc38187 Human AML
	924	22	0.6	25	9	ADC38189	Adc38189 Human AML
	925	22	0.6	25	9	ADC38186	Adc38186 Human AML
	926	22	0.6	25	9	ADC38188	Adc38188 Human AML
	927	22	0.6	30	7	ABZ81777	Abz81777 Huntingto
c	928	22	0.6	52	7	ABZ81774	Abz81774 Oligonucl
c	929	22	0.6	52	7	ABZ81756	Abz81756 Huntingto
	930	22	0.6	138	3	AAA15871	Aaa15871 DNA encod
c	931	22	0.6	172	7	ABQ80313	Abq80313 Human lut
c	932	22	0.6	172	7	ACC83027	Acc83027 Human lut
c	933	22	0.6	196	3	AAZ99412	Aaz99412 Trans-spl
c	934	22	0.6	196	6	ABQ73501	Abq73501 Pre-trans
c	935	22	0.6	267	2	AAZ31736	Aaz31736 Human CG
c	936	22	0.6	267	2	AAZ31735	Aaz31735 Human CG
	937	22	0.6	294	3	AAA15879	Aaa15879 DNA encod
	938	22	0.6	300	2	AAZ13093	Aaz13093 Human gen
	939	22	0.6	316	4	AAI20017	Aai20017 Probe #99
	940	22	0.6	316	4	ABA65045	Aba65045 Human foe
	941	22	0.6	316	4	AAI45215	Aai45215 Probe #13
	942	22	0.6	316	4	ABA47161	Aba47161 Human bre
	943	22	0.6	316	4	ABA32153	Aba32153 Probe #10
	944	22	0.6	316	4	AAK39207	Aak39207 Human bon
	945	22	0.6	316	4	AAK13469	Aak13469 Human bra
	946	22	0.6	316	4	ABS38793	Abs38793 Human liv
	947	22	0.6	316	5	AAI05725	Aai05725 Probe #57
	948	22	0.6	316	6	ABS13291	Abs13291 Human gen
	949	22	0.6	358	2	AAV87567	Aav87567 EST clone
	950	22	0.6	362	3	AAA15880	Aaa15880 DNA encod
	951	22	0.6	387	4	ABL28401	Abl28401 Drosophil
	952	22	0.6	387	9	ADC37658	Adc37658 Human ang
	953	22	0.6	396	6	ABQ98092	Abq98092 Mouse ES
c	954	22	0.6	399	3	AAZ94093	Aaz94093 Haematopo
c	955	22	0.6	426	1	AAN60524	Aan60524 Sequence
	956	22	0.6	436	4	AAI10775	Aai10775 Probe #70
	957	22	0.6	436	4	ABA52425	Aba52425 Human foe
	958	22	0.6	436	4	AAI32033	Aai32033 Probe #71
	959	22	0.6	436	4	ABA22220	Aba22220 Probe #68
	960	22	0.6	436	4	AAK26145	Aak26145 Human bon
	961	22	0.6	436	4	AAK00694	Aak00694 Human bra
	962	22	0.6	436	4	ABS25735	Abs25735 Human liv
	963	22	0.6	436	5	AAI00701	Aai00701 Probe #69
	964	22	0.6	436	6	ABS00730	Abs00730 Human gen
	965	22	0.6	500	9	ADC37673	Adc37673 Human ang
c	966	22	0.6	503	7	ABQ80312	Abq80312 Full leng
c	967	22	0.6	503	7	ACC83026	Acc83026 Human lut
c	968	22	0.6	508	2	AAZ31752	Aaz31752 Human CG
	969	22	0.6	512	9	ADE81405	Ade81405 Arabidops
	970	22	0.6	526	6	ABI99619	Abi99619 Mouse isc
c	971	22	0.6	539	2	AAV04780	Aav04780 Human cho
c	972	22	0.6	539	2	AAV18517	Aav18517 Human bet

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c 973     22    0.6    539  2  AAV04779              Aav04779 Human cho
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c 975     22    0.6    539  3  AAA73833              Aaa73833 Human cho
  976     22    0.6    543  2  AAQ23092              Aaq23092 Antigen t
  977     22    0.6    549  4  AAD08808              Aad08808 Human sin
c 978     22    0.6    575  2  AAT03240              Aat03240 Human CG
c 979     22    0.6    575  4  AAS08507              Aas08507 DNA encod
c 980     22    0.6    575  4  AAD08807              Aad08807 Human sin
c 981     22    0.6    587  2  AAZ31734              Aaz31734 Human cho
c 982     22    0.6    595  5  AAS80859              Aas80859 DNA encod
  983     22    0.6    627  4  ABL23497              Abl23497 Drosophil
  984     22    0.6    633  4  ABL27793              Abl27793 Drosophil
  985     22    0.6    686  6  ABS77041              Abs77041 Frog embr
  986     22    0.6    717  4  AAD08788              Aad08788 Human sin
  987     22    0.6    717  4  AAD08800              Aad08800 Human sin
  988     22    0.6    717  4  AAD08798              Aad08798 Human sin
  989     22    0.6    718  4  AAD08790              Aad08790 Human sin
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c 992     22    0.6    725  2  AAZ31750              Aaz31750 Human CG
  993     22    0.6    726  4  AAD08796              Aad08796 Human sin
  994     22    0.6    726  4  AAD08794              Aad08794 Human sin
c 995     22    0.6    729  2  AAZ31748              Aaz31748 Human CG
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c 997     22    0.6    729  2  AAZ31749              Aaz31749 Human CG
  998     22    0.6    731  6  ABA90389              Aba90389 Drosophil
c 999     22    0.6    743  2  AAT03233              Aat03233 Single ch
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ALIGNMENTS

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RESULT 1
ADE34151
ID   ADE34151 standard; DNA; 3951 BP.
XX
AC   ADE34151;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human DNA encoding misshapen/NIKs-related kinase, Mink3a.
XX
KW   Human; misshapen/NIKs-related kinase; Mink3a; ds; antiinflammatory;
KW   immunosuppressive; cytostatic; germinal centre kinase;
KW   c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;
KW   growth factor induced-ERK activation; proliferation;
KW   cell proliferation disorder; cell survival;
KW   intracellular signal transduction; apoptosis; morphological change;
KW   cell migration; gene therapy; inflammatory disease; autoimmune disease;
KW   immunodeficiency; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7..3945
FT                   /*tag=  a
FT                   /product= "Mink3a"
XX
PN   US2003077597-A1.
XX
PD   24-APR-2003.
XX
PF   19-OCT-2001; 2001US-00029115.
XX
PR   19-OCT-2001; 2001US-00029115.
XX
PA   (LUOY/) LUO Y.
PA   (FUCA/) FU C A.
PA   (SHEN/) SHEN M.
XX
PI   Luo Y,  Fu CA,  Shen M;
XX
DR   WPI; 2003-635076/60.
DR   P-PSDB; ADE34150.
XX
PT   New misshapen/NIKs-related kinase nucleic acids and proteins useful in
PT   gene therapy and for treating disorders, e.g. acute and chronic
PT   inflammatory diseases.
XX
PS   Claim 3; SEQ ID NO 1; 53pp; English.
XX
CC   The invention relates to a recombinant nucleic acid capable of
CC   hybridising to a Human DNA encoding misshapen/NIKs-related kinase
CC   (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as
CC   ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or
CC   their complements. Also included are a recombinant polypeptide at least
CC   95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,
CC   ADE34152 and ADE34154), screening for a candidate bioactive agent capable
CC   of modulating c-JUN N-terminal kinase (JNK) or extracellular signal
CC   response kinase (ERK) phosphorylation or activity, screening for a
CC   candidate bioactive agent capable of modulating growth factor induced-ERK
CC   activation in a mammalian cell, screening for a candidate bioactive agent
CC   capable of modulating proliferation in a mammalian cell, diagnosing a
CC   mammalian cell proliferation disorder, a medicament for treating a
CC   mammalian cell proliferation disorder and screening for a candidate agent
CC   capable of modulating cell survival. The MINK3 (misshapen/NIKs-related
CC   kinase) nucleic acids are useful in the modulation of intracellular
CC   signal transduction, cell proliferation, apoptosis, morphological change
CC   and migration of mammalian cells. MINK3 nucleic acids and proteins are
CC   specifically useful in gene therapy, and for treating, preventing or
CC   diagnosing acute and chronic inflammatory diseases, autoimmune diseases
CC   and diseases characterised by immunodeficiency. The compositions may also
CC   be used to treat MINK3 dysfunction related disorders, e.g. cancer. The
CC   nucleotide sequences may also be used as hybridisation probes, in
CC   chromosome and gene mapping, and in generating antisense RNA and DNA. The
CC   present sequence encodes Mink3a.
XX
SQ   Sequence 3951 BP; 928 A; 1196 C; 1199 G; 628 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 3951;  DB 9;  Length 3951;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3951;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCCTTATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 CGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC 180
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Qy        241 CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGAT 300
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Qy        301 GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG 360
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Db        301 GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG 360

Qy        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420
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Db        361 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC 420

Qy        421 AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT 480
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Db        421 AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT 480
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Qy        481 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG 540
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Db        481 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG 540

Qy        541 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG 600
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Db        541 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG 600

Qy        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660
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Db        601 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT 660

Qy        661 CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 720

Qy        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGCGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG 780

Qy        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA 840

Qy        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC 900

Qy        901 CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG 960

Qy        961 ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG 1020

Qy       1021 CCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTC 1080

Qy       1081 CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAG 1140

Qy       1141 CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA 1200

Qy       1201 GAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG 1260

Qy       1261 CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG 1320

Qy       1321 GAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG 1380

Qy       1381 CAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCC 1440

Qy       1441 CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCT 1500

Qy       1501 GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC 1560

Qy       1561 TGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC 1620

Qy       1621 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCC 1680

Qy       1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG 1740

Qy       1741 CACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC 1800

Qy       1801 CCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGC 1860

Qy       1861 CAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC 1920

Qy       1921 CGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCC 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCC 1980

Qy       1981 CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGC 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGC 2040

Qy       2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT 2100

Qy       2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGG 2160

Qy       2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC 2220

Qy       2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC 2280

Qy       2281 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGG 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGG 2340

Qy       2341 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAG 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAG 2400

Qy       2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG 2460

Qy       2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGG 2520

Qy       2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG 2580

Qy       2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG 2640

Qy       2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2641 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA 2700

Qy       2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG 2760

Qy       2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG 2820

Qy       2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG 2880

Qy       2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAAT 2940

Qy       2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTC 3000

Qy       3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC 3060

Qy       3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA 3120

Qy       3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA 3180

Qy       3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGAC 3240

Qy       3241 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC 3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC 3300

Qy       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 TACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG 3360

Qy       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC 3420

Qy       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG 3480

Qy       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTAT 3540

Qy       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC 3600

Qy       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660

Qy       3661 ACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTG 3720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 ACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTG 3720

Qy       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780

Qy       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840

Qy       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA 3900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA 3900

Qy       3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
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RESULT 2
ADE34155
ID   ADE34155 standard; DNA; 4033 BP.
XX
AC   ADE34155;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human DNA encoding misshapen/NIKs-related kinase, Mink3c.
XX
KW   Human; misshapen/NIKs-related kinase; Mink3c; ds; antiinflammatory;
KW   immunosuppressive; cytostatic; germinal centre kinase;
KW   c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;
KW   growth factor induced-ERK activation; proliferation;
KW   cell proliferation disorder; cell survival;
KW   intracellular signal transduction; apoptosis; morphological change;
KW   cell migration; gene therapy; inflammatory disease; autoimmune disease;
KW   immunodeficiency; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             203..4033
FT                   /*tag=  a
FT                   /product= "Mink3c"
XX
PN   US2003077597-A1.
XX
PD   24-APR-2003.
XX
PF   19-OCT-2001; 2001US-00029115.
XX
PR   19-OCT-2001; 2001US-00029115.
XX
PA   (LUOY/) LUO Y.
PA   (FUCA/) FU C A.
PA   (SHEN/) SHEN M.
XX
PI   Luo Y,  Fu CA,  Shen M;
XX
DR   WPI; 2003-635076/60.
DR   P-PSDB; ADE34154.
XX
PT   New misshapen/NIKs-related kinase nucleic acids and proteins useful in
PT   gene therapy and for treating disorders, e.g. acute and chronic
PT   inflammatory diseases.
XX
PS   Claim 3; SEQ ID NO 5; 53pp; English.
XX
CC   The invention relates to a recombinant nucleic acid capable of
CC   hybridising to a Human DNA encoding misshapen/NIKs-related kinase
CC   (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as
CC   ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or
CC   their complements. Also included are a recombinant polypeptide at least
CC   95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,
CC   ADE34152 and ADE34154), screening for a candidate bioactive agent capable
CC   of modulating c-JUN N-terminal kinase (JNK) or extracellular signal
CC   response kinase (ERK) phosphorylation or activity, screening for a
CC   candidate bioactive agent capable of modulating growth factor induced-ERK
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CC   activation in a mammalian cell, screening for a candidate bioactive agent
CC   capable of modulating proliferation in a mammalian cell, diagnosing a
CC   mammalian cell proliferation disorder, a medicament for treating a
CC   mammalian cell proliferation disorder and screening for a candidate agent
CC   capable of modulating cell survival. The MINK3 (misshapen/NIKs-related
CC   kinase) nucleic acids are useful in the modulation of intracellular
CC   signal transduction, cell proliferation, apoptosis, morphological change
CC   and migration of mammalian cells. MINK3 nucleic acids and proteins are
CC   specifically useful in gene therapy, and for treating, preventing or
CC   diagnosing acute and chronic inflammatory diseases, autoimmune diseases
CC   and diseases characterised by immunodeficiency. The compositions may also
CC   be used to treat MINK3 dysfunction related disorders, e.g. cancer. The
CC   nucleotide sequences may also be used as hybridisation probes, in
CC   chromosome and gene mapping, and in generating antisense RNA and DNA. The
CC   present sequence encodes Mink3c.
XX
SQ   Sequence 4033 BP; 959 A; 1213 C; 1210 G; 651 T; 0 U; 0 Other;

  Query Match             48.3%;  Score 1907;  DB 9;  Length 4033;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2197;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy       1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1836 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1895

Qy       1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1896 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1955

Qy       1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1956 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 2015

Qy       1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2016 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2075

Qy       1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2076 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2135

Qy       2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2136 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2195

Qy       2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2196 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2255

Qy       2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2256 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2315

Qy       2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2316 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2375

Qy       2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2376 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2435

Qy       2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2436 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2495

Qy       2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2496 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2555

Qy       2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
              |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       2556 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2612

Qy       2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2613 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2672

Qy       2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2673 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2732

Qy       2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2733 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2792

Qy       2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2793 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2852

Qy       2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2853 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2912

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2913 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2972

Qy       2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2973 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 3032

Qy       2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3033 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3092

Qy       3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3093 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3152

Qy       3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3153 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3212

Qy       3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3213 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3272

Qy       3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3273 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3332

Qy       3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3333 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3392

Qy       3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3393 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3452

Qy       3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3453 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3512

Qy       3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3513 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3572

Qy       3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       3573 TCTATGGCTCCAGTGCTGGCTTCCATGCTGCGGATGTCGACTCGGGGAACAGCTATGACA 3632

Qy       3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3633 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3692
```

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Qy       3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3693 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3752

Qy       3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3753 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3812

Qy       3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3813 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3872

Qy       3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3873 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3932

Qy       3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3933 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3992

Qy       3905 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||||
Db       3993 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4033
```

```
RESULT 3
AAL48627
ID   AAL48627 standard; cDNA; 3888 BP.
XX
AC   AAL48627;
XX
DT   11-OCT-2002  (first entry)
XX
DE   Human insulin receptor signaling modifier cDNA SEQ ID NO: 37.
XX
KW   Human; insulin receptor signaling; insulin receptor signaling modifier;
KW   ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200255664-A2.
XX
PD   18-JUL-2002.
XX
PF   11-JAN-2002; 2002WO-US001048.
XX
PR   12-JAN-2001; 2001US-0261226P.
PR   12-JAN-2001; 2001US-0261303P.
PR   12-JAN-2001; 2001US-0261304P.
PR   12-JAN-2001; 2001US-0261335P.
PR   12-JAN-2001; 2001US-0261336P.
PR   12-JAN-2001; 2001US-0261361P.
PR   12-JAN-2001; 2001US-0261456P.
PR   12-JAN-2001; 2001US-0261457P.
PR   12-JAN-2001; 2001US-0261458P.
PR   12-JAN-2001; 2001US-0261459P.
PR   12-JAN-2001; 2001US-0261461P.
PR   12-JAN-2001; 2001US-0261518P.
PR   12-JAN-2001; 2001US-0261531P.
PR   12-JAN-2001; 2001US-0261532P.
PR   12-JAN-2001; 2001US-0261589P.
PR   12-JAN-2001; 2001US-0261590P.
PR   12-JAN-2001; 2001US-0261694P.
PR   12-JAN-2001; 2001US-0261695P.
PR   12-JAN-2001; 2001US-0261697P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Seidel-Dugan C,  Ferguson KC,  Kidd T;
XX
DR   WPI; 2002-599664/64.
DR   P-PSDB; AAO18508.
XX
PT   Identifying an insulin receptor signaling modulator, useful as drug
PT   targets for treating diabetes or metabolic disorders, comprises
PT   contacting an assay system comprising insulin receptor signaling
PT   modifiers with a test agent.
XX
PS   Disclosure; Page 118-120; 232pp; English.
XX
CC   The present invention relates to a method of identifying a candidate
CC   insulin receptor (INR) signaling modulating agent, involving contacting
CC   an assay system comprising an insulin receptor signaling modifier (ISM)
CC   polypeptide or nucleic acid with a test agent, and detecting a test agent
CC   -biased activity of the assay system. The method is useful for
CC   identifying candidate INR signaling modulating agents. ISM genes may be
CC   used as drug targets for treatment of disorders related to INR signaling
CC   such as diabetes or metabolic syndrome. ISM nucleic acids and
CC   polypeptides are useful for identifying and testing agents that modulate
CC   ISM function and for other applications related to the involvement of ISM
CC   in INR signaling, and for identifying subjects having a predisposition to
CC   such diseases associated with INR signaling. The present sequence is an
CC   ISM coding sequence described in the exemplification of the invention
XX
SQ   Sequence 3888 BP; 917 A; 1168 C; 1182 G; 621 T; 0 U; 0 Other;

  Query Match             43.1%;  Score 1701;  DB 6;  Length 3888;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1801;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       2143 AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCA 2202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 AGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCA 2145

Qy       2203 GCCTCTCACGGGCACCTCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCC 2262
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2146 GCCTCTCACGGGCACCTCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCC 2205

Qy       2263 TCCAAACTGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCAC 2322
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2206 TCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCAC 2265

Qy       2323 CGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 CGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG 2325

Qy       2383 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 GCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGC 2385

Qy       2443 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 AGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 2445

Qy       2503 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 GGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAG 2505

Qy       2563 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 GAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCT 2565

Qy       2623 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 GAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTG 2625

Qy       2683 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 GTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGAT 2685

Qy       2743 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 GGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACG 2745

Qy       2803 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2746 ATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACA 2805

Qy       2863 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2806 GCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGT 2865

Qy       2923 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2866 TCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGG 2925

Qy       2983 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 3042
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2926 AAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTG 2985

Qy       3043 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2986 CTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTAT 3045

Qy       3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3046 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3105

Qy       3163 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3106 ATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAAC 3165

Qy       3223 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3166 AAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGAC 3225

Qy       3283 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3226 ATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATC 3285

Qy       3343 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3286 GCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATG 3345

Qy       3403 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3346 GCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAG 3405

Qy       3463 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3406 GAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTC 3465

Qy       3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3466 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCC 3525

Qy       3583 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3526 CATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGAC 3585

Qy       3643 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3586 GAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGG 3645

Qy       3703 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3646 GAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAA 3705

Qy       3763 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3706 GCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGA 3765

Qy       3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3766 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGC 3825

Qy       3883 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3826 TCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGG 3885

Qy       3943 TGA 3945
              |||
Db       3886 TGA 3888
```

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RESULT 4
AAZ40485
ID   AAZ40485 standard; DNA; 4133 BP.
XX
AC   AAZ40485;
XX
DT   18-FEB-2000  (first entry)
XX
DE   Human ZC3 DNA.
XX
KW   Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
KW   antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
KW   neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW   vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7;
KW   ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist;
KW   antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW   inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW   rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW   myocardial infarction; cardiovascular disease; stroke; renal failure;
KW   oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW   amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW   ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW   mesangial disorder; growth regulation; wound healing; T cell activation;
KW   immunosuppressant; ss.
XX
OS   Homo sapiens.
XX
PN   WO9953036-A2.
XX
PD   21-OCT-1999.
XX
PF   13-APR-1999;   99WO-US008150.
XX
PR   14-APR-1998;   98US-0081784P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman G,  Martinez R,  Whyte D;
XX
DR   WPI; 1999-611301/52.
DR   P-PSDB; AAY55933.
XX
PT   Novel kinase-related polypeptides used for the diagnosis and treatment of
PT   kinase-related diseases and disorders.
XX
PS   Disclosure; Page 267-269; 387pp; English.
XX
CC   This sequence represents the coding sequence for a novel STE20-related
CC   protein kinase. The invention relates to nucleic acid molecule encoding a
CC   kinase polypeptide selected from STLK2, STLK3, STLK4, STLK5, STLK6,
CC   STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The
CC   proteins are used to identify agonists and antagonists, and to raise
CC   antibodies. The polynucleotides are useful in gene therapy protocols. The
CC   polynucleotides, polypeptides, antibodies, antagonists and agonists may
CC   be used to treat diseases such as immune-related disorders and diseases
CC   (e.g. rheumatoid arthritis, artherosclerosis, chronic inflammatory bowel
CC   disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis,
CC   atherosclerosis, rhinitis, autoimmunity, and organ transplantation,
CC   chronic inflammatory pelvic disease, multiple sclerosis, organ
CC   transplantation, myocardial infarction, cardiovascular disease, stroke,
CC   renal failure, oxidative stress-related neurodegenerative disorders (e.g.
CC   amylotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome),
CC   cancer, cardiomyopathies, ischemic disorders, inflammatory disorders,
CC   diabetes mellitus, fibrotic and mesangial disorders. The proteins may
CC   also be useful for cell growth regulation (e.g. in wound healing), T cell
CC   activation, mitosis control, and as immunosuppressants
XX
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SQ   Sequence 4133 BP; 960 A; 1258 C; 1246 G; 669 T; 0 U; 0 Other;

  Query Match             42.9%;  Score 1694;  DB 2;  Length 4133;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2084;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy   1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1784 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1843

Qy   1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1844 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1903

Qy   1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCAGCCTGGGTCCGCC 1924
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1904 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCAGCCTGGGTCCGCC 1963

Qy   1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1964 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2023

Qy   1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2024 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2083

Qy   2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2084 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2143

Qy   2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2144 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2203

Qy   2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2204 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2263

Qy   2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
          ||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||
Db   2264 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2323

Qy   2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2324 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2383

Qy   2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2384 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2443

Qy   2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2444 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2503

Qy   2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
          |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db   2504 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2560

Qy   2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2561 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2620

Qy   2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2621 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2680

Qy   2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2681 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2740

Qy   2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2741 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2800

Qy   2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2801 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2860

Qy   2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2861 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2920

Qy   2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2921 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2980

Qy   2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2981 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3040

Qy   3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3041 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3100

Qy   3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3101 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3160

Qy   3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3161 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3220

Qy   3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   3221 ACAAACTGCGGGTGTATTACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3280

Qy   3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3281 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3340

Qy   3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3341 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3400

Qy   3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3401 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3460

Qy   3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3461 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3520

Qy   3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3521 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3580

Qy   3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3581 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3640

Qy   3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3641 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3700

Qy   3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3701 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3760

Qy   3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3761 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3820

Qy   3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTC 3834
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3821 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTC 3870
```

```
RESULT 5
AAK52286
ID   AAK52286 standard; cDNA; 4863 BP.
XX
AC   AAK52286;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 831.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM79153.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 1; Page 2771-2777; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 4863 BP; 1072 A; 1509 C; 1447 G; 835 T; 0 U; 0 Other;

  Query Match             42.7%;  Score 1689;  DB 4;  Length 4863;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1739;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 244

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 304

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 364

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 424

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 484

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 544

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 604

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 664

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 724

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 784

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1085 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1144

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1384
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Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1685 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1744

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924
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RESULT 6
AAL48626
ID   AAL48626 standard; cDNA; 4863 BP.
XX
AC   AAL48626;
XX
DT   11-OCT-2002  (first entry)
XX
DE   Human insulin receptor signaling modifier cDNA SEQ ID NO: 35.
XX
KW   Human; insulin receptor signaling; insulin receptor signaling modifier;
KW   ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200255664-A2.
XX
PD   18-JUL-2002.
XX
PF   11-JAN-2002; 2002WO-US001048.
XX
PR   12-JAN-2001; 2001US-0261226P.
PR   12-JAN-2001; 2001US-0261303P.
PR   12-JAN-2001; 2001US-0261304P.
PR   12-JAN-2001; 2001US-0261335P.
PR   12-JAN-2001; 2001US-0261336P.
PR   12-JAN-2001; 2001US-0261361P.
PR   12-JAN-2001; 2001US-0261456P.
PR   12-JAN-2001; 2001US-0261457P.
PR   12-JAN-2001; 2001US-0261458P.
PR   12-JAN-2001; 2001US-0261459P.
PR   12-JAN-2001; 2001US-0261461P.
PR   12-JAN-2001; 2001US-0261518P.
PR   12-JAN-2001; 2001US-0261531P.
PR   12-JAN-2001; 2001US-0261532P.
PR   12-JAN-2001; 2001US-0261589P.
PR   12-JAN-2001; 2001US-0261590P.
PR   12-JAN-2001; 2001US-0261694P.
PR   12-JAN-2001; 2001US-0261695P.
PR   12-JAN-2001; 2001US-0261697P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Seidel-Dugan C,  Ferguson KC,  Kidd T;
XX
DR   WPI; 2002-599664/64.
DR   P-PSDB; AAO18507.
XX
PT   Identifying an insulin receptor signaling modulator, useful as drug
PT   targets for treating diabetes or metabolic disorders, comprises
PT   contacting an assay system comprising insulin receptor signaling
PT   modifiers with a test agent.
XX
PS   Disclosure; Page 110-112; 232pp; English.
XX
CC   The present invention relates to a method of identifying a candidate
CC   insulin receptor (INR) signaling modulating agent, involving contacting
CC   an assay system comprising an insulin receptor signaling modifier (ISM)
CC   polypeptide or nucleic acid with a test agent, and detecting a test agent
CC   -biased activity of the assay system. The method is useful for
CC   identifying candidate INR signaling modulating agents. ISM genes may be
CC   used as drug targets for treatment of disorders related to INR signaling
CC   such as diabetes or metabolic syndrome. ISM nucleic acids and
CC   polypeptides are useful for identifying and testing agents that modulate
CC   ISM function and for other applications related to the involvement of ISM
CC   in INR signaling, and for identifying subjects having a predisposition to
CC   such diseases associated with INR signaling. The present sequence is an
CC   ISM coding sequence described in the exemplification of the invention
XX
SQ   Sequence 4863 BP; 1072 A; 1509 C; 1447 G; 835 T; 0 U; 0 Other;

  Query Match             42.7%;  Score 1689;  DB 6;  Length 4863;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1739;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 244

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 304

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 364

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 424

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 484

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 544

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 604

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 664

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          665 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 724

Qy          547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          725 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 784

Qy          607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy          667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy          727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy          787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy          847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy          907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1085 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1144

Qy          967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy         1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy         1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy         1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1325 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1384

Qy         1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy         1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy         1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
                |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db         1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy         1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy         1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

Qy         1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1685 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1744

Qy         1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy         1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy         1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924


RESULT 7
AAL61132
ID   AAL61132 standard; DNA; 4863 BP.
XX
AC   AAL61132;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Human MINK2 antisense transcript DNA.
XX
KW   Transcript; therapy; systemic lupus erythematosus; inflammatory disease;
KW   cardiovascular; gastrointestinal disease; atherosclerosis; skin disease;
KW   rheumatoid disorder; autoimmune disease; diabetes; multiple sclerosis;
KW   cancer; neuroprotective; human; MINK2; antisense; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003046220-A1.
XX
PD   05-JUN-2003.
XX
PF   11-NOV-2002; 2002WO-IL000904.
XX
PR   26-NOV-2001; 2001US-00993398.
PR   24-JUL-2002; 2002US-00201605.
XX
PA   (COMP-) COMPUGEN LTD.
XX
PI   Levanon E,  Pollock S,  Nemzer S,  Shoshan A,  Khosravi R,  Walach S;
PI   Levine Z,  Bernstein J,  Dahari D,  Wasserman A,  Rotman G;
XX
DR   WPI; 2003-505211/47.
XX
PT   Identifying putative naturally occurring antisense transcripts, useful
PT   for quantifying gene expression levels, and detecting and/or treating
PT   inflammatory, autoimmune or cardiovascular diseases, diabetes, arthritis
PT   and cancer.
XX
PS   Example; Page 214-216; 230pp; English.
XX
CC   The invention relates to methods and systems for identifying naturally
CC   occurring antisense transcripts. The method is useful for quantifying
CC   gene expression levels and for detecting, quantifying or specifically
CC   regulating antisense and respective sense transcripts thereby enabling
CC   detection and treatment of a wide range or disorders, such as systemic
CC   lupus erythematosus, inflammatory diseases, rheumatoid disorders,
CC   autoimmune diseases, diabetes, multiple sclerosis, cardiovascular and
CC   gastrointestinal diseases, atherosclerosis, skin diseases and cancer. The
CC   present sequence is human MINK2 transcript DNA used to illustrate the
CC   method of the invention
XX
SQ   Sequence 4863 BP; 1072 A; 1509 C; 1447 G; 835 T; 0 U; 0 Other;

  Query Match             42.7%;  Score 1689;  DB 8;  Length 4863;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1739;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy            7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          185 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 244

Qy           67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 304

Qy         127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 364

Qy         187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         365 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 424

Qy         247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         425 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 484

Qy         307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         485 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 544

Qy         367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         545 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 604

Qy         427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         605 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 664

Qy         487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         665 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 724

Qy         547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         725 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 784

Qy         607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy         667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy         727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy         787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy         847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy         907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1085 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1144

Qy         967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy        1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy        1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy        1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1325 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1384

Qy        1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy        1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy        1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy        1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy        1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

Qy        1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1685 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1744

Qy        1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy        1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy        1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924
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RESULT 8
ADE34153
ID   ADE34153 standard; DNA; 4414 BP.
XX
AC   ADE34153;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human DNA encoding misshapen/NIKs-related kinase, Mink3b.
XX
KW   Human; misshapen/NIKs-related kinase; Mink3b; ds; antiinflammatory;
KW   immunosuppressive; cytostatic; germinal centre kinase;
KW   c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;
KW   growth factor induced-ERK activation; proliferation;
KW   cell proliferation disorder; cell survival;
KW   intracellular signal transduction; apoptosis; morphological change;
KW   cell migration; gene therapy; inflammatory disease; autoimmune disease;
KW   immunodeficiency; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             209..2587
FT                   /*tag=  a
FT                   /product= "Mink3b"
XX
PN   US2003077597-A1.
XX
PD   24-APR-2003.
XX
PF   19-OCT-2001; 2001US-00029115.
XX
PR   19-OCT-2001; 2001US-00029115.
XX
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PA   (LUOY/) LUO Y.
PA   (FUCA/) FU C A.
PA   (SHEN/) SHEN M.
XX
PI   Luo Y,  Fu CA,  Shen M;
XX
DR   WPI; 2003-635076/60.
DR   P-PSDB; ADE34152.
XX
PT   New misshapen/NIKs-related kinase nucleic acids and proteins useful in
PT   gene therapy and for treating disorders, e.g. acute and chronic
PT   inflammatory diseases.
XX
PS   Claim 3; SEQ ID NO 3; 53pp; English.
XX
CC   The invention relates to a recombinant nucleic acid capable of
CC   hybridising to a Human DNA encoding misshapen/NIKs-related kinase
CC   (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as
CC   ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or
CC   their complements. Also included are a recombinant polypeptide at least
CC   95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,
CC   ADE34152 and ADE34154), screening for a candidate bioactive agent capable
CC   of modulating c-JUN N-terminal kinase (JNK) or extracellular signal
CC   response kinase (ERK) phosphorylation or activity, screening for a
CC   candidate bioactive agent capable of modulating growth factor induced-ERK
CC   activation in a mammalian cell, screening for a candidate bioactive agent
CC   capable of modulating proliferation in a mammalian cell, diagnosing a
CC   mammalian cell proliferation disorder, a medicament for treating a
CC   mammalian cell proliferation disorder and screening for a candidate agent
CC   capable of modulating cell survival. The MINK3 (misshapen/NIKs-related
CC   kinase) nucleic acids are useful in the modulation of intracellular
CC   signal transduction, cell proliferation, apoptosis, morphological change
CC   and migration of mammalian cells. MINK3 nucleic acids and proteins are
CC   specifically useful in gene therapy, and for treating, preventing or
CC   diagnosing acute and chronic inflammatory diseases, autoimmune diseases
CC   and diseases characterised by immunodeficiency. The compositions may also
CC   be used to treat MINK3 dysfunction related disorders, e.g. cancer. The
CC   nucleotide sequences may also be used as hybridisation probes, in
CC   chromosome and gene mapping, and in generating antisense RNA and DNA. The
CC   present sequence encodes Mink3b.
XX
SQ   Sequence 4414 BP; 1010 A; 1339 C; 1317 G; 748 T; 0 U; 0 Other;

  Query Match             42.6%;  Score 1683;  DB 9;  Length 4414;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1683;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         64 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 160

Qy        124 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 220

Qy        184 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 280

Qy        244 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 340

Qy        304 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 400

Qy        364 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 460

Qy        424 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 520

Qy        484 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 580

Qy        544 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 640

Qy        604 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 700

Qy        664 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 760

Qy        724 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 820

Qy        784 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 880

Qy        844 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 940

Qy        904 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 963
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 1000

Qy        964 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1001 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1060

Qy       1024 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1083
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1120

Qy       1084 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1180

Qy       1144 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1240

Qy       1204 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1241 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1300

Qy       1264 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1360

Qy       1324 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1420

Qy       1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1421 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1480

Qy       1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1481 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1540

Qy       1504 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1541 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1600
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Qy       1564 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1601 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1660

Qy       1624 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1661 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1720

Qy       1684 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1721 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1780

Qy       1744 AAG 1746
              |||
Db       1781 AAG 1783


RESULT 9
AAD17762
ID   AAD17762 standard; DNA; 3735 BP.
XX
AC   AAD17762;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human novel STE20-like protein, NOV-3d encoding DNA.
XX
KW   Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;
KW   trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;
KW   immunological disorder; neurodegenerative disorder; Alzheimer's disease;
KW   Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;
KW   human immunodeficiency virus; HIV; fertility disorder; neuroprotective;
KW   cytostatic; nootropic; anti-infertility; cancer; chromosome 17;
KW   NOV-3d protein; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3735
FT                   /*tag=  a
FT                   /product= "Human novel STE20-like protein, NOV-3d"
XX
PN   WO200162928-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US006151.
XX
PR   25-FEB-2000; 2000US-0184951P.
PR   28-FEB-2000; 2000US-0185548P.
PR   01-MAR-2000; 2000US-0185967P.
PR   18-APR-2000; 2000US-0197723P.
PR   27-APR-2000; 2000US-0199957P.
PR   23-FEB-2001; 2001US-00789390.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Vernet CAM,  Fernandes E,  Shimkets RA,  Macdougall J,  Spaderna SK;
XX
DR   WPI; 2001-582051/65.
DR   P-PSDB; AAE10614.
XX
PT   New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like
PT   polypeptide for diagnosing and treating pathological disorders, such as
PT   Parkinson's disease and for use in pharmocogenomics.
XX
PS   Claim 9; Page 67-68; 189pp; English.
XX
CC   The invention relates to novel human polypeptides referred as NOV-X and
CC   their corresponding nucleic acid sequences. NOV-X collectively include
CC   NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-
CC   3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and
CC   NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin
CC   inhibitor-like polypeptides. NOV-X is used to identify a potential
CC   therapeutic agent that can modulate its activity and can be used for
CC   treating a pathology related to aberrant expression or aberrant
CC   physiological interactions of NOV-X. NOV-X or its DNA is used to
CC   determine the presence or predisposition to a disease associated with
CC   altered levels of NOV-X. NOV-X, its DNA and its antibody are used to
CC   treat or prevent a pathology associated with NOV-X. The pathological
CC   states that can be treated or prevented are haematopoietic, cancer,
CC   immunological, tumour, neurodegenerative (e.g. Alzheimer's and
CC   Parkinson's disease), human immunodeficiency virus (HIV) illness and
CC   fertility disorders. NOV-X and its DNA are used in pharmacogenomics for
CC   predictive medicine. NOV-X DNA is used in gene therapy. The present
CC   sequence is a DNA encoding human novel STE20-like protein, NOV-3d. NOV-3d
CC   gene is located at chromosome 17
XX
SQ   Sequence 3735 BP; 880 A; 1105 C; 1137 G; 613 T; 0 U; 0 Other;

  Query Match             40.5%;  Score 1599;  DB 5;  Length 3735;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2137 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2196

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2197 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2256

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2257 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2316

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2317 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2376

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2377 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2436

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2437 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2496

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2497 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2556

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2557 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2616

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2617 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2676

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2677 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2736

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2737 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 2796

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2797 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 2856

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2857 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 2916
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Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2917 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 2976

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2977 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3036

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3037 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3096

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
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Db       3097 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3156

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3157 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3216

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3217 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3276

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3277 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3336

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3337 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3396

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
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Db       3397 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3456

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3457 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3516

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3517 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3576

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3577 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3636

Qy       3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3637 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3696

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||
Db       3697 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3735
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RESULT 10

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AAD17761
ID   AAD17761 standard; DNA; 3822 BP.
XX
AC   AAD17761;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human novel STE20-like protein, NOV-3c encoding DNA.
XX
KW   Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;
KW   trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;
KW   immunological disorder; neurodegenerative disorder; Alzheimer's disease;
KW   Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;
KW   human immunodeficiency virus; HIV; fertility disorder; neuroprotective;
KW   cytostatic; nootropic; anti-infertility; cancer; chromosome 17;
KW   NOV-3c protein; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3822
FT                   /*tag=  a
FT                   /product= "Human novel STE20-like protein, NOV-3c"
XX
PN   WO200162928-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US006151.
XX
PR   25-FEB-2000; 2000US-0184951P.
PR   28-FEB-2000; 2000US-0185548P.
PR   01-MAR-2000; 2000US-0185967P.
PR   18-APR-2000; 2000US-0197723P.
PR   27-APR-2000; 2000US-0199957P.
PR   23-FEB-2001; 2001US-00789390.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Vernet CAM,  Fernandes E,  Shimkets RA,  Macdougall J,  Spaderna SK;
XX
DR   WPI; 2001-582051/65.
DR   P-PSDB; AAE10613.
XX
PT   New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like
PT   polypeptide for diagnosing and treating pathological disorders, such as
PT   Parkinson's disease and for use in pharmacogenomics.
XX
PS   Claim 9; Page 58-59; 189pp; English.
XX
CC   The invention relates to novel human polypeptides referred as NOV-X and
CC   their corresponding nucleic acid sequences. NOV-X collectively include
CC   NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-
CC   3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and
CC   NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin
CC   inhibitor-like polypeptides. NOV-X is used to identify a potential
CC   therapeutic agent that can modulate its activity and can be used for
CC   treating a pathology related to aberrant expression or aberrant
CC   physiological interactions of NOV-X. NOV-X or its DNA is used to
CC   determine the presence or predisposition to a disease associated with
CC   altered levels of NOV-X. NOV-X, its DNA and its antibody are used to
CC   treat or prevent a pathology associated with NOV-X. The pathological
CC   states that can be treated or prevented are haematopoietic, cancer,
CC   immunological, tumour, neurodegenerative (e.g. Alzheimer's and
CC   Parkinson's disease), human immunodeficiency virus (HIV) illness and
CC   fertility disorders. NOV-X and its DNA are used in pharmacogenomics for
CC   predictive medicine. NOV-X DNA is used in gene therapy. The present
CC   sequence is a DNA encoding human novel STE20-like protein, NOV-3c. NOV-3c
CC   gene is located at chromosome 17
XX
SQ   Sequence 3822 BP; 904 A; 1129 C; 1165 G; 624 T; 0 U; 0 Other;

  Query Match             40.5%;  Score 1599;  DB 5;  Length 3822;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
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Db       2224 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2283

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2284 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2343

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2344 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2403
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Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2404 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2463

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2464 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2523

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2524 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2583

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
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Db       2584 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2643

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2644 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2703

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2704 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2763

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2764 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2823

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2824 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 2883

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2884 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 2943

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2944 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3003

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3004 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3063

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3064 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3123

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3124 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3183

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3184 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3243

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3244 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3303

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3304 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3363

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3364 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3423

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3424 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3483

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3484 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3543

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3544 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3603

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3604 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3663

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3664 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3723

Qy       3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3724 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3783

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||
Db       3784 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3822
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RESULT 11
AAD17760
ID   AAD17760 standard; DNA; 3912 BP.
XX
AC   AAD17760;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human novel STE20-like protein, NOV-3b encoding DNA.
XX
KW   Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;
KW   trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;
KW   immunological disorder; neurodegenerative disorder; Alzheimer's disease;
KW   Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;
KW   human immunodeficiency virus; HIV; fertility disorder; neuroprotective;
KW   cytostatic; nootropic; anti-infertility; cancer; chromosome 17;
KW   NOV-3b protein; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3912
FT                   /*tag=  a
FT                   /product= "Human novel STE20-like protein, NOV-3b"
XX
PN   WO200162928-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US006151.
XX
PR   25-FEB-2000; 2000US-0184951P.
PR   28-FEB-2000; 2000US-0185548P.
PR   01-MAR-2000; 2000US-0185967P.
PR   18-APR-2000; 2000US-0197723P.
PR   27-APR-2000; 2000US-0199957P.
PR   23-FEB-2001; 2001US-00789390.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Vernet CAM,  Fernandes E,  Shimkets RA,  Macdougall J,  Spaderna SK;
XX
DR   WPI; 2001-582051/65.
DR   P-PSDB; AAE10612.
XX
PT   New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like
PT   polypeptide for diagnosing and treating pathological disorders, such as
PT   Parkinson's disease and for use in pharmocogenomics.
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XX
PS   Claim 9; Page 51-52; 189pp; English.
XX
CC   The invention relates to novel human polypeptides referred as NOV-X and
CC   their corresponding nucleic acid sequences. NOV-X collectively include
CC   NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-
CC   3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and
CC   NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin
CC   inhibitor-like polypeptides. NOV-X is used to identify a potential
CC   therapeutic agent that can modulate its activity and can be used for
CC   treating a pathology related to aberrant expression or aberrant
CC   physiological interactions of NOV-X. NOV-X or its DNA is used to
CC   determine the presence or predisposition to a disease associated with
CC   altered levels of NOV-X. NOV-X, its DNA and its antibody are used to
CC   treat or prevent a pathology associated with NOV-X. The pathological
CC   states that can be treated or prevented are haematopoietic, cancer,
CC   immunological, tumour, neurodegenerative (e.g. Alzheimer's and
CC   Parkinson's disease), human immunodeficiency virus (HIV) illness and
CC   fertility disorders. NOV-X and its DNA are used in pharmacogenomics for
CC   predictive medicine. NOV-X DNA is used in gene therapy. The present
CC   sequence is a DNA encoding human novel STE20-like protein, NOV-3b. NOV-3b
CC   gene is located at chromosome 17
XX
SQ   Sequence 3912 BP; 924 A; 1171 C; 1187 G; 630 T; 0 U; 0 Other;

  Query Match             40.5%;  Score 1599;  DB 5;  Length 3912;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2373

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2433

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2493

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2553

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2613

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2673

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2733

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2793

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2853

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2913

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 2973

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2974 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3033

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3093

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3153

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3213

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3273

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3333

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
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Db       3334 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3393

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3453

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3513

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3573

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
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Db       3574 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3633

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3634 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3693

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3694 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3753

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3754 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3813

Qy       3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3814 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3873

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||
Db       3874 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3912


RESULT 12
AAD17759
ID   AAD17759 standard; DNA; 3999 BP.
XX
AC   AAD17759;
XX
DT   10-DEC-2001  (first entry)
XX
```

```
DE   Human novel STE20-like protein, NOV-3a encoding DNA.
XX
KW   Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;
KW   trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;
KW   immunological disorder; neurodegenerative disorder; Alzheimer's disease;
KW   Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;
KW   human immunodeficiency virus; HIV; fertility disorder; neuroprotective;
KW   cytostatic; nootropic; anti-infertility; cancer; chromosome 17;
KW   NOV-3a protein; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3999
FT                   /*tag=  a
FT                   /product= "Human novel STE20-like protein, NOV-3a"
XX
PN   WO200162928-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US006151.
XX
PR   25-FEB-2000; 2000US-0184951P.
PR   28-FEB-2000; 2000US-0185548P.
PR   01-MAR-2000; 2000US-0185967P.
PR   18-APR-2000; 2000US-0197723P.
PR   27-APR-2000; 2000US-0199957P.
PR   23-FEB-2001; 2001US-00789390.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Vernet CAM,  Fernandes E,  Shimkets RA,  Macdougall J,  Spaderna SK;
XX
DR   WPI; 2001-582051/65.
DR   P-PSDB; AAE10611.
XX
PT   New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like
PT   polypeptide for diagnosing and treating pathological disorders, such as
PT   Parkinson's disease and for use in pharmocogenomics.
XX
PS   Claim 9; Page 44-45; 189pp; English.
XX
CC   The invention relates to novel human polypeptides referred as NOV-X and
CC   their corresponding nucleic acid sequences. NOV-X collectively include
CC   NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-
CC   3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and
CC   NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin
CC   inhibitor-like polypeptides. NOV-X is used to identify a potential
CC   therapeutic agent that can modulate its activity and can be used for
CC   treating a pathology related to aberrant expression or aberrant
CC   physiological interactions of NOV-X. NOV-X or its DNA is used to
CC   determine the presence or predisposition to a disease associated with
CC   altered levels of NOV-X. NOV-X, its DNA and its antibody are used to
CC   treat or prevent a pathology associated with NOV-X. The pathological
CC   states that can be treated or prevented are haematopoietic, cancer,
CC   immunological, tumour, neurodegenerative (e.g. Alzheimer's and
CC   Parkinson's disease), human immunodeficiency virus (HIV) illness and
CC   fertility disorders. NOV-X and its DNA are used in pharmacogenomics for
CC   predictive medicine. NOV-X DNA is used in gene therapy. The present
CC   sequence is a DNA encoding human novel STE20-like protein, NOV-3a. NOV-3a
CC   gene is located at chromosome 17
XX
SQ   Sequence 3999 BP; 948 A; 1195 C; 1215 G; 641 T; 0 U; 0 Other;

  Query Match             40.5%;  Score 1599;  DB 5;  Length 3999;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2460

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2520

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2580

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2640

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2700

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2760

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2820

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2880

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2940

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 3000

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3060

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3120

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3180

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3240

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3300

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3360

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3420

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3480

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3540

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3541 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3600

Qy        3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3601 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3660

Qy        3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3661 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3720

Qy        3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3721 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3780

Qy        3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3781 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3840

Qy        3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3841 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3900

Qy        3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3901 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3960

Qy        3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
               |||||||||||||||||||||||||||||||||||||||
Db        3961 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3999
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RESULT 13
AAS88207

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ID   AAS88207 standard; cDNA; 7132 BP.
XX
AC   AAS88207;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #24011.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG24020.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 1; SEQ ID NO 24011; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC   coding sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 7132 BP; 1569 A; 2123 C; 2159 G; 1280 T; 0 U; 1 Other;

  Query Match             33.9%;  Score 1340;  DB 5;  Length 7132;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 217

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 277

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 337

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 397

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 457

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 517

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 577

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 637

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 697

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 757

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        758 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 817

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 877
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Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        878 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 937

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        938 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 997

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        998 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1057

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1058 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1117

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1118 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1177

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1178 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1237

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1238 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1297

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1298 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1357

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1358 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1417

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1418 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1477

Qy       1327 GAGCGGCGGCAGGCGGAGCG 1346
              ||||||||||||||||||||
Db       1478 GAGCGGCGGCAGGCGGAGCG 1497
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RESULT 14
AAC98909
ID   AAC98909 standard; cDNA; 2345 BP.
XX
AC   AAC98909;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:137.
XX
KW   Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;
KW   diagnosis; identification; cytostatic; neuroprotective; nootropic;
KW   immunomodulatory; relaxant; contraceptive; gynaecological;
KW   antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW   linkage analysis; tissue identification; tissue typing; forensic; neural;
KW   immune system; muscular; reproductive; gastrointestinal; pulmonary;
KW   cardiovascular; renal; proliferative; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055320-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005989.
XX
PR   12-MAR-1999;   99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-579444/54.
DR   P-PSDB; AAB54144.
XX
PT   New nucleic acid that is a pancreatic cancer antigen for preventing,
PT   treating, or ameliorating a medical condition, particular pancreatic
PT   cancer, or for use in assays for diagnosing a pathological condition.
XX
PS   Claim 1; Page 596-597; 1379pp; English.
XX
CC   AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC   proteins, called pancreatic cancer antigens, given in AAB54008 to
CC   AAB54466. The human pancreatic cancer antigens have cytostatic,
CC   neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC   gynaecological, cardiant and antiinflammatory activities, and can be used
CC   in gene therapy. The polynucleotide and proteins can be used for
CC   preventing, treating, or ameliorating a medical condition or in assays
CC   for diagnosing a pathological condition or a susceptibility to one in a
CC   subject. Binding partners to the proteins and the activity of the
CC   proteins can be identified. The pancreatic cancer antigens can be used to
CC   detect, treat or prevent pancreatic disorders, especially cancer.
CC   Agonists and antagonists to the antigens can be screened for. The
CC   pancreatic cancer antigen polynucleotides can be used to design nucleic
CC   acid hybridisation probes that can be used in chromosome mapping, linkage
CC   analysis, tissue identification and/or typing and a variety of forensic
CC   and diagnostic methods. The proteins can be used to generate antibodies
CC   which are used to purify, detect and target the polypeptides, including
CC   both in vivo and in vitro diagnostic and therapeutic methods. The
CC   proteins can be used to treat or prevent neural, immune system, muscular,
CC   reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC   proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 2345 BP; 499 A; 693 C; 671 G; 467 T; 0 U; 15 Other;

  Query Match             26.1%;  Score 1030;  DB 3;  Length 2345;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1180;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2763 TCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGAT 2822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGAT 410

Qy       2823 CTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGG 2882
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 TTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGG 470

Qy       2883 CACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCC 2942
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 CACTCGGTTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCC 530

Qy       2943 CACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAA 3002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 CACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAA 590

Qy       3003 CTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGG 3062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 CTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGG 650

Qy       3063 GCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACG 3122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 GCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACG 710

Qy       3123 CTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAG 3182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 CTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAG 770

Qy       3183 GAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCC 3242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 GAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCC 830
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Qy       3243 AGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTA 3302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 AGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTA 890

Qy       3303 CCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGA 3362
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        891 CCGTKTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGA 950

Qy       3363 GGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGA 3422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        951 GGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGA 1010

Qy       3423 CCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGT 3482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1011 CCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGT 1070

Qy       3483 CATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGA 3542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1071 CATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGA 1130

Qy       3543 CATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCC 3602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 CATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCC 1190

Qy       3603 CAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACAC 3662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 CAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACAC 1250

Qy       3663 GTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGC 3722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 GTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGC 1310

Qy       3723 CTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGT 3782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 CTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGT 1370

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Qy       3843 GTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGT 3902
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RESULT 15
ABL39593
ID   ABL39593 standard; cDNA; 1964 BP.
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AC   ABL39593;
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DT   09-MAY-2002  (first entry)
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DE   Human cancer suppressing gene PP928 encoding cDNA SEQ ID NO:30.
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KW   Human; cancer suppression; cancer; gene; ss.
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OS   Homo sapiens.
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FH   Key             Location/Qualifiers
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FT                   /*tag=  a
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PN   CN1313318-A.
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PD   19-SEP-2001.
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PF   14-MAR-2000; 2000CN-00111997.
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PR   14-MAR-2000; 2000CN-00111997.
XX
PA   (SHAN-) SHANGHAI INST ONCOLOGY.
XX
PI   Gu J,  Yang S;
XX
DR   WPI; 2002-042196/06.
DR   P-PSDB; ABB06007.
XX
PT   New human protein able to suppress growth of cancer cells and its
PT   encoding polynucleotide.
XX
PS   Claim 5; Page 44-46 (Disclosure); 65pp; Chinese.
XX
CC   The present invention describes human proteins with cancer suppressing
CC   activity. ALso described are the polynucleotides encoding the proteins
CC   and a process for preparing the proteins by DNA recombination. The
CC   proteins and polynucleotides can be used in the treatment of diseases
CC   such as cancer. The present sequence encodes a human cancer suppressing
CC   protein from the present invention
XX
SQ   Sequence 1964 BP; 450 A; 583 C; 518 G; 413 T; 0 U; 0 Other;

  Query Match             24.6%;  Score 970;  DB 6;  Length 1964;
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Qy       3103 GGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTC 3162
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SUMMARIES

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	150	22	0.6	1345	3	US-08-659-188-7	Sequence 7, Appli
	151	22	0.6	1345	3	US-08-655-227-7	Sequence 7, Appli
	152	22	0.6	1345	3	US-08-655-241-7	Sequence 7, Appli
	153	22	0.6	1345	3	US-09-149-976-7	Sequence 7, Appli
	154	22	0.6	1345	4	US-09-398-326-7	Sequence 7, Appli
c	155	22	0.6	1408	1	US-08-222-124-10	Sequence 10, Appl
c	156	22	0.6	1408	2	US-08-842-657A-10	Sequence 10, Appl
c	157	22	0.6	1414	1	US-08-222-124-9	Sequence 9, Appli
c	158	22	0.6	1414	2	US-08-842-657A-9	Sequence 9, Appli
c	159	22	0.6	1578	4	US-09-016-434-1377	Sequence 1377, Ap
c	160	22	0.6	1665	3	US-08-766-354A-29	Sequence 29, Appl
c	161	22	0.6	1809	1	US-08-453-956-24	Sequence 24, Appl
c	162	22	0.6	1809	1	US-08-086-631-24	Sequence 24, Appl
c	163	22	0.6	1809	2	US-08-452-930-24	Sequence 24, Appl
c	164	22	0.6	1809	5	PCT-US93-08174-24	Sequence 24, Appl
	165	22	0.6	3501	1	US-08-524-757-5	Sequence 5, Appli
	166	22	0.6	3502	4	US-09-976-594-659	Sequence 659, App
	167	22	0.6	3909	4	US-09-016-434-1119	Sequence 1119, Ap
	168	22	0.6	4262	4	US-09-521-511C-10	Sequence 10, Appl
	169	22	0.6	9997	1	US-08-246-982A-15	Sequence 15, Appl
	170	22	0.6	9997	1	US-08-453-265-15	Sequence 15, Appl
	171	22	0.6	10103	2	US-08-457-273B-7	Sequence 7, Appli
	172	21	0.5	21	4	US-09-688-188B-58	Sequence 58, Appl
	173	21	0.5	21	4	US-09-291-417D-58	Sequence 58, Appl
c	174	21	0.5	390	1	US-08-661-168-7	Sequence 7, Appli
	175	21	0.5	397	3	US-09-253-691-3	Sequence 3, Appli
c	176	21	0.5	639	4	US-09-336-536-57	Sequence 57, Appl
	177	21	0.5	1080	2	US-08-918-727-2	Sequence 2, Appli
	178	21	0.5	1080	3	US-09-205-680A-2	Sequence 2, Appli
	179	21	0.5	1093	4	US-09-010-147B-1	Sequence 1, Appli
	180	21	0.5	1144	1	US-08-014-943A-1	Sequence 1, Appli
	181	21	0.5	1144	1	US-08-486-421-2	Sequence 2, Appli
	182	21	0.5	1144	1	US-08-470-911-2	Sequence 2, Appli
	183	21	0.5	1144	2	US-08-486-809-2	Sequence 2, Appli
c	184	21	0.5	1686	4	US-09-833-381-2019	Sequence 2019, Ap
	185	21	0.5	1776	2	US-08-531-927B-1	Sequence 1, Appli
	186	21	0.5	1776	3	US-09-041-886-12	Sequence 12, Appl
c	187	21	0.5	1858	4	US-09-336-536-56	Sequence 56, Appl
	188	21	0.5	1884	3	US-08-753-007A-5	Sequence 5, Appli
	189	21	0.5	1884	3	US-09-398-496-5	Sequence 5, Appli
c	190	21	0.5	2104	1	US-07-984-044A-4	Sequence 4, Appli
c	191	21	0.5	2104	1	US-08-458-393-4	Sequence 4, Appli
	192	21	0.5	2568	4	US-09-489-039A-5258	Sequence 5258, Ap
c	193	21	0.5	2736	4	US-09-489-039A-6366	Sequence 6366, Ap
	194	21	0.5	3609	4	US-09-799-875-6	Sequence 6, Appli
	195	21	0.5	5983	4	US-09-799-875-4	Sequence 4, Appli
	196	21	0.5	6794	4	US-09-491-356C-2	Sequence 2, Appli
	197	21	0.5	55298	4	US-09-491-356C-1	Sequence 1, Appli
	198	20	0.5	20	4	US-09-688-188B-59	Sequence 59, Appl
	199	20	0.5	20	4	US-09-291-417D-59	Sequence 59, Appl
c	200	20	0.5	252	2	US-08-623-906A-1	Sequence 1, Appli
c	201	20	0.5	314	3	US-09-060-410-6	Sequence 6, Appli
c	202	20	0.5	314	4	US-09-723-458-6	Sequence 6, Appli
	203	20	0.5	328	4	US-09-016-434-986	Sequence 986, App
	204	20	0.5	448	4	US-09-669-751-88	Sequence 88, Appl
c	205	20	0.5	822	4	US-09-228-986-38	Sequence 38, Appl
c	206	20	0.5	879	1	US-08-243-545-1	Sequence 1, Appli
c	207	20	0.5	879	2	US-08-993-962-1	Sequence 1, Appli
c	208	20	0.5	879	3	US-09-160-841-1	Sequence 1, Appli
c	209	20	0.5	879	4	US-08-669-692-1	Sequence 1, Appli
c	210	20	0.5	879	4	US-08-444-626-1	Sequence 1, Appli
c	211	20	0.5	879	5	PCT-US94-05365-1	Sequence 1, Appli
c	212	20	0.5	1017	5	PCT-US94-05150-21	Sequence 21, Appl
c	213	20	0.5	1383	3	US-09-400-742-7	Sequence 7, Appli
c	214	20	0.5	1383	3	US-08-618-651A-7	Sequence 7, Appli
c	215	20	0.5	1383	4	US-09-215-252-6	Sequence 6, Appli
c	216	20	0.5	1383	4	US-09-970-989A-6	Sequence 6, Appli
	217	20	0.5	1866	3	US-08-909-742-1	Sequence 1, Appli
	218	20	0.5	1866	3	US-09-412-289-1	Sequence 1, Appli
c	219	20	0.5	1909	4	US-09-461-657B-16	Sequence 16, Appl
c	220	20	0.5	2097	4	US-09-461-657B-14	Sequence 14, Appl
	221	20	0.5	2450	4	US-09-620-312D-336	Sequence 336, App
	222	20	0.5	2513	4	US-09-620-312D-337	Sequence 337, App
c	223	20	0.5	2787	4	US-09-254-594-2	Sequence 2, Appli
c	224	20	0.5	2799	4	US-09-461-657B-11	Sequence 11, Appl
	225	20	0.5	2900	4	US-09-620-312D-673	Sequence 673, App
c	226	20	0.5	2987	3	US-07-757-342D-1	Sequence 1, Appli
c	227	20	0.5	2987	4	US-09-461-657B-1	Sequence 1, Appli
	228	20	0.5	3110	4	US-09-023-655-1072	Sequence 1072, Ap
	229	20	0.5	3116	4	US-09-976-594-283	Sequence 283, App
	230	20	0.5	3132	2	US-08-224-482-3	Sequence 3, Appli
	231	20	0.5	3132	3	US-09-205-921-1	Sequence 1, Appli
	232	20	0.5	3132	4	US-09-300-958A-32	Sequence 32, Appl
	233	20	0.5	3132	4	US-09-702-705-320	Sequence 320, App
	234	20	0.5	3132	4	US-09-736-457-320	Sequence 320, App
	235	20	0.5	3132	4	US-09-614-124B-320	Sequence 320, App
	236	20	0.5	3132	4	US-09-671-325-320	Sequence 320, App
	237	20	0.5	3132	4	US-09-589-184-320	Sequence 320, App
	238	20	0.5	3137	4	US-09-620-312D-714	Sequence 714, App
c	239	20	0.5	3195	4	US-09-254-594-1	Sequence 1, Appli
	240	20	0.5	3223	2	US-08-620-694A-9	Sequence 9, Appli
	241	20	0.5	3223	3	US-09-022-255-9	Sequence 9, Appli
	242	20	0.5	3223	3	US-09-022-696-9	Sequence 9, Appli
	243	20	0.5	3223	3	US-08-978-773-3	Sequence 3, Appli
	244	20	0.5	3223	3	US-09-022-253-9	Sequence 9, Appli
	245	20	0.5	3223	3	US-09-022-260-9	Sequence 9, Appli
	246	20	0.5	3223	3	US-09-022-259-9	Sequence 9, Appli

	247	20	0.5	3223	3	US-09-022-257-9	Sequence 9, Appli
	248	20	0.5	3223	4	US-09-549-679-9	Sequence 9, Appli
	249	20	0.5	3715	3	US-09-041-886-10	Sequence 10, Appl
	250	20	0.5	3862	4	US-10-164-595-5	Sequence 5, Appli
	251	20	0.5	3985	4	US-10-164-595-3	Sequence 3, Appli
c	252	20	0.5	4079	4	US-09-016-434-1208	Sequence 1208, Ap
c	253	20	0.5	4132	4	US-09-300-958A-10	Sequence 10, Appl
	254	20	0.5	4196	4	US-09-688-188B-19	Sequence 19, Appl
	255	20	0.5	4196	4	US-09-291-417D-19	Sequence 19, Appl
c	256	20	0.5	4262	4	US-09-521-511C-10	Sequence 10, Appl
	257	20	0.5	4296	3	US-09-060-410-3	Sequence 3, Appli
	258	20	0.5	4296	4	US-09-723-458-3	Sequence 3, Appli
	259	20	0.5	4797	4	US-09-976-594-988	Sequence 988, App
	260	20	0.5	4954	4	US-09-506-066E-1	Sequence 1, Appli
	261	20	0.5	8600	4	US-09-457-708-1	Sequence 1, Appli
	262	20	0.5	8600	4	US-09-950-046A-1	Sequence 1, Appli
c	263	19	0.5	19	4	US-09-688-188B-62	Sequence 62, Appl
c	264	19	0.5	19	4	US-09-291-417D-62	Sequence 62, Appl
	265	19	0.5	34	2	US-08-861-459-12	Sequence 12, Appl
	266	19	0.5	203	3	US-09-043-303-7	Sequence 7, Appli
c	267	19	0.5	211	4	US-09-099-631A-13	Sequence 13, Appl
	268	19	0.5	238	4	US-09-491-356C-15	Sequence 15, Appl
	269	19	0.5	250	1	US-08-480-552-16	Sequence 16, Appl
	270	19	0.5	250	3	US-08-929-208-16	Sequence 16, Appl
	271	19	0.5	250	4	US-09-568-315-16	Sequence 16, Appl
	272	19	0.5	253	4	US-09-491-356C-13	Sequence 13, Appl
	273	19	0.5	265	4	US-09-491-356C-14	Sequence 14, Appl
	274	19	0.5	265	4	US-09-491-356C-16	Sequence 16, Appl
	275	19	0.5	265	4	US-09-491-356C-17	Sequence 17, Appl
	276	19	0.5	265	4	US-09-491-356C-18	Sequence 18, Appl
c	277	19	0.5	286	4	US-09-313-294A-4130	Sequence 4130, Ap
c	278	19	0.5	300	4	US-09-328-352-4065	Sequence 4065, Ap
c	279	19	0.5	301	3	US-08-905-223-267	Sequence 267, App
	280	19	0.5	447	2	US-08-387-942C-33	Sequence 33, Appl
c	281	19	0.5	455	4	US-09-227-357-70	Sequence 70, Appl
c	282	19	0.5	504	3	US-09-328-111-123	Sequence 123, App
	283	19	0.5	516	4	US-09-489-039A-5930	Sequence 5930, Ap
c	284	19	0.5	590	4	US-09-118-554-67	Sequence 67, Appl
c	285	19	0.5	590	4	US-09-118-627-67	Sequence 67, Appl
c	286	19	0.5	590	4	US-09-602-877A-67	Sequence 67, Appl
c	287	19	0.5	608	4	US-09-669-751-247	Sequence 247, App
	288	19	0.5	738	4	US-08-722-570-13	Sequence 13, Appl
	289	19	0.5	738	4	US-08-932-411A-13	Sequence 13, Appl
c	290	19	0.5	742	3	US-08-966-317-2	Sequence 2, Appli
c	291	19	0.5	742	4	US-09-489-770-2	Sequence 2, Appli
c	292	19	0.5	795	4	US-09-404-879A-86	Sequence 86, Appl
c	293	19	0.5	795	4	US-09-338-933-86	Sequence 86, Appl
c	294	19	0.5	795	4	US-09-215-681-86	Sequence 86, Appl
c	295	19	0.5	795	4	US-09-216-003A-86	Sequence 86, Appl
	296	19	0.5	991	4	US-09-344-529-3	Sequence 3, Appli
	297	19	0.5	1027	4	US-09-344-529-1	Sequence 1, Appli
	298	19	0.5	1333	1	US-08-910-973-21	Sequence 21, Appl
	299	19	0.5	1333	4	US-09-499-227-21	Sequence 21, Appl
	300	19	0.5	1392	4	US-09-489-039A-5663	Sequence 5663, Ap
	301	19	0.5	1416	3	US-08-866-928B-2	Sequence 2, Appli
	302	19	0.5	1416	4	US-09-685-836-2	Sequence 2, Appli
	303	19	0.5	1467	4	US-09-620-312D-662	Sequence 662, App
c	304	19	0.5	1472	4	US-09-668-097A-29	Sequence 29, Appl
	305	19	0.5	1788	1	US-08-035-928-1	Sequence 1, Appli
c	306	19	0.5	1812	2	US-08-735-041A-3	Sequence 3, Appli
c	307	19	0.5	1812	3	US-09-190-476B-3	Sequence 3, Appli
c	308	19	0.5	1812	3	US-09-190-889A-3	Sequence 3, Appli
c	309	19	0.5	1812	3	US-09-190-938B-3	Sequence 3, Appli
	310	19	0.5	1849	2	US-08-665-926-7	Sequence 7, Appli
	311	19	0.5	1849	3	US-08-740-223A-9	Sequence 9, Appli
	312	19	0.5	1849	4	US-09-202-491-1	Sequence 1, Appli
	313	19	0.5	1849	4	US-09-709-188-9	Sequence 9, Appli
	314	19	0.5	1853	1	US-08-553-110-2	Sequence 2, Appli
	315	19	0.5	1897	1	US-08-453-477-1	Sequence 1, Appli
	316	19	0.5	1897	1	US-08-453-461-1	Sequence 1, Appli
	317	19	0.5	1898	1	US-08-342-411A-1	Sequence 1, Appli
c	318	19	0.5	2072	3	US-08-675-816-5	Sequence 5, Appli
c	319	19	0.5	2103	2	US-08-735-041A-5	Sequence 5, Appli
c	320	19	0.5	2103	2	US-08-735-041A-7	Sequence 7, Appli
c	321	19	0.5	2103	3	US-09-190-476B-5	Sequence 5, Appli
c	322	19	0.5	2103	3	US-09-190-476B-7	Sequence 7, Appli
c	323	19	0.5	2103	3	US-09-190-889A-5	Sequence 5, Appli
c	324	19	0.5	2103	3	US-09-190-889A-7	Sequence 7, Appli
c	325	19	0.5	2103	3	US-09-190-938B-5	Sequence 5, Appli
c	326	19	0.5	2103	3	US-09-190-938B-7	Sequence 7, Appli
c	327	19	0.5	2142	4	US-09-540-236-1675	Sequence 1675, Ap
	328	19	0.5	2289	2	US-08-463-081B-30	Sequence 30, Appl
	329	19	0.5	2289	2	US-08-461-379A-30	Sequence 30, Appl
	330	19	0.5	2289	2	US-08-462-390B-30	Sequence 30, Appl
	331	19	0.5	2289	3	US-08-463-074B-30	Sequence 30, Appl
	332	19	0.5	2289	3	US-08-465-585C-30	Sequence 30, Appl
	333	19	0.5	2289	3	US-08-652-446-30	Sequence 30, Appl
c	334	19	0.5	2307	4	US-09-620-312D-1098	Sequence 1098, Ap
	335	19	0.5	2806	4	US-09-653-839-9	Sequence 9, Appli
c	336	19	0.5	2823	4	US-09-704-611-4	Sequence 4, Appli
c	337	19	0.5	2892	4	US-09-704-611-3	Sequence 3, Appli
	338	19	0.5	2946	1	US-08-473-122-1	Sequence 1, Appli
	339	19	0.5	2946	2	US-08-472-478-1	Sequence 1, Appli
	340	19	0.5	2946	2	US-08-463-081B-7	Sequence 7, Appli
	341	19	0.5	2946	2	US-08-461-379A-7	Sequence 7, Appli
	342	19	0.5	2946	2	US-08-462-390B-7	Sequence 7, Appli
	343	19	0.5	2946	3	US-08-463-074B-7	Sequence 7, Appli
	344	19	0.5	2946	3	US-08-465-585C-7	Sequence 7, Appli
	345	19	0.5	2946	3	US-08-652-446-7	Sequence 7, Appli
	346	19	0.5	2946	4	US-08-481-659C-1	Sequence 1, Appli
	347	19	0.5	2984	5	PCT-US93-00893-1	Sequence 1, Appli
c	348	19	0.5	2984	5	PCT-US93-00893-2	Sequence 2, Appli
c	349	19	0.5	3018	4	US-09-016-434-1468	Sequence 1468, Ap
	350	19	0.5	3156	4	US-09-134-001C-2168	Sequence 2168, Ap
	351	19	0.5	3231	4	US-09-866-028-14	Sequence 14, Appl
	352	19	0.5	3302	4	US-09-620-312D-475	Sequence 475, App
c	353	19	0.5	3470	4	US-09-976-594-345	Sequence 345, App
	354	19	0.5	3853	4	US-09-245-248B-53	Sequence 53, Appl
	355	19	0.5	3879	3	US-08-916-352-1	Sequence 1, Appli
c	356	19	0.5	3942	3	US-09-162-484-19	Sequence 19, Appl
	357	19	0.5	4168	4	US-09-266-225D-17	Sequence 17, Appl
	358	19	0.5	4250	4	US-09-706-594-6	Sequence 6, Appli
	359	19	0.5	4279	3	US-09-041-886-22	Sequence 22, Appl
	360	19	0.5	4323	4	US-09-620-312D-134	Sequence 134, App
c	361	19	0.5	4358	3	US-08-675-816-7	Sequence 7, Appli
	362	19	0.5	5325	4	US-10-164-595-17	Sequence 17, Appl
	363	19	0.5	5334	4	US-10-164-595-21	Sequence 21, Appl
	364	19	0.5	5581	4	US-10-164-595-19	Sequence 19, Appl
	365	19	0.5	5630	2	US-08-937-931-1	Sequence 1, Appli
	366	19	0.5	5630	3	US-09-285-502-1	Sequence 1, Appli
	367	19	0.5	5630	4	US-09-709-126-1	Sequence 1, Appli
	368	19	0.5	5630	4	US-09-871-385A-1	Sequence 1, Appli
c	369	19	0.5	5633	4	US-09-023-655-1490	Sequence 1490, Ap
	370	19	0.5	5816	3	US-08-857-076-11	Sequence 11, Appl
	371	19	0.5	12588	2	US-08-387-942C-1	Sequence 1, Appli
c	372	19	0.5	13011	2	US-08-791-849A-14	Sequence 14, Appl
c	373	19	0.5	13910	3	US-09-263-933-1	Sequence 1, Appli
c	374	19	0.5	13910	3	US-09-263-933-8	Sequence 8, Appli
c	375	19	0.5	13910	3	US-09-263-933-15	Sequence 15, Appl
c	376	19	0.5	13910	4	US-09-919-901-1	Sequence 1, Appli
c	377	19	0.5	13910	4	US-09-919-901-8	Sequence 8, Appli
c	378	19	0.5	13910	4	US-09-919-901-15	Sequence 15, Appl
	379	19	0.5	16075	3	US-09-096-942-1	Sequence 1, Appli
	380	19	0.5	16075	3	US-09-096-867-1	Sequence 1, Appli
c	381	19	0.5	22255	4	US-09-616-289-51	Sequence 51, Appl
	382	19	0.5	34094	4	US-09-292-034-1	Sequence 1, Appli
	383	19	0.5	43804	4	US-09-171-461-1	Sequence 1, Appli
c	384	19	0.5	90050	3	US-09-245-041-5	Sequence 5, Appli
c	385	19	0.5	119211	4	US-09-596-002-40	Sequence 40, Appl
	386	19	0.5	246240	2	US-08-724-394A-20	Sequence 20, Appl
	387	19	0.5	246240	2	US-08-724-394A-21	Sequence 21, Appl
	388	19	0.5	246240	2	US-08-724-394A-22	Sequence 22, Appl
	389	19	0.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	390	19	0.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	391	18	0.5	18	4	US-09-205-995-48	Sequence 48, Appl
	392	18	0.5	36	2	US-08-863-639A-31	Sequence 31, Appl

c	393	18	0.5	54	1	US-07-941-651-3	Sequence 3, Appli
c	394	18	0.5	54	1	US-08-279-996-3	Sequence 3, Appli
c	395	18	0.5	54	4	US-09-479-645A-174	Sequence 174, App
c	396	18	0.5	90	1	US-08-123-702-21	Sequence 21, Appl
	397	18	0.5	148	4	US-09-205-995-78	Sequence 78, Appl
c	398	18	0.5	228	6	5273901-10	Patent No. 5273901
c	399	18	0.5	228	6	5482709-9	Patent No. 5482709
	400	18	0.5	247	4	US-09-621-976-602	Sequence 602, App
c	401	18	0.5	278	4	US-09-313-294A-3318	Sequence 3318, Ap
c	402	18	0.5	288	5	PCT-US94-04361-13	Sequence 13, Appl
	403	18	0.5	290	4	US-09-233-086-4	Sequence 4, Appli
	404	18	0.5	345	4	US-09-489-039A-3837	Sequence 3837, Ap
	405	18	0.5	393	4	US-09-621-976-3004	Sequence 3004, Ap
	406	18	0.5	408	4	US-09-134-000C-1915	Sequence 1915, Ap
c	407	18	0.5	413	4	US-09-621-976-2185	Sequence 2185, Ap
c	408	18	0.5	417	4	US-09-328-352-3846	Sequence 3846, Ap
	409	18	0.5	423	1	US-08-470-179-91	Sequence 91, Appl
c	410	18	0.5	432	4	US-09-060-299-5	Sequence 5, Appli
c	411	18	0.5	432	4	US-09-402-923A-5	Sequence 5, Appli
	412	18	0.5	435	4	US-09-252-991A-5863	Sequence 5863, Ap
c	413	18	0.5	443	4	US-09-621-976-12875	Sequence 12875, A
	414	18	0.5	444	2	US-09-109-266-5	Sequence 5, Appli
c	415	18	0.5	465	6	5496550-9	Patent No. 5496550
c	416	18	0.5	466	6	5496550-7	Patent No. 5496550
c	417	18	0.5	484	6	5496550-5	Patent No. 5496550
c	418	18	0.5	552	4	US-09-621-976-11006	Sequence 11006, A
c	419	18	0.5	570	3	US-09-122-443-1	Sequence 1, Appli
c	420	18	0.5	570	4	US-09-558-089-1	Sequence 1, Appli
c	421	18	0.5	570	4	US-09-558-087-1	Sequence 1, Appli
	422	18	0.5	593	4	US-09-691-538A-12	Sequence 12, Appl
c	423	18	0.5	604	4	US-08-831-399-3	Sequence 3, Appli
c	424	18	0.5	604	4	US-09-366-862-3	Sequence 3, Appli
c	425	18	0.5	604	4	US-09-368-772-3	Sequence 3, Appli
c	426	18	0.5	647	4	US-09-669-751-54	Sequence 54, Appl
	427	18	0.5	683	4	US-09-023-655-415	Sequence 415, App
c	428	18	0.5	687	5	PCT-US94-04361-25	Sequence 25, Appl
	429	18	0.5	688	3	US-08-998-416-915	Sequence 915, App
c	430	18	0.5	732	4	US-09-479-645A-63	Sequence 63, Appl
c	431	18	0.5	792	1	US-08-300-903A-1	Sequence 1, Appli
c	432	18	0.5	792	4	US-08-988-197-1	Sequence 1, Appli
	433	18	0.5	809	2	US-08-370-909-1	Sequence 1, Appli
	434	18	0.5	809	3	US-09-056-105-22	Sequence 22, Appl
c	435	18	0.5	817	3	US-08-998-416-443	Sequence 443, App
c	436	18	0.5	846	4	US-09-976-594-797	Sequence 797, App
	437	18	0.5	867	4	US-09-489-039A-5593	Sequence 5593, Ap
c	438	18	0.5	978	3	US-08-927-219-50	Sequence 50, Appl
	439	18	0.5	990	4	US-09-489-039A-7102	Sequence 7102, Ap
c	440	18	0.5	1026	4	US-09-687-637B-2	Sequence 2, Appli
	441	18	0.5	1035	4	US-09-579-664B-6	Sequence 6, Appli
c	442	18	0.5	1037	1	US-08-240-124-1	Sequence 1, Appli
c	443	18	0.5	1037	1	US-08-453-943-1	Sequence 1, Appli
c	444	18	0.5	1037	2	US-09-057-121-1	Sequence 1, Appli
c	445	18	0.5	1037	3	US-09-358-734-1	Sequence 1, Appli
c	446	18	0.5	1037	4	US-09-181-585-3	Sequence 3, Appli
c	447	18	0.5	1059	4	US-09-489-039A-1984	Sequence 1984, Ap
c	448	18	0.5	1070	1	US-08-299-567-8	Sequence 8, Appli
c	449	18	0.5	1097	2	US-08-978-404B-4	Sequence 4, Appli
c	450	18	0.5	1097	4	US-09-620-312D-472	Sequence 472, App
c	451	18	0.5	1103	2	US-09-016-366A-24	Sequence 24, Appl
	452	18	0.5	1120	3	US-08-586-165-1	Sequence 1, Appli
c	453	18	0.5	1159	4	US-09-181-585-1	Sequence 1, Appli
	454	18	0.5	1198	3	US-09-319-989-1	Sequence 1, Appli
	455	18	0.5	1218	4	US-09-252-991A-9482	Sequence 9482, Ap
c	456	18	0.5	1219	2	US-08-978-404B-7	Sequence 7, Appli
	457	18	0.5	1281	4	US-09-328-352-2286	Sequence 2286, Ap
	458	18	0.5	1281	4	US-09-489-039A-3590	Sequence 3590, Ap
c	459	18	0.5	1287	4	US-09-252-991A-5766	Sequence 5766, Ap
c	460	18	0.5	1290	4	US-09-252-991A-9349	Sequence 9349, Ap
c	461	18	0.5	1329	4	US-09-252-991A-5804	Sequence 5804, Ap
	462	18	0.5	1376	4	US-09-443-184-44	Sequence 44, Appl
	463	18	0.5	1390	4	US-09-205-258-124	Sequence 124, App
c	464	18	0.5	1441	3	US-08-927-219-78	Sequence 78, Appl
c	465	18	0.5	1471	4	US-09-181-585-2	Sequence 2, Appli
c	466	18	0.5	1497	4	US-09-620-312D-366	Sequence 366, App
	467	18	0.5	1517	3	US-08-963-602-6	Sequence 6, Appli
	468	18	0.5	1518	2	US-08-820-170A-20	Sequence 20, Appl
	469	18	0.5	1518	3	US-09-055-699-20	Sequence 20, Appl
	470	18	0.5	1518	3	US-09-273-565-20	Sequence 20, Appl
	471	18	0.5	1518	4	US-09-565-538-20	Sequence 20, Appl
	472	18	0.5	1518	4	US-09-661-468-20	Sequence 20, Appl
	473	18	0.5	1518	4	US-09-976-165-20	Sequence 20, Appl
	474	18	0.5	1578	3	US-09-416-050A-1	Sequence 1, Appli
	475	18	0.5	1578	3	US-09-664-800-1	Sequence 1, Appli
	476	18	0.5	1578	3	US-09-665-309-1	Sequence 1, Appli
	477	18	0.5	1578	3	US-09-661-569-1	Sequence 1, Appli
	478	18	0.5	1588	4	US-09-490-291-7	Sequence 7, Appli
c	479	18	0.5	1596	4	US-09-489-039A-2553	Sequence 2553, Ap
c	480	18	0.5	1614	4	US-09-016-434-1151	Sequence 1151, Ap
c	481	18	0.5	1615	3	US-08-308-814-1	Sequence 1, Appli
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	483	18	0.5	1677	2	US-08-684-101-1	Sequence 1, Appli
	484	18	0.5	1677	3	US-09-205-814-1	Sequence 1, Appli
	485	18	0.5	1710	1	US-07-903-103-3	Sequence 3, Appli
	486	18	0.5	1710	1	US-08-044-619A-3	Sequence 3, Appli
	487	18	0.5	1710	1	US-08-283-911-3	Sequence 3, Appli
	488	18	0.5	1710	1	US-08-245-500A-4	Sequence 4, Appli
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	493	18	0.5	1710	1	US-08-390-517A-4	Sequence 4, Appli
	494	18	0.5	1710	1	US-08-390-515A-4	Sequence 4, Appli
	495	18	0.5	1710	2	US-08-801-718-4	Sequence 4, Appli
	496	18	0.5	1710	3	US-09-073-567-12	Sequence 12, Appl
	497	18	0.5	1710	4	US-09-170-159A-4	Sequence 4, Appli
	498	18	0.5	1710	4	US-09-480-718-45	Sequence 45, Appl
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	502	18	0.5	1857	4	US-09-252-991A-5847	Sequence 5847, Ap
	503	18	0.5	1858	3	US-08-813-574-1	Sequence 1, Appli
	504	18	0.5	1860	2	US-08-372-652-7	Sequence 7, Appli
	505	18	0.5	1860	5	PCT-US95-16311-7	Sequence 7, Appli
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c	508	18	0.5	1881	4	US-09-833-381-1406	Sequence 1406, Ap
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	512	18	0.5	1934	3	US-08-776-844-1	Sequence 1, Appli
	513	18	0.5	1934	4	US-09-909-325-1	Sequence 1, Appli
	514	18	0.5	1934	4	US-09-909-326-1	Sequence 1, Appli
	515	18	0.5	1949	3	US-09-146-221-1	Sequence 1, Appli
	516	18	0.5	1959	1	US-08-342-411A-3	Sequence 3, Appli
	517	18	0.5	1959	5	PCT-US94-12883-4	Sequence 4, Appli
	518	18	0.5	1995	1	US-08-425-069-3	Sequence 3, Appli
	519	18	0.5	1995	2	US-08-317-844B-3	Sequence 3, Appli
c	520	18	0.5	2023	4	US-09-491-522-6	Sequence 6, Appli
c	521	18	0.5	2036	3	US-08-923-454A-17	Sequence 17, Appl
c	522	18	0.5	2065	3	US-08-335-865J-8	Sequence 8, Appli
	523	18	0.5	2077	4	US-09-921-099A-16	Sequence 16, Appl
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	525	18	0.5	2117	4	US-09-581-105-4	Sequence 4, Appli
	526	18	0.5	2190	4	US-09-625-188-19	Sequence 19, Appl
c	527	18	0.5	2196	4	US-09-252-991A-9319	Sequence 9319, Ap
c	528	18	0.5	2205	3	US-08-888-077A-41	Sequence 41, Appl
	529	18	0.5	2338	1	US-08-425-069-1	Sequence 1, Appli
	530	18	0.5	2338	2	US-08-317-844B-1	Sequence 1, Appli
	531	18	0.5	2341	4	US-09-620-312D-423	Sequence 423, App
c	532	18	0.5	2362	4	US-09-907-794A-194	Sequence 194, App
c	533	18	0.5	2362	4	US-09-905-125A-194	Sequence 194, App
c	534	18	0.5	2362	4	US-09-902-775A-194	Sequence 194, App
c	535	18	0.5	2398	4	US-09-687-637B-21	Sequence 21, Appl
	536	18	0.5	2413	3	US-09-613-182-10	Sequence 10, Appl
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	541	18	0.5	2509	3	US-09-146-221-5	Sequence 5, Appli
	542	18	0.5	2544	4	US-09-235-451-33	Sequence 33, Appl
	543	18	0.5	2561	3	US-09-146-221-7	Sequence 7, Appli
c	544	18	0.5	2563	1	US-08-423-441-1	Sequence 1, Appli
c	545	18	0.5	2624	4	US-09-370-838-19	Sequence 19, Appl
	546	18	0.5	2636	2	US-08-820-170A-21	Sequence 21, Appl
	547	18	0.5	2636	3	US-09-055-699-21	Sequence 21, Appl
	548	18	0.5	2636	3	US-09-273-565-21	Sequence 21, Appl
	549	18	0.5	2636	4	US-09-565-538-21	Sequence 21, Appl
	550	18	0.5	2636	4	US-09-661-468-21	Sequence 21, Appl
	551	18	0.5	2636	4	US-09-976-165-21	Sequence 21, Appl
	552	18	0.5	2682	1	US-07-855-793-3	Sequence 3, Appli
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	559	18	0.5	3106	4	US-09-392-714-4	Sequence 4, Appli
	560	18	0.5	3231	1	US-08-195-152-1	Sequence 1, Appli
	561	18	0.5	3231	4	US-08-754-311B-1	Sequence 1, Appli
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	571	18	0.5	3288	4	US-09-549-679-1	Sequence 1, Appli
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	574	18	0.5	3312	5	PCT-US94-04190-1	Sequence 1, Appli
	575	18	0.5	3463	4	US-09-533-220A-1	Sequence 1, Appli
	576	18	0.5	3500	3	US-09-197-636-7	Sequence 7, Appli
c	577	18	0.5	3518	4	US-09-412-210-2	Sequence 2, Appli
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	580	18	0.5	3681	1	US-08-909-984A-3	Sequence 3, Appli
	581	18	0.5	3681	1	US-08-909-983-3	Sequence 3, Appli
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c	583	18	0.5	3695	1	US-08-203-676-1	Sequence 1, Appli
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	585	18	0.5	3771	1	US-08-185-432-3	Sequence 3, Appli
c	586	18	0.5	3771	1	US-08-185-432-23	Sequence 23, Appl
	587	18	0.5	3807	4	US-09-645-456A-8	Sequence 8, Appli
	588	18	0.5	3807	4	US-09-425-324A-8	Sequence 8, Appli
	589	18	0.5	3807	4	US-09-645-791-8	Sequence 8, Appli
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	591	18	0.5	3831	4	US-09-645-456A-5	Sequence 5, Appli
	592	18	0.5	3831	4	US-09-425-324A-5	Sequence 5, Appli
	593	18	0.5	3831	4	US-09-645-791-5	Sequence 5, Appli
	594	18	0.5	3894	4	US-09-645-456A-7	Sequence 7, Appli
	595	18	0.5	3894	4	US-09-425-324A-7	Sequence 7, Appli
	596	18	0.5	3894	4	US-09-645-791-7	Sequence 7, Appli
	597	18	0.5	3918	4	US-09-645-456A-3	Sequence 3, Appli
	598	18	0.5	3918	4	US-09-425-324A-3	Sequence 3, Appli
	599	18	0.5	3918	4	US-09-645-791-3	Sequence 3, Appli
	600	18	0.5	3937	3	US-08-586-165-8	Sequence 8, Appli
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	602	18	0.5	3972	4	US-09-645-456A-6	Sequence 6, Appli
	603	18	0.5	3972	4	US-09-425-324A-6	Sequence 6, Appli
	604	18	0.5	3972	4	US-09-645-791-6	Sequence 6, Appli
	605	18	0.5	3996	4	US-09-645-456A-2	Sequence 2, Appli
	606	18	0.5	3996	4	US-09-425-324A-2	Sequence 2, Appli
	607	18	0.5	3996	4	US-09-645-791-2	Sequence 2, Appli
	608	18	0.5	3997	3	US-08-821-994-72	Sequence 72, Appl
	609	18	0.5	4055	4	US-09-688-188B-10	Sequence 10, Appl
	610	18	0.5	4055	4	US-09-291-417D-10	Sequence 10, Appl
	611	18	0.5	4059	4	US-09-645-456A-4	Sequence 4, Appli
	612	18	0.5	4059	4	US-09-425-324A-4	Sequence 4, Appli
	613	18	0.5	4059	4	US-09-645-791-4	Sequence 4, Appli
	614	18	0.5	4062	4	US-09-620-312D-348	Sequence 348, App
	615	18	0.5	4080	2	US-08-446-345-35	Sequence 35, Appl
	616	18	0.5	4083	4	US-09-579-664B-7	Sequence 7, Appli
	617	18	0.5	4083	4	US-09-645-456A-1	Sequence 1, Appli
	618	18	0.5	4083	4	US-09-425-324A-1	Sequence 1, Appli
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	621	18	0.5	4112	2	US-08-452-567-2	Sequence 2, Appli
	622	18	0.5	4112	2	US-08-452-427-2	Sequence 2, Appli
	623	18	0.5	4112	3	US-09-085-407-2	Sequence 2, Appli
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	625	18	0.5	4171	4	US-09-667-422-3	Sequence 3, Appli
	626	18	0.5	4181	3	US-09-393-569-1	Sequence 1, Appli
	627	18	0.5	4182	4	US-09-667-422-2	Sequence 2, Appli
	628	18	0.5	4203	4	US-09-667-422-1	Sequence 1, Appli
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	634	18	0.5	4616	2	US-08-452-567-1	Sequence 1, Appli
	635	18	0.5	4616	2	US-08-452-427-1	Sequence 1, Appli
	636	18	0.5	4616	3	US-09-085-407-1	Sequence 1, Appli
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	638	18	0.5	4803	3	US-09-197-636-1	Sequence 1, Appli
	639	18	0.5	4803	3	US-09-197-636-3	Sequence 3, Appli
	640	18	0.5	4810	1	US-08-188-281B-3	Sequence 3, Appli
	641	18	0.5	4810	1	US-08-453-552-7	Sequence 7, Appli
	642	18	0.5	4810	2	US-08-710-637-7	Sequence 7, Appli
	643	18	0.5	4810	5	PCT-US93-00907-7	Sequence 7, Appli
	644	18	0.5	4810	5	PCT-US94-07280-3	Sequence 3, Appli
	645	18	0.5	4810	5	PCT-US95-01087-3	Sequence 3, Appli
c	646	18	0.5	4843	4	US-09-060-299-2	Sequence 2, Appli
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	648	18	0.5	4849	2	US-08-540-804-13	Sequence 13, Appl
	649	18	0.5	4849	2	US-08-218-265-13	Sequence 13, Appl
	650	18	0.5	4849	3	US-08-521-872-13	Sequence 13, Appl
	651	18	0.5	4849	3	US-08-590-399-13	Sequence 13, Appl
	652	18	0.5	4911	4	US-09-718-692-1	Sequence 1, Appli
	653	18	0.5	4911	4	US-09-718-852-1	Sequence 1, Appli
	654	18	0.5	4911	4	US-09-718-815-1	Sequence 1, Appli
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	656	18	0.5	5063	1	US-08-185-432-1	Sequence 1, Appli
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c	658	18	0.5	5098	4	US-09-402-923A-1	Sequence 1, Appli
c	659	18	0.5	5117	3	US-08-854-585-1	Sequence 1, Appli
c	660	18	0.5	5117	4	US-09-447-533-1	Sequence 1, Appli
c	661	18	0.5	5117	5	PCT-US95-05512-1	Sequence 1, Appli
	662	18	0.5	5125	1	US-08-453-552-11	Sequence 11, Appl
	663	18	0.5	5125	2	US-08-710-637-11	Sequence 11, Appl
	664	18	0.5	5125	5	PCT-US93-00907-11	Sequence 11, Appl
	665	18	0.5	5243	2	US-08-414-335-2	Sequence 2, Appli
	666	18	0.5	5267	3	US-08-976-255-2	Sequence 2, Appli
	667	18	0.5	5323	1	US-08-453-552-9	Sequence 9, Appli
	668	18	0.5	5323	2	US-08-710-637-9	Sequence 9, Appli
	669	18	0.5	5323	5	PCT-US93-00907-9	Sequence 9, Appli
c	670	18	0.5	5414	4	US-08-628-829-13	Sequence 13, Appl
c	671	18	0.5	5621	4	US-09-566-921-106	Sequence 106, App
	672	18	0.5	5828	4	US-09-023-655-1386	Sequence 1386, Ap
c	673	18	0.5	5962	6	5386025-5	Patent No. 5386025
c	674	18	0.5	5975	1	US-08-404-354B-1	Sequence 1, Appli
c	675	18	0.5	5975	1	US-08-314-083B-1	Sequence 1, Appli
c	676	18	0.5	5975	1	US-08-435-675B-1	Sequence 1, Appli
c	677	18	0.5	5975	1	US-08-336-257A-3	Sequence 3, Appli
c	678	18	0.5	5975	3	US-08-884-599-1	Sequence 1, Appli
	679	18	0.5	6152	1	US-08-557-139-1	Sequence 1, Appli
	680	18	0.5	6513	1	US-08-338-702-7	Sequence 7, Appli
	681	18	0.5	6513	1	US-08-337-339-7	Sequence 7, Appli
	682	18	0.5	6513	1	US-08-724-095-7	Sequence 7, Appli
	683	18	0.5	6513	5	PCT-US95-14262-7	Sequence 7, Appli
	684	18	0.5	6513	5	PCT-US95-14378-7	Sequence 7, Appli

	685	18	0.5	6519	2	US-08-808-793-24	Sequence 24, Appl
c	686	18	0.5	6692	4	US-09-491-522-1	Sequence 1, Appli
	687	18	0.5	7478	4	US-09-618-425-10	Sequence 10, Appl
	688	18	0.5	7498	2	US-08-816-693A-1	Sequence 1, Appli
	689	18	0.5	7498	3	US-08-885-291-1	Sequence 1, Appli
	690	18	0.5	7498	3	US-09-496-672-1	Sequence 1, Appli
	691	18	0.5	8252	1	US-08-046-585-15	Sequence 15, Appl
	692	18	0.5	8252	1	US-08-393-703-15	Sequence 15, Appl
	693	18	0.5	8252	5	PCT-US93-11721-15	Sequence 15, Appl
c	694	18	0.5	10014	3	US-08-927-219-130	Sequence 130, App
c	695	18	0.5	13993	4	US-09-220-132-20	Sequence 20, Appl
c	696	18	0.5	14070	4	US-09-108-006C-2	Sequence 2, Appli
	697	18	0.5	14561	4	US-09-392-714-1	Sequence 1, Appli
	698	18	0.5	15602	4	US-09-844-634-17	Sequence 17, Appl
	699	18	0.5	22671	4	US-08-976-259-14	Sequence 14, Appl
c	700	18	0.5	44848	4	US-09-435-739-42	Sequence 42, Appl
	701	18	0.5	50000	4	US-09-146-053-4	Sequence 4, Appli
	702	18	0.5	118067	4	US-09-497-855A-32	Sequence 32, Appl
	703	18	0.5	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	704	17	0.4	18	2	US-08-863-639A-17	Sequence 17, Appl
c	705	17	0.4	21	2	US-08-267-803B-66	Sequence 66, Appl
	706	17	0.4	21	2	US-08-863-639A-28	Sequence 28, Appl
	707	17	0.4	21	2	US-08-863-639A-40	Sequence 40, Appl
c	708	17	0.4	21	2	US-08-863-639A-60	Sequence 60, Appl
	709	17	0.4	21	2	US-08-863-639A-66	Sequence 66, Appl
c	710	17	0.4	21	2	US-08-863-639A-69	Sequence 69, Appl
c	711	17	0.4	21	2	US-08-863-639A-87	Sequence 87, Appl
	712	17	0.4	24	2	US-08-863-639A-94	Sequence 94, Appl
	713	17	0.4	30	1	US-08-068-747-6	Sequence 6, Appli
c	714	17	0.4	30	1	US-08-068-747-11	Sequence 11, Appl
	715	17	0.4	30	2	US-08-863-639A-30	Sequence 30, Appl
	716	17	0.4	30	3	US-09-135-994-4	Sequence 4, Appli
	717	17	0.4	30	4	US-09-684-843A-4	Sequence 4, Appli
	718	17	0.4	31	2	US-08-570-155-14	Sequence 14, Appl
	719	17	0.4	31	5	PCT-US95-02861-14	Sequence 14, Appl
c	720	17	0.4	33	2	US-08-863-639A-29	Sequence 29, Appl
	721	17	0.4	33	4	US-09-475-947A-251	Sequence 251, App
c	722	17	0.4	42	3	US-09-162-484-7	Sequence 7, Appli
c	723	17	0.4	43	2	US-08-531-927B-17	Sequence 17, Appl
c	724	17	0.4	47	2	US-08-039-198B-18	Sequence 18, Appl
c	725	17	0.4	47	2	US-08-182-067-23	Sequence 23, Appl
c	726	17	0.4	47	2	US-08-465-313-23	Sequence 23, Appl
	727	17	0.4	47	4	US-09-422-978-1690	Sequence 1690, Ap
	728	17	0.4	50	3	US-08-732-218-5	Sequence 5, Appli
c	729	17	0.4	51	1	US-08-068-747-1	Sequence 1, Appli
c	730	17	0.4	51	4	US-09-443-199C-1053	Sequence 1053, Ap
c	731	17	0.4	51	4	US-09-443-199C-1054	Sequence 1054, Ap
c	732	17	0.4	52	3	US-09-332-769-3	Sequence 3, Appli
c	733	17	0.4	52	3	US-09-456-153-3	Sequence 3, Appli
c	734	17	0.4	52	4	US-09-455-627-3	Sequence 3, Appli
c	735	17	0.4	52	4	US-09-426-533-3	Sequence 3, Appli
c	736	17	0.4	52	4	US-09-609-205-4	Sequence 4, Appli
c	737	17	0.4	52	4	US-09-516-945-3	Sequence 3, Appli
c	738	17	0.4	52	4	US-09-757-218-4	Sequence 4, Appli
c	739	17	0.4	52	4	US-09-516-757-3	Sequence 3, Appli
c	740	17	0.4	52	4	US-09-516-750-3	Sequence 3, Appli
c	741	17	0.4	52	4	US-09-342-577-4	Sequence 4, Appli
c	742	17	0.4	52	4	US-09-516-756-3	Sequence 3, Appli
c	743	17	0.4	52	4	US-09-828-061A-4	Sequence 4, Appli
c	744	17	0.4	52	4	US-09-463-917-3	Sequence 3, Appli
c	745	17	0.4	52	4	US-09-347-673-4	Sequence 4, Appli
c	746	17	0.4	52	4	US-09-757-213-4	Sequence 4, Appli
c	747	17	0.4	52	4	US-09-656-653-3	Sequence 3, Appli
c	748	17	0.4	52	4	US-09-757-251-4	Sequence 4, Appli
c	749	17	0.4	52	4	US-09-828-259A-4	Sequence 4, Appli
c	750	17	0.4	52	4	US-09-719-878-4	Sequence 4, Appli
c	751	17	0.4	52	4	US-09-757-217A-4	Sequence 4, Appli
c	752	17	0.4	52	4	US-09-828-325A-4	Sequence 4, Appli
c	753	17	0.4	52	4	US-09-756-248-3	Sequence 3, Appli
c	754	17	0.4	53	4	US-09-136-080E-50	Sequence 50, Appl
	755	17	0.4	54	4	US-09-479-645A-177	Sequence 177, App
	756	17	0.4	54	4	US-09-479-645A-203	Sequence 203, App
	757	17	0.4	59	4	US-08-407-620A-45	Sequence 45, Appl
c	758	17	0.4	64	1	US-08-388-672A-13	Sequence 13, Appl
c	759	17	0.4	64	3	US-09-080-554-13	Sequence 13, Appl
	760	17	0.4	68	1	US-08-208-886C-23	Sequence 23, Appl
	761	17	0.4	68	1	US-08-704-744-23	Sequence 23, Appl
	762	17	0.4	68	1	US-08-469-557-23	Sequence 23, Appl
	763	17	0.4	68	2	US-08-290-793B-23	Sequence 23, Appl
c	764	17	0.4	69	1	US-08-374-641-2	Sequence 2, Appli
	765	17	0.4	76	4	US-09-136-080E-6	Sequence 6, Appli
	766	17	0.4	78	1	US-08-446-102-1	Sequence 1, Appli
c	767	17	0.4	78	1	US-08-446-102-2	Sequence 2, Appli
c	768	17	0.4	78	3	US-08-617-010C-15	Sequence 15, Appl
c	769	17	0.4	78	3	US-09-566-591-15	Sequence 15, Appl
c	770	17	0.4	78	4	US-08-744-481A-25	Sequence 25, Appl
	771	17	0.4	80	4	US-09-136-080E-4	Sequence 4, Appli
c	772	17	0.4	91	4	US-09-091-952A-15	Sequence 15, Appl
c	773	17	0.4	94	4	US-09-091-952A-14	Sequence 14, Appl
	774	17	0.4	103	3	US-08-513-968-56	Sequence 56, Appl
c	775	17	0.4	103	4	US-09-136-080E-7	Sequence 7, Appli
c	776	17	0.4	106	2	US-08-613-235-15	Sequence 15, Appl
c	777	17	0.4	117	1	US-08-467-420A-68	Sequence 68, Appl
c	778	17	0.4	117	1	US-08-470-110A-68	Sequence 68, Appl
c	779	17	0.4	117	1	US-08-667-769A-68	Sequence 68, Appl
c	780	17	0.4	117	2	US-08-940-371-68	Sequence 68, Appl
c	781	17	0.4	117	5	PCT-US95-17082A-68	Sequence 68, Appl
c	782	17	0.4	121	2	US-08-483-636-71	Sequence 71, Appl
c	783	17	0.4	121	2	US-08-483-632-71	Sequence 71, Appl
c	784	17	0.4	141	1	US-08-661-627-4	Sequence 4, Appli
	785	17	0.4	154	1	US-08-469-802B-6	Sequence 6, Appli
	786	17	0.4	154	2	US-08-267-803B-6	Sequence 6, Appli
	787	17	0.4	160	2	US-08-332-766A-13	Sequence 13, Appl
	788	17	0.4	165	3	US-09-043-303-17	Sequence 17, Appl
	789	17	0.4	168	1	US-08-469-802B-4	Sequence 4, Appli
	790	17	0.4	168	2	US-08-267-803B-4	Sequence 4, Appli
	791	17	0.4	171	1	US-08-469-802B-5	Sequence 5, Appli
	792	17	0.4	171	2	US-08-267-803B-5	Sequence 5, Appli
c	793	17	0.4	189	3	US-08-905-223-253	Sequence 253, App
c	794	17	0.4	192	2	US-08-442-809A-49	Sequence 49, Appl
	795	17	0.4	195	1	US-08-469-802B-2	Sequence 2, Appli
	796	17	0.4	195	2	US-08-267-803B-2	Sequence 2, Appli
c	797	17	0.4	216	4	US-09-621-976-15427	Sequence 15427, A
	798	17	0.4	228	6	5273901-10	Patent No. 5273901
	799	17	0.4	228	6	5482709-9	Patent No. 5482709
	800	17	0.4	234	1	US-08-469-802B-3	Sequence 3, Appli
	801	17	0.4	234	2	US-08-267-803B-3	Sequence 3, Appli
c	802	17	0.4	243	4	US-09-833-381-107	Sequence 107, App
c	803	17	0.4	248	3	US-08-959-381A-6	Sequence 6, Appli
c	804	17	0.4	248	4	US-09-621-976-9776	Sequence 9776, Ap
c	805	17	0.4	263	2	US-08-332-766A-12	Sequence 12, Appl
c	806	17	0.4	268	4	US-09-313-294A-909	Sequence 909, App
	807	17	0.4	270	4	US-09-146-054-8	Sequence 8, Appli
	808	17	0.4	270	4	US-09-664-977A-8	Sequence 8, Appli
	809	17	0.4	278	4	US-09-313-294A-2240	Sequence 2240, Ap
c	810	17	0.4	278	4	US-09-016-434-333	Sequence 333, App
	811	17	0.4	283	2	US-08-332-766A-21	Sequence 21, Appl
	812	17	0.4	286	2	US-08-332-766A-6	Sequence 6, Appli
	813	17	0.4	299	4	US-09-313-294A-6279	Sequence 6279, Ap
	814	17	0.4	300	3	US-09-135-994-3	Sequence 3, Appli
	815	17	0.4	300	4	US-09-684-843A-3	Sequence 3, Appli
	816	17	0.4	308	3	US-09-094-207A-2	Sequence 2, Appli
	817	17	0.4	313	4	US-09-118-464-11	Sequence 11, Appl
	818	17	0.4	318	2	US-08-318-157B-18	Sequence 18, Appl
	819	17	0.4	318	4	US-09-672-609-20	Sequence 20, Appl
c	820	17	0.4	318	4	US-09-118-554-40	Sequence 40, Appl
c	821	17	0.4	318	4	US-09-118-627-40	Sequence 40, Appl
	822	17	0.4	318	4	US-09-025-403A-20	Sequence 20, Appl
c	823	17	0.4	318	4	US-09-602-877A-40	Sequence 40, Appl
	824	17	0.4	318	4	US-09-253-794-18	Sequence 18, Appl
	825	17	0.4	321	1	US-08-459-310-13	Sequence 13, Appl
	826	17	0.4	321	1	US-08-459-310-16	Sequence 16, Appl
c	827	17	0.4	323	4	US-09-621-976-81	Sequence 81, Appl
	828	17	0.4	325	2	US-08-531-927B-3	Sequence 3, Appli
	829	17	0.4	330	4	US-09-672-609-21	Sequence 21, Appl
	830	17	0.4	330	4	US-09-025-403A-21	Sequence 21, Appl

	831	17	0.4	330	4	US-09-343-698-7	Sequence 7, Appli
	832	17	0.4	330	4	US-08-325-955-7	Sequence 7, Appli
	833	17	0.4	333	1	US-08-491-845-15	Sequence 15, Appl
	834	17	0.4	333	2	US-08-483-636-72	Sequence 72, Appl
	835	17	0.4	333	2	US-08-483-632-72	Sequence 72, Appl
	836	17	0.4	336	2	US-08-859-649-32	Sequence 32, Appl
	837	17	0.4	336	4	US-08-207-861-32	Sequence 32, Appl
	838	17	0.4	336	4	US-08-859-648-32	Sequence 32, Appl
	839	17	0.4	339	1	US-08-467-420A-69	Sequence 69, Appl
	840	17	0.4	339	1	US-08-470-110A-69	Sequence 69, Appl
	841	17	0.4	339	1	US-08-667-769A-69	Sequence 69, Appl
	842	17	0.4	339	2	US-08-940-371-69	Sequence 69, Appl
	843	17	0.4	339	3	US-08-513-968-81	Sequence 81, Appl
c	844	17	0.4	339	4	US-09-621-976-44	Sequence 44, Appl
	845	17	0.4	339	5	PCT-US95-17082A-69	Sequence 69, Appl
	846	17	0.4	340	4	US-08-407-620A-14	Sequence 14, Appl
	847	17	0.4	342	2	US-08-428-257A-79	Sequence 79, Appl
	848	17	0.4	342	3	US-07-987-264-61	Sequence 61, Appl
c	849	17	0.4	348	4	US-09-621-976-17781	Sequence 17781, A
c	850	17	0.4	355	3	US-08-301-162-9	Sequence 9, Appli
c	851	17	0.4	355	4	US-09-461-240-9	Sequence 9, Appli
c	852	17	0.4	355	4	US-09-968-927-9	Sequence 9, Appli
c	853	17	0.4	357	4	US-09-621-976-14210	Sequence 14210, A
	854	17	0.4	373	4	US-08-407-620A-31	Sequence 31, Appl
	855	17	0.4	379	3	US-08-646-265A-42	Sequence 42, Appl
	856	17	0.4	379	3	US-08-646-265A-46	Sequence 46, Appl
	857	17	0.4	379	3	US-08-646-265A-56	Sequence 56, Appl
	858	17	0.4	379	3	US-08-646-265A-64	Sequence 64, Appl
	859	17	0.4	379	3	US-08-646-265A-76	Sequence 76, Appl
	860	17	0.4	379	3	US-08-646-265A-80	Sequence 80, Appl
	861	17	0.4	379	3	US-08-646-265A-84	Sequence 84, Appl
	862	17	0.4	379	3	US-08-646-265A-86	Sequence 86, Appl
	863	17	0.4	379	3	US-08-646-265A-90	Sequence 90, Appl
	864	17	0.4	381	2	US-08-353-372A-37	Sequence 37, Appl
	865	17	0.4	381	4	US-08-057-430A-29	Sequence 29, Appl
	866	17	0.4	386	1	US-08-463-128-5	Sequence 5, Appli
	867	17	0.4	386	1	US-08-463-128-9	Sequence 9, Appli
	868	17	0.4	386	1	US-08-463-298-5	Sequence 5, Appli
	869	17	0.4	386	1	US-08-463-298-9	Sequence 9, Appli
	870	17	0.4	386	2	US-08-436-339A-5	Sequence 5, Appli
	871	17	0.4	386	2	US-08-436-339A-9	Sequence 9, Appli
	872	17	0.4	386	4	US-08-454-899G-30	Sequence 30, Appl
	873	17	0.4	386	4	US-08-454-899G-62	Sequence 62, Appl
	874	17	0.4	386	4	US-08-454-899G-66	Sequence 66, Appl
	875	17	0.4	386	5	PCT-US94-10395-4	Sequence 4, Appli
	876	17	0.4	386	5	PCT-US94-10395-6	Sequence 6, Appli
	877	17	0.4	390	1	US-08-208-886C-16	Sequence 16, Appl
	878	17	0.4	390	1	US-08-704-744-16	Sequence 16, Appl
	879	17	0.4	390	1	US-08-469-557-16	Sequence 16, Appl
	880	17	0.4	390	2	US-08-290-793B-16	Sequence 16, Appl
	881	17	0.4	393	1	US-08-208-886C-27	Sequence 27, Appl
	882	17	0.4	393	1	US-08-704-744-27	Sequence 27, Appl
	883	17	0.4	393	1	US-08-469-557-27	Sequence 27, Appl
	884	17	0.4	393	2	US-08-290-793B-27	Sequence 27, Appl
c	885	17	0.4	402	4	US-09-833-381-1448	Sequence 1448, Ap
c	886	17	0.4	412	4	US-09-612-033B-5	Sequence 5, Appli
	887	17	0.4	412	4	US-09-833-381-1376	Sequence 1376, Ap
c	888	17	0.4	427	4	US-09-397-787-219	Sequence 219, App
c	889	17	0.4	432	4	US-08-956-171E-541	Sequence 541, App
	890	17	0.4	434	4	US-09-397-787-295	Sequence 295, App
	891	17	0.4	435	4	US-09-252-991A-9921	Sequence 9921, Ap
c	892	17	0.4	438	3	US-08-648-322-1	Sequence 1, Appli
c	893	17	0.4	438	4	US-08-857-389-1	Sequence 1, Appli
c	894	17	0.4	447	4	US-09-252-991A-8401	Sequence 8401, Ap
	895	17	0.4	454	4	US-09-621-976-740	Sequence 740, App
	896	17	0.4	458	4	US-09-621-976-17616	Sequence 17616, A
c	897	17	0.4	459	4	US-09-148-545-36	Sequence 36, Appl
	898	17	0.4	463	4	US-09-621-976-741	Sequence 741, App
c	899	17	0.4	465	4	US-09-252-991A-453	Sequence 453, App
c	900	17	0.4	470	4	US-09-621-976-362	Sequence 362, App
c	901	17	0.4	471	4	US-09-252-991A-10011	Sequence 10011, A
	902	17	0.4	477	3	US-08-706-391B-6	Sequence 6, Appli
	903	17	0.4	477	3	US-09-135-994-1	Sequence 1, Appli

	904	17	0.4	477	4	US-09-684-843A-1	Sequence 1, Appli
c	905	17	0.4	478	4	US-09-621-976-2311	Sequence 2311, Ap
	906	17	0.4	490	4	US-09-679-686B-13	Sequence 13, Appl
	907	17	0.4	491	4	US-09-621-976-2690	Sequence 2690, Ap
c	908	17	0.4	505	4	US-09-621-976-2322	Sequence 2322, Ap
	909	17	0.4	506	1	US-08-469-802B-7	Sequence 7, Appli
	910	17	0.4	506	2	US-08-267-803B-7	Sequence 7, Appli
	911	17	0.4	510	2	US-08-184-009-150	Sequence 150, App
	912	17	0.4	510	2	US-08-458-356-150	Sequence 150, App
	913	17	0.4	510	3	US-08-460-736-150	Sequence 150, App
	914	17	0.4	510	4	US-09-535-370-150	Sequence 150, App
	915	17	0.4	510	4	US-09-833-381-1723	Sequence 1723, Ap
	916	17	0.4	511	4	US-09-556-877-271	Sequence 271, App
	917	17	0.4	511	4	US-09-620-412C-271	Sequence 271, App
	918	17	0.4	511	4	US-09-598-419-271	Sequence 271, App
	919	17	0.4	513	4	US-09-252-991A-411	Sequence 411, App
	920	17	0.4	518	4	US-09-621-976-18651	Sequence 18651, A
	921	17	0.4	524	3	US-08-513-968-49	Sequence 49, Appl
c	922	17	0.4	525	4	US-09-621-976-11737	Sequence 11737, A
	923	17	0.4	533	4	US-09-443-041A-3	Sequence 3, Appli
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	932	17	0.4	600	4	US-09-669-751-177	Sequence 177, App
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ALIGNMENTS

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RESULT 1
US-09-688-188B-11
; Sequence 11, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0328
;  CURRENT APPLICATION NUMBER: US/09/688,188B
;  CURRENT FILING DATE:  2000-10-16
;  PRIOR APPLICATION NUMBER: 09/291,417
;  PRIOR FILING DATE: 1999-04-14
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-688-188B-11

  Query Match             45.2%;  Score 1787;  DB 4;  Length 4133;
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RESULT 2
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; Sequence 11, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 038602/0329
;  CURRENT APPLICATION NUMBER: US/09/291,417D
;  CURRENT FILING DATE:  1999-04-13
;  PRIOR APPLICATION NUMBER: 60/081,784
;  PRIOR FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-291-417D-11

  Query Match             45.2%;  Score 1787;  DB 4;  Length 4133;
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Db       2384 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2443

Qy       2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2444 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2503

Qy       2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
              |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       2504 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2560

Qy       2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2561 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2620

Qy       2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2621 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2680
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Qy       2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2681 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2740

Qy       2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2741 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2800

Qy       2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2801 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2860

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2861 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2920

Qy       2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2921 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2980

Qy       2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2981 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3040

Qy       3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3041 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3100

Qy       3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3101 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3160

Qy       3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3161 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3220

Qy       3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       3221 ACAAACTGCGGGTGTATTACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3280

Qy       3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3281 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3340

Qy       3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3341 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3400

Qy       3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3401 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3460

Qy       3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3461 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3520

Qy       3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3521 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3580

Qy       3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3581 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3640

Qy       3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3641 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3700

Qy       3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3701 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3760

Qy       3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3761 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3820

Qy       3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3821 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3880

Qy       3845 GTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3881 GTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3940

Qy       3905 ACTTCATGACTCTGAACCGTAAC 3927
              |||||||||||||||||||||||
Db       3941 ACTTCATGACTCTGAACCGTAAC 3963

RESULT 3
US-09-579-664B-1
; Sequence 1, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
;  APPLICANT: Immunex Corporation
;  APPLICANT:  Bird, Timothy A.
;  APPLICANT:  Virca, G. Duke
;  APPLICANT:  Martin, Unja
;  APPLICANT:  Anderson, Dirk M.
;  TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
;  FILE REFERENCE: 2923-A
;  CURRENT APPLICATION NUMBER: US/09/579,664B
;  CURRENT FILING DATE:  2000-05-26
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 896
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-579-664B-1

  Query Match              1.2%;  Score 47;  DB 4;  Length 896;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-11;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTC 53
              |||||||||||||||||||||||||||||||||||||||||||||||
Db         71 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTC 117

RESULT 4
US-09-976-594-368
; Sequence 368, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 368
;   LENGTH: 2913
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 2125081CB1
US-09-976-594-368

  Query Match              0.8%;  Score 31;  DB 4;  Length 2913;
  Best Local Similarity   100.0%;  Pred. No. 0.00043;
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  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        566 CTTTCATTGGGACTCCCTACTGGATGGCTCC 596
              |||||||||||||||||||||||||||||||
Db        545 CTTTCATTGGGACTCCCTACTGGATGGCTCC 575


RESULT 5
US-08-864-038A-1/c
; Sequence 1, Application US/08864038A
; Patent No. 6001592
;  GENERAL INFORMATION:
;    APPLICANT:  Kunio NAKASHIMA et al.
;    TITLE OF INVENTION:  NOVEL POLYPEPTIDE GENE cDNA, VECTOR
;    TITLE OF INVENTION:  CONTAINING SAID cDNA, HOST CELLS TRANSFORMED WITH SAID
;    TITLE OF INVENTION:  VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
;    TITLE OF INVENTION:  SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
;    TITLE OF INVENTION:  TO SAID POLYPEPTIDE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  812-5 Hirano
;      STREET:  Isshinden
;      CITY:  Tsu-city
;      STATE:  Mie-prefecture
;      COUNTRY:  JAPAN
;      ZIP:  514-01
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Word Perfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,038A
;      FILING DATE:  May 28, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8-184459
;      FILING DATE:  15-July-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  C. Bruce Hamburg
;      REGISTRATION NUMBER:  22,389
;      REFERENCE/DOCKET NUMBER:  F-5610
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)986-2340
;      TELEFAX:  (212)953-7733
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2214
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    ORIGINAL SOURCE:
;      ORGANISM:  Pinctada fucata
;      CELL TYPE:  mantle epithelial cell
US-08-864-038A-1

  Query Match             0.7%;  Score 29;  DB 3;  Length 2214;
  Best Local Similarity   100.0%;  Pred. No. 0.0033;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1120 CAGCAGCAGCTGCAGCAGCAGCAGCAGCG 1148
              |||||||||||||||||||||||||||||
Db       1657 CAGCAGCAGCTGCAGCAGCAGCAGCAGCG 1629


RESULT 6
US-08-864-038A-2/c
; Sequence 2, Application US/08864038A
; Patent No. 6001592
;  GENERAL INFORMATION:
;    APPLICANT:  Kunio NAKASHIMA et al.
;    TITLE OF INVENTION:  NOVEL POLYPEPTIDE GENE cDNA, VECTOR
;    TITLE OF INVENTION:  CONTAINING SAID cDNA, HOST CELLS TRANSFORMED WITH SAID
;    TITLE OF INVENTION:  VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
;    TITLE OF INVENTION:  SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
;    TITLE OF INVENTION:  TO SAID POLYPEPTIDE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  812-5 Hirano
;      STREET:  Isshinden
;      CITY:  Tsu-city
;      STATE:  Mie-prefecture
;      COUNTRY:  JAPAN
;      ZIP:  514-01
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Word Perfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,038A
;      FILING DATE:  May 28, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8-184459
;      FILING DATE:  15-July-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  C. Bruce Hamburg
;      REGISTRATION NUMBER:  22,389
;      REFERENCE/DOCKET NUMBER:  F-5610
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)986-2340
;      TELEFAX:  (212)953-7733
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3331
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pinctada fucata
;      CELL TYPE:  mantle epithelial cell
;    FEATURE:  mRNA
;      LOCATION:  from 1 to 3331
;      IDENTIFICATION METHOD:  E (by experiment)
US-08-864-038A-2

  Query Match             0.7%;  Score 29;  DB 3;  Length 3331;
  Best Local Similarity   100.0%;  Pred. No. 0.0033;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1120 CAGCAGCAGCTGCAGCAGCAGCAGCAGCG 1148
              |||||||||||||||||||||||||||||
Db       1706 CAGCAGCAGCTGCAGCAGCAGCAGCAGCG 1678


RESULT 7
US-08-864-038A-4/c
; Sequence 4, Application US/08864038A
; Patent No. 6001592
;  GENERAL INFORMATION:
;    APPLICANT:  Kunio NAKASHIMA et al.
;    TITLE OF INVENTION:  NOVEL POLYPEPTIDE GENE cDNA, VECTOR
;    TITLE OF INVENTION:  CONTAINING SAID cDNA, HOST CELLS TRANSFORMED WITH SAID
;    TITLE OF INVENTION:  VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
;    TITLE OF INVENTION:  SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
;    TITLE OF INVENTION:  TO SAID POLYPEPTIDE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  812-5 Hirano
;      STREET:  Isshinden
;      CITY:  Tsu-city
;      STATE:  Mie-prefecture
;      COUNTRY:  JAPAN
;      ZIP:  514-01
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
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;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Microsoft Windows 95
;       SOFTWARE:  Word Perfect 6.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/864,038A
;       FILING DATE:  May 28, 1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 8-184459
;       FILING DATE:  15-July-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  C. Bruce Hamburg
;       REGISTRATION NUMBER:  22,389
;       REFERENCE/DOCKET NUMBER:  F-5610
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)986-2340
;       TELEFAX:  (212)953-7733
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3331
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Pinctada fucata
;       CELL TYPE:  mantle epithelial cell
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  from 50 to 2263
;       IDENTIFICATION METHOD:  P (by similarity to some other pattern)
US-08-864-038A-4

  Query Match             0.7%;  Score 29;  DB 3;  Length 3331;
  Best Local Similarity   100.0%;  Pred. No. 0.0033;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1120 CAGCAGCAGCTGCAGCAGCAGCAGCAGCG 1148
              |||||||||||||||||||||||||||||
Db       1706 CAGCAGCAGCTGCAGCAGCAGCAGCAGCG 1678


RESULT 8
US-09-976-594-560
; Sequence 560, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 560
;   LENGTH: 8411
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 1327024.5
;   NAME/KEY: unsure
;   LOCATION: 8361, 8372, 8381, 8388, 8398, 8405-8406
;   OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-560

  Query Match             0.7%;  Score 27;  DB 4;  Length 8411;
  Best Local Similarity   100.0%;  Pred. No. 0.024;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1118 AGCAGCAGCAGCTGCAGCAGCAGCAGC 1144
              |||||||||||||||||||||||||||
Db       4073 AGCAGCAGCAGCTGCAGCAGCAGCAGC 4099

RESULT 9
US-09-043-303-14
; Sequence 14, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
;  APPLICANT: TSUJI, Shoji
;  APPLICANT: SANPEI, Kazujiro
;  TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
;  TITLE OF INVENTION: Primers Therefor
;  FILE REFERENCE: 0760-0241P
;  CURRENT APPLICATION NUMBER: US/09/043,303
;  CURRENT FILING DATE: 1998-05-18
;  EARLIER APPLICATION NUMBER: PCT/JP96/01999
;  EARLIER FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 57
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-043-303-14

  Query Match             0.7%;  Score 26;  DB 3;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.084;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||||||
Db          9 GCAGCAGCAGCAACAGCAGCAGCAGC 34


RESULT 10
US-09-043-303-13
; Sequence 13, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
;  APPLICANT: TSUJI, Shoji
;  APPLICANT: SANPEI, Kazujiro
;  TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
;  TITLE OF INVENTION: Primers Therefor
;  FILE REFERENCE: 0760-0241P
;  CURRENT APPLICATION NUMBER: US/09/043,303
;  CURRENT FILING DATE: 1998-05-18
;  EARLIER APPLICATION NUMBER: PCT/JP96/01999
;  EARLIER FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 69
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-043-303-13

  Query Match             0.7%;  Score 26;  DB 3;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||||||
Db         30 GCAGCAGCAGCAACAGCAGCAGCAGC 55


RESULT 11
US-09-043-303-10
; Sequence 10, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
;  APPLICANT: TSUJI, Shoji
;  APPLICANT: SANPEI, Kazujiro
```

```
;  TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
;  TITLE OF INVENTION: Primers Therefor
;  FILE REFERENCE: 0760-0241P
;  CURRENT APPLICATION NUMBER: US/09/043,303
;  CURRENT FILING DATE: 1998-05-18
;  EARLIER APPLICATION NUMBER: PCT/JP96/01999
;  EARLIER FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 75
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-043-303-10

  Query Match             0.7%;  Score 26;  DB 3;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
              ||||||||||||||||||||||||||
Db         15 GCAGCAGCAGCAACAGCAGCAGCAGC 40

RESULT 12
US-09-043-303-11
; Sequence 11, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
;  APPLICANT: TSUJI, Shoji
;  APPLICANT: SANPEI, Kazujiro
;  TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
;  TITLE OF INVENTION: Primers Therefor
;  FILE REFERENCE: 0760-0241P
;  CURRENT APPLICATION NUMBER: US/09/043,303
;  CURRENT FILING DATE: 1998-05-18
;  EARLIER APPLICATION NUMBER: PCT/JP96/01999
;  EARLIER FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 78
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-043-303-11

  Query Match             0.7%;  Score 26;  DB 3;  Length 78;
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RESULT 13
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; Sequence 12, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
;  APPLICANT: TSUJI, Shoji
;  APPLICANT: SANPEI, Kazujiro
;  TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
;  TITLE OF INVENTION: Primers Therefor
;  FILE REFERENCE: 0760-0241P
;  CURRENT APPLICATION NUMBER: US/09/043,303
;  CURRENT FILING DATE: 1998-05-18
;  EARLIER APPLICATION NUMBER: PCT/JP96/01999
;  EARLIER FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 78
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-043-303-12

  Query Match             0.7%;  Score 26;  DB 3;  Length 78;
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Qy       1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
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RESULT 14
US-09-205-995-75
; Sequence 75, Application US/09205995
; Patent No. 6368855
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Minzhen
;  APPLICANT:  Qiu, Gang
;  APPLICANT:  Humphreys, Robert
;  TITLE OF INVENTION:  CANCER CELL VACCINE
;  FILE REFERENCE:  U.S. Application 09/205,995, (CIP)
;  CURRENT APPLICATION NUMBER: US/09/205,995
;  CURRENT FILING DATE:  1998-12-04
;  PRIOR APPLICATION NUMBER:  09/036,746
;  PRIOR FILING DATE:  1998-03-09
;  PRIOR APPLICATION NUMBER:  08/661,627
;  PRIOR FILING DATE:  1996-06-11
;  NUMBER OF SEQ ID NOS:  79
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 75
;   LENGTH: 107
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Reverse gene
;   OTHER INFORMATION: construct corresponding to a  specific region of
;   OTHER INFORMATION: the mouse Ii gene.
US-09-205-995-75

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RESULT 15
US-09-205-995-72
; Sequence 72, Application US/09205995
; Patent No. 6368855
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Minzhen
;  APPLICANT:  Qiu, Gang
;  APPLICANT:  Humphreys, Robert
;  TITLE OF INVENTION:  CANCER CELL VACCINE
;  FILE REFERENCE:  U.S. Application 09/205,995, (CIP)
;  CURRENT APPLICATION NUMBER: US/09/205,995
;  CURRENT FILING DATE:  1998-12-04
;  PRIOR APPLICATION NUMBER:  09/036,746
;  PRIOR FILING DATE:  1998-03-09
;  PRIOR APPLICATION NUMBER:  08/661,627
;  PRIOR FILING DATE:  1996-06-11
;  NUMBER OF SEQ ID NOS:  79
;  SOFTWARE:  PatentIn Ver. 2.0
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;   ORGANISM: Artificial Sequence
;   FEATURE:
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;   OTHER INFORMATION: Description of Artificial Sequence: Reverse gene
;   OTHER INFORMATION: construct corresponding to a  specific region of
;   OTHER INFORMATION: the mouse Ii gene.
US-09-205-995-72

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Perfect score:  3951
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SUMMARIES

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	21	205	5.2	507	14	US-10-029-386-3818	Sequence 3818, Ap
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	24	160	4.0	507	14	US-10-029-386-12798	Sequence 12798, A
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	156	26	0.7	77038	15	US-10-085-117-151	Sequence 151, App
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	173	25	0.6	4621	14	US-10-379-616-9	Sequence 9, Appli
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	176	25	0.6	5718	14	US-10-270-333-8	Sequence 8, Appli
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	183	24	0.6	455	9	US-09-864-761-2102	Sequence 2102, Ap
	184	24	0.6	472	9	US-09-864-761-2216	Sequence 2216, Ap
c	185	24	0.6	506	14	US-10-029-386-7031	Sequence 7031, Ap
c	186	24	0.6	597	9	US-09-893-737-235	Sequence 235, App
	187	24	0.6	615	15	US-10-027-632-97052	Sequence 97052, A
	188	24	0.6	615	15	US-10-027-632-97053	Sequence 97053, A
	189	24	0.6	615	15	US-10-027-632-319129	Sequence 319129,
	190	24	0.6	615	15	US-10-027-632-319130	Sequence 319130,
c	191	24	0.6	1018	9	US-09-864-761-19967	Sequence 19967, A
	192	24	0.6	1578	13	US-10-105-929-10	Sequence 10, Appl
	193	24	0.6	1578	14	US-10-365-227-10	Sequence 10, Appl
	194	24	0.6	2157	14	US-10-029-386-25369	Sequence 25369, A
	195	24	0.6	2219	12	US-10-424-599-103265	Sequence 103265,
	196	24	0.6	2261	15	US-10-374-780A-598	Sequence 598, App
	197	24	0.6	3423	14	US-10-092-390-1	Sequence 1, Appli
	198	24	0.6	3552	14	US-10-365-227-19	Sequence 19, Appl
	199	24	0.6	5184	14	US-10-247-671-55	Sequence 55, Appl
	200	24	0.6	8147	13	US-10-109-886-9	Sequence 9, Appli
c	201	24	0.6	106323	9	US-09-803-661-3	Sequence 3, Appli
c	202	24	0.6	106323	14	US-10-300-827-3	Sequence 3, Appli
c	203	23	0.6	23	10	US-09-291-417-60	Sequence 60, Appl
	204	23	0.6	23	10	US-09-291-417-61	Sequence 61, Appl
	205	23	0.6	96	9	US-09-864-761-25975	Sequence 25975, A
c	206	23	0.6	169	10	US-09-930-213-653	Sequence 653, App
c	207	23	0.6	216	9	US-09-728-444-25	Sequence 25, Appl
	208	23	0.6	355	12	US-10-424-599-77754	Sequence 77754, A
	209	23	0.6	526	14	US-10-029-386-11510	Sequence 11510, A
	210	23	0.6	562	14	US-10-255-536-15	Sequence 15, Appl
c	211	23	0.6	574	12	US-10-424-599-118379	Sequence 118379,
	212	23	0.6	577	9	US-09-864-761-9506	Sequence 9506, Ap
	213	23	0.6	599	12	US-10-424-599-69970	Sequence 69970, A
	214	23	0.6	688	15	US-10-027-632-33554	Sequence 33554, A
	215	23	0.6	789	15	US-10-374-780A-1571	Sequence 1571, Ap
	216	23	0.6	927	13	US-10-029-180-97	Sequence 97, Appl
	217	23	0.6	1353	15	US-10-191-803-99	Sequence 99, Appl
	218	23	0.6	1385	14	US-10-393-590-43	Sequence 43, Appl
	219	23	0.6	1385	14	US-10-393-567-43	Sequence 43, Appl
	220	23	0.6	1385	14	US-10-394-087-43	Sequence 43, Appl
	221	23	0.6	1455	9	US-09-801-368-333	Sequence 333, App
	222	23	0.6	1455	15	US-10-369-493-45717	Sequence 45717, A
	223	23	0.6	1745	9	US-09-819-252-1	Sequence 1, Appli
	224	23	0.6	1745	9	US-09-922-217-1051	Sequence 1051, Ap
	225	23	0.6	1745	9	US-09-833-263-1051	Sequence 1051, Ap
	226	23	0.6	1745	13	US-10-025-380-1051	Sequence 1051, Ap
	227	23	0.6	3178	13	US-10-108-605-124	Sequence 124, App
	228	23	0.6	3178	13	US-10-108-605-128	Sequence 128, App
	229	23	0.6	3455	11	US-09-946-290-11	Sequence 11, Appl
c	230	23	0.6	4065	9	US-09-808-571A-3	Sequence 3, Appli
	231	23	0.6	4248	14	US-10-198-846-11546	Sequence 11546, A
	232	23	0.6	5482	14	US-10-199-937-138	Sequence 138, App
	233	23	0.6	5607	13	US-10-108-605-92	Sequence 92, Appl
c	234	23	0.6	5718	14	US-10-270-333-8	Sequence 8, Appli

	235	23	0.6	9400	14	US-10-270-333-7	Sequence 7, Appli
	236	23	0.6	44577	15	US-10-034-650-4	Sequence 4, Appli
c	237	23	0.6	158001	16	US-10-211-179-11	GENERAL INFORMATI
c	238	23	0.6	165961	15	US-10-085-117-241	Sequence 241, App
	239	22	0.6	30	14	US-10-215-432-43	Sequence 43, Appl
c	240	22	0.6	52	14	US-10-215-432-24	Sequence 24, Appl
	241	22	0.6	54	15	US-10-418-182-300	Sequence 300, App
	242	22	0.6	138	9	US-09-244-694-129	Sequence 129, App
	243	22	0.6	169	14	US-10-029-386-24226	Sequence 24226, A
	244	22	0.6	169	14	US-10-029-386-24541	Sequence 24541, A
	245	22	0.6	181	15	US-10-195-722-2	Sequence 2, Appli
c	246	22	0.6	196	9	US-09-756-095-63	Sequence 63, Appl
c	247	22	0.6	196	10	US-09-941-492-63	Sequence 63, Appl
c	248	22	0.6	196	10	US-09-756-096A-63	Sequence 63, Appl
c	249	22	0.6	196	10	US-09-838-858-63	Sequence 63, Appl
	250	22	0.6	294	9	US-09-244-694-137	Sequence 137, App
	251	22	0.6	316	9	US-09-864-761-17473	Sequence 17473, A
	252	22	0.6	358	13	US-10-040-739-45	Sequence 45, Appl
	253	22	0.6	362	9	US-09-244-694-138	Sequence 138, App
	254	22	0.6	396	9	US-09-728-446-1360	Sequence 1360, Ap
c	255	22	0.6	399	9	US-09-789-919-17	Sequence 17, Appl
	256	22	0.6	436	9	US-09-864-761-686	Sequence 686, App
c	257	22	0.6	500	14	US-10-029-386-11303	Sequence 11303, A
	258	22	0.6	502	9	US-09-783-590-8065	Sequence 8065, Ap
	259	22	0.6	512	10	US-09-770-961-176	Sequence 176, App
	260	22	0.6	521	12	US-10-425-114-34711	Sequence 34711, A
c	261	22	0.6	539	9	US-09-466-320-15	Sequence 15, Appl
c	262	22	0.6	539	14	US-10-050-875-1	Sequence 1, Appli
	263	22	0.6	572	14	US-10-029-386-10526	Sequence 10526, A
	264	22	0.6	588	14	US-10-029-386-10841	Sequence 10841, A
c	265	22	0.6	655	15	US-10-027-632-33446	Sequence 33446, A
	266	22	0.6	683	12	US-10-424-599-44799	Sequence 44799, A
	267	22	0.6	686	9	US-09-910-943-275	Sequence 275, App
	268	22	0.6	718	12	US-10-424-599-44791	Sequence 44791, A
	269	22	0.6	731	14	US-10-161-051-32	Sequence 32, Appl
	270	22	0.6	797	10	US-09-949-029-27	Sequence 27, Appl
	271	22	0.6	808	12	US-10-425-114-5381	Sequence 5381, Ap
	272	22	0.6	887	14	US-10-180-375-83	Sequence 83, Appl
c	273	22	0.6	893	9	US-09-760-294-3	Sequence 3, Appli
c	274	22	0.6	893	9	US-09-760-294-5	Sequence 5, Appli
c	275	22	0.6	893	9	US-09-760-294-6	Sequence 6, Appli
c	276	22	0.6	893	9	US-09-760-294-7	Sequence 7, Appli
c	277	22	0.6	893	9	US-09-760-294-8	Sequence 8, Appli
c	278	22	0.6	893	9	US-09-760-294-9	Sequence 9, Appli
c	279	22	0.6	893	9	US-09-760-294-10	Sequence 10, Appl
	280	22	0.6	897	12	US-10-424-599-127609	Sequence 127609,
	281	22	0.6	957	10	US-09-373-658-73	Sequence 73, Appl
	282	22	0.6	957	10	US-09-373-658-74	Sequence 74, Appl
	283	22	0.6	957	11	US-09-989-687-73	Sequence 73, Appl
	284	22	0.6	957	11	US-09-989-687-74	Sequence 74, Appl
c	285	22	0.6	1070	9	US-09-789-919-67	Sequence 67, Appl
	286	22	0.6	1089	10	US-09-373-658-75	Sequence 75, Appl
	287	22	0.6	1089	11	US-09-989-687-75	Sequence 75, Appl
	288	22	0.6	1089	14	US-10-267-430-1	Sequence 1, Appli
	289	22	0.6	1125	12	US-10-425-114-34515	Sequence 34515, A
	290	22	0.6	1164	14	US-10-180-375-89	Sequence 89, Appl
	291	22	0.6	1312	12	US-10-425-114-17429	Sequence 17429, A
	292	22	0.6	1345	9	US-09-853-450-7	Sequence 7, Appli
c	293	22	0.6	1360	14	US-10-017-161-1345	Sequence 1345, Ap
c	294	22	0.6	1360	15	US-10-292-798-1105	Sequence 1105, Ap
c	295	22	0.6	1388	15	US-10-264-049-518	Sequence 518, App
	296	22	0.6	1427	14	US-10-029-386-20199	Sequence 20199, A
	297	22	0.6	1431	12	US-10-424-599-127608	Sequence 127608,
	298	22	0.6	1434	14	US-10-161-051-44	Sequence 44, Appl
	299	22	0.6	1527	12	US-10-425-114-4772	Sequence 4772, Ap
c	300	22	0.6	1551	14	US-10-032-585-6468	Sequence 6468, Ap
c	301	22	0.6	1578	15	US-10-305-720-1377	Sequence 1377, Ap
c	302	22	0.6	1622	14	US-10-029-386-22666	Sequence 22666, A
	303	22	0.6	1671	15	US-10-374-780A-834	Sequence 834, App
	304	22	0.6	1791	9	US-09-416-384A-6	Sequence 6, Appli
c	305	22	0.6	1839	14	US-10-125-692-9	Sequence 9, Appli
	306	22	0.6	1861	12	US-10-425-114-24826	Sequence 24826, A
	307	22	0.6	1890	15	US-10-094-749-742	Sequence 742, App
	308	22	0.6	1939	12	US-10-424-599-44796	Sequence 44796, A
	309	22	0.6	2018	12	US-10-425-114-25076	Sequence 25076, A
c	310	22	0.6	2034	13	US-10-010-065-5	Sequence 5, Appli
c	311	22	0.6	2034	14	US-10-225-567A-133	Sequence 133, App
	312	22	0.6	2049	12	US-10-425-114-3601	Sequence 3601, Ap
	313	22	0.6	2109	14	US-10-161-051-19	Sequence 19, Appl
	314	22	0.6	2133	15	US-10-104-047-1791	Sequence 1791, Ap
	315	22	0.6	2135	12	US-10-425-114-17550	Sequence 17550, A
	316	22	0.6	2264	15	US-10-108-260A-790	Sequence 790, App
	317	22	0.6	2387	12	US-10-425-114-30696	Sequence 30696, A
	318	22	0.6	2769	14	US-10-128-714-1594	Sequence 1594, Ap
	319	22	0.6	2826	14	US-10-128-714-7594	Sequence 7594, Ap
c	320	22	0.6	3206	16	US-10-293-965-8	Sequence 8, Appli
	321	22	0.6	3308	14	US-10-147-026-3	Sequence 3, Appli
	322	22	0.6	3368	14	US-10-128-714-6594	Sequence 6594, Ap
	323	22	0.6	3909	14	US-10-007-926A-175	Sequence 175, App
	324	22	0.6	3909	15	US-10-305-720-1119	Sequence 1119, Ap
	325	22	0.6	4276	15	US-10-144-194A-89	Sequence 89, Appl
	326	22	0.6	4320	15	US-10-259-194A-345	Sequence 345, App
	327	22	0.6	4330	15	US-10-144-194A-91	Sequence 91, Appl
	328	22	0.6	4769	14	US-10-128-714-594	Sequence 594, App
	329	22	0.6	4824	15	US-10-144-194A-41	Sequence 41, Appl
	330	22	0.6	5067	15	US-10-374-979-78	Sequence 78, Appl
	331	22	0.6	5299	14	US-10-270-333-73	Sequence 73, Appl
	332	22	0.6	5368	14	US-10-128-714-5594	Sequence 5594, Ap
	333	22	0.6	22929	14	US-10-017-161-591	Sequence 591, App
	334	21	0.5	21	10	US-09-291-417-58	Sequence 58, Appl
c	335	21	0.5	51	15	US-10-418-182-240	Sequence 240, App
c	336	21	0.5	89	9	US-09-864-761-17177	Sequence 17177, A
c	337	21	0.5	97	9	US-09-864-761-17641	Sequence 17641, A
	338	21	0.5	157	14	US-10-029-386-18878	Sequence 18878, A
	339	21	0.5	313	10	US-09-814-353-145	Sequence 145, App
	340	21	0.5	313	10	US-09-814-353-6538	Sequence 6538, Ap
c	341	21	0.5	341	15	US-10-062-674-378	Sequence 378, App
	342	21	0.5	417	10	US-09-814-353-12923	Sequence 12923, A
c	343	21	0.5	418	9	US-09-954-456-1573	Sequence 1573, Ap
	344	21	0.5	424	9	US-09-933-797-197	Sequence 197, App
	345	21	0.5	425	10	US-09-918-995-37194	Sequence 37194, A
	346	21	0.5	443	10	US-09-918-995-1790	Sequence 1790, Ap
	347	21	0.5	468	9	US-09-920-300A-615	Sequence 615, App
	348	21	0.5	468	13	US-10-033-528-615	Sequence 615, App
	349	21	0.5	468	14	US-10-099-926-615	Sequence 615, App
c	350	21	0.5	469	9	US-09-864-761-367	Sequence 367, App
c	351	21	0.5	469	9	US-09-864-761-861	Sequence 861, App
	352	21	0.5	480	10	US-09-918-995-21611	Sequence 21611, A
c	353	21	0.5	487	15	US-10-027-632-85428	Sequence 85428, A
c	354	21	0.5	487	15	US-10-027-632-293029	Sequence 293029,
c	355	21	0.5	548	9	US-09-867-701-1427	Sequence 1427, Ap
	356	21	0.5	548	15	US-10-027-632-127974	Sequence 127974,
	357	21	0.5	553	14	US-10-029-386-5122	Sequence 5122, Ap
	358	21	0.5	560	9	US-09-867-701-1428	Sequence 1428, Ap
	359	21	0.5	832	15	US-10-264-237-535	Sequence 535, App
	360	21	0.5	1054	15	US-10-447-839A-10	Sequence 10, Appl
	361	21	0.5	1061	9	US-09-822-849A-171	Sequence 171, App
	362	21	0.5	1080	9	US-09-974-298-3	Sequence 3, Appli
	363	21	0.5	1080	9	US-09-984-245-102	Sequence 102, App
	364	21	0.5	1080	10	US-09-966-262-102	Sequence 102, App
	365	21	0.5	1080	10	US-09-983-966-102	Sequence 102, App
	366	21	0.5	1080	10	US-09-492-026-2	Sequence 2, Appli
	367	21	0.5	1080	14	US-10-143-090-102	Sequence 102, App
	368	21	0.5	1094	12	US-10-424-599-27534	Sequence 27534, A
	369	21	0.5	1099	9	US-09-984-245-27	Sequence 27, Appl
	370	21	0.5	1099	10	US-09-966-262-27	Sequence 27, Appl
	371	21	0.5	1099	10	US-09-983-966-27	Sequence 27, Appl
	372	21	0.5	1099	14	US-10-143-090-27	Sequence 27, Appl
	373	21	0.5	1189	9	US-09-925-299-135	Sequence 135, App
	374	21	0.5	1189	10	US-09-925-299-135	Sequence 135, App
	375	21	0.5	1191	12	US-10-425-114-11802	Sequence 11802, A
	376	21	0.5	1320	15	US-10-374-780A-740	Sequence 740, App
	377	21	0.5	1484	12	US-10-425-114-8031	Sequence 8031, Ap
	378	21	0.5	1495	12	US-10-425-114-8618	Sequence 8618, Ap
	379	21	0.5	1573	12	US-10-424-599-38758	Sequence 38758, A
	380	21	0.5	1674	9	US-09-922-364A-22	Sequence 22, Appl

	381	21	0.5	1674	9	US-09-254-590-22	Sequence 22, Appl
	382	21	0.5	1674	13	US-10-115-695-22	Sequence 22, Appl
	383	21	0.5	1674	14	US-10-116-561-22	Sequence 22, Appl
	384	21	0.5	1674	14	US-10-115-671-22	Sequence 22, Appl
	385	21	0.5	1674	14	US-10-115-415-22	Sequence 22, Appl
	386	21	0.5	1674	14	US-10-116-260-22	Sequence 22, Appl
	387	21	0.5	1674	14	US-10-115-688-22	Sequence 22, Appl
c	388	21	0.5	1686	9	US-09-833-381-2019	Sequence 2019, Ap
	389	21	0.5	1790	14	US-10-210-120-91	Sequence 91, Appl
	390	21	0.5	1817	12	US-10-425-114-793	Sequence 793, App
	391	21	0.5	1857	15	US-10-202-348-5	Sequence 5, Appli
c	392	21	0.5	1858	9	US-09-796-858-21	Sequence 21, Appl
	393	21	0.5	1884	13	US-10-096-241-5	Sequence 5, Appli
	394	21	0.5	1918	15	US-10-369-493-36239	Sequence 36239, A
	395	21	0.5	1959	14	US-10-102-524-1862	Sequence 1862, Ap
	396	21	0.5	2146	12	US-10-424-599-44790	Sequence 44790, A
c	397	21	0.5	2259	14	US-10-287-290-6	Sequence 6, Appli
	398	21	0.5	2521	10	US-09-814-353-19176	Sequence 19176, A
	399	21	0.5	2614	10	US-09-822-846-491	Sequence 491, App
c	400	21	0.5	2621	14	US-10-128-714-159	Sequence 159, App
c	401	21	0.5	2621	14	US-10-128-714-5159	Sequence 5159, Ap
	402	21	0.5	2709	15	US-10-202-348-7	Sequence 7, Appli
	403	21	0.5	3008	15	US-10-104-047-1315	Sequence 1315, Ap
c	404	21	0.5	3063	12	US-10-425-114-15761	Sequence 15761, A
	405	21	0.5	3181	13	US-10-098-841-282	Sequence 282, App
	406	21	0.5	3256	15	US-10-264-049-770	Sequence 770, App
	407	21	0.5	3348	14	US-10-260-715-5	Sequence 5, Appli
	408	21	0.5	3595	15	US-10-104-047-1860	Sequence 1860, Ap
	409	21	0.5	3609	9	US-09-799-875-6	Sequence 6, Appli
c	410	21	0.5	3630	15	US-10-027-632-113827	Sequence 113827,
	411	21	0.5	3743	14	US-10-102-524-1769	Sequence 1769, Ap
	412	21	0.5	3743	15	US-10-331-496A-75	Sequence 75, Appl
	413	21	0.5	3829	15	US-10-302-267-97	Sequence 97, Appl
	414	21	0.5	3829	15	US-10-374-780A-2341	Sequence 2341, Ap
	415	21	0.5	4381	15	US-10-288-798-31	Sequence 31, Appl
	416	21	0.5	5162	14	US-10-205-219-176	Sequence 176, App
	417	21	0.5	5248	10	US-09-822-846-76	Sequence 76, Appl
	418	21	0.5	5263	10	US-09-374-046A-19	Sequence 19, Appl
	419	21	0.5	5263	14	US-10-102-524-1847	Sequence 1847, Ap
	420	21	0.5	5263	15	US-10-331-496A-76	Sequence 76, Appl
	421	21	0.5	5983	9	US-09-799-875-4	Sequence 4, Appli
	422	21	0.5	6604	9	US-09-880-107-1748	Sequence 1748, Ap
	423	21	0.5	6912	14	US-10-260-715-3	Sequence 3, Appli
c	424	21	0.5	53226	9	US-09-818-264-3	Sequence 3, Appli
	425	20	0.5	20	10	US-09-291-417-59	Sequence 59, Appl
	426	20	0.5	137	9	US-09-933-797-782	Sequence 782, App
c	427	20	0.5	137	9	US-09-933-797-782	Sequence 782, App
c	428	20	0.5	185	14	US-10-029-386-14729	Sequence 14729, A
	429	20	0.5	256	9	US-09-764-878-337	Sequence 337, App
	430	20	0.5	256	14	US-10-079-854-337	Sequence 337, App
	431	20	0.5	272	12	US-10-424-599-76029	Sequence 76029, A
	432	20	0.5	302	12	US-10-424-599-69390	Sequence 69390, A
c	433	20	0.5	314	9	US-09-960-352-1020	Sequence 1020, Ap
c	434	20	0.5	314	15	US-10-445-735-6	Sequence 6, Appli
	435	20	0.5	328	15	US-10-305-720-986	Sequence 986, App
	436	20	0.5	334	15	US-10-242-535A-11055	Sequence 11055, A
c	437	20	0.5	375	9	US-09-960-352-8599	Sequence 8599, Ap
	438	20	0.5	380	14	US-10-125-852-16	Sequence 16, Appl
c	439	20	0.5	407	12	US-10-424-599-37512	Sequence 37512, A
	440	20	0.5	422	9	US-09-738-973-337	Sequence 337, App
	441	20	0.5	422	9	US-09-854-133-337	Sequence 337, App
	442	20	0.5	422	14	US-10-144-649A-337	Sequence 337, App
	443	20	0.5	435	15	US-10-027-632-181730	Sequence 181730,
	444	20	0.5	435	15	US-10-027-632-308272	Sequence 308272,
c	445	20	0.5	441	9	US-09-893-737-41	Sequence 41, Appl
	446	20	0.5	448	14	US-10-255-536-88	Sequence 88, Appl
	447	20	0.5	449	10	US-09-918-995-26938	Sequence 26938, A
c	448	20	0.5	458	10	US-09-814-353-1817	Sequence 1817, Ap
c	449	20	0.5	458	10	US-09-814-353-8164	Sequence 8164, Ap
c	450	20	0.5	464	9	US-09-864-761-11104	Sequence 11104, A
	451	20	0.5	492	12	US-10-424-599-117670	Sequence 117670,
c	452	20	0.5	500	10	US-09-918-995-23606	Sequence 23606, A
	453	20	0.5	501	10	US-09-918-995-32151	Sequence 32151, A
	454	20	0.5	505	10	US-09-918-995-32788	Sequence 32788, A
	455	20	0.5	510	10	US-09-918-995-32344	Sequence 32344, A
	456	20	0.5	511	10	US-09-770-961-187	Sequence 187, App
c	457	20	0.5	512	9	US-09-864-761-25347	Sequence 25347, A
c	458	20	0.5	513	10	US-09-814-353-14548	Sequence 14548, A
	459	20	0.5	519	10	US-09-918-995-32641	Sequence 32641, A
c	460	20	0.5	520	14	US-10-029-386-18331	Sequence 18331, A
	461	20	0.5	528	15	US-10-260-238-736	Sequence 736, App
	462	20	0.5	548	15	US-10-027-632-91892	Sequence 91892, A
	463	20	0.5	548	15	US-10-027-632-91893	Sequence 91893, A
	464	20	0.5	548	15	US-10-027-632-317835	Sequence 317835,
	465	20	0.5	548	15	US-10-027-632-317836	Sequence 317836,
c	466	20	0.5	554	9	US-09-864-761-7357	Sequence 7357, Ap
	467	20	0.5	554	10	US-09-918-995-32092	Sequence 32092, A
	468	20	0.5	574	15	US-10-027-632-322377	Sequence 322377,
c	469	20	0.5	575	9	US-09-864-761-8628	Sequence 8628, Ap
	470	20	0.5	592	13	US-10-042-417-31	Sequence 31, Appl
	471	20	0.5	593	9	US-09-783-252-20	Sequence 20, Appl
c	472	20	0.5	595	14	US-10-029-386-1026	Sequence 1026, Ap
c	473	20	0.5	597	14	US-10-029-386-4575	Sequence 4575, Ap
c	474	20	0.5	603	15	US-10-027-632-230862	Sequence 230862,
c	475	20	0.5	603	15	US-10-027-632-230863	Sequence 230863,
c	476	20	0.5	618	15	US-10-027-632-269245	Sequence 269245,
	477	20	0.5	622	12	US-10-425-114-35963	Sequence 35963, A
c	478	20	0.5	630	15	US-10-027-632-128316	Sequence 128316,
	479	20	0.5	635	14	US-10-178-213-37	Sequence 37, Appl
c	480	20	0.5	659	14	US-10-029-386-20268	Sequence 20268, A
c	481	20	0.5	698	14	US-10-029-386-22908	Sequence 22908, A
	482	20	0.5	791	15	US-10-369-493-27376	Sequence 27376, A
	483	20	0.5	792	14	US-10-125-852-19	Sequence 19, Appl
c	484	20	0.5	809	15	US-10-027-632-153176	Sequence 153176,
c	485	20	0.5	809	15	US-10-027-632-153177	Sequence 153177,
c	486	20	0.5	809	15	US-10-027-632-153178	Sequence 153178,
c	487	20	0.5	822	14	US-10-101-464A-38	Sequence 38, Appl
	488	20	0.5	863	12	US-10-425-114-19709	Sequence 19709, A
c	489	20	0.5	879	8	US-08-994-468-1	Sequence 1, Appli
c	490	20	0.5	879	9	US-09-983-806-1	Sequence 1, Appli
c	491	20	0.5	879	13	US-10-095-449-1	Sequence 1, Appli
c	492	20	0.5	879	14	US-10-314-035-1	Sequence 1, Appli
	493	20	0.5	885	9	US-09-801-368-201	Sequence 201, App
c	494	20	0.5	893	12	US-10-425-114-2011	Sequence 2011, Ap
c	495	20	0.5	897	15	US-10-369-493-34404	Sequence 34404, A
c	496	20	0.5	907	14	US-10-106-698-1382	Sequence 1382, Ap
	497	20	0.5	915	10	US-09-764-891-1411	Sequence 1411, Ap
	498	20	0.5	961	12	US-10-425-114-6612	Sequence 6612, Ap
	499	20	0.5	988	14	US-10-180-375-85	Sequence 85, Appl
	500	20	0.5	1010	12	US-10-425-114-16293	Sequence 16293, A
	501	20	0.5	1035	12	US-10-425-114-26560	Sequence 26560, A
	502	20	0.5	1063	15	US-10-374-780A-1789	Sequence 1789, Ap
	503	20	0.5	1066	12	US-10-425-114-33268	Sequence 33268, A
	504	20	0.5	1135	12	US-10-425-114-23292	Sequence 23292, A
c	505	20	0.5	1194	11	US-09-764-875-86	Sequence 86, Appl
	506	20	0.5	1196	12	US-10-425-114-2655	Sequence 2655, Ap
c	507	20	0.5	1204	15	US-10-158-057-31	Sequence 31, Appl
c	508	20	0.5	1221	12	US-10-425-114-4972	Sequence 4972, Ap
c	509	20	0.5	1224	15	US-10-027-632-124644	Sequence 124644,
c	510	20	0.5	1312	15	US-10-027-632-122831	Sequence 122831,
	511	20	0.5	1315	14	US-10-125-852-17	Sequence 17, Appl
	512	20	0.5	1324	14	US-10-149-819-26	Sequence 26, Appl
	513	20	0.5	1339	12	US-10-425-114-26400	Sequence 26400, A
c	514	20	0.5	1383	9	US-09-967-768A-189	Sequence 189, App
c	515	20	0.5	1383	9	US-09-970-989-6	Sequence 6, Appli
c	516	20	0.5	1383	10	US-09-873-367C-250	Sequence 250, App
	517	20	0.5	1410	12	US-10-425-114-6681	Sequence 6681, Ap
	518	20	0.5	1425	12	US-10-425-114-25156	Sequence 25156, A
	519	20	0.5	1481	14	US-10-050-704-29	Sequence 29, Appl
	520	20	0.5	1516	12	US-10-425-114-30842	Sequence 30842, A
c	521	20	0.5	1522	9	US-09-962-436-20	Sequence 20, Appl
c	522	20	0.5	1522	9	US-09-954-531-612	Sequence 612, App
c	523	20	0.5	1581	12	US-10-425-114-25878	Sequence 25878, A
	524	20	0.5	1632	15	US-10-085-117-168	Sequence 168, App
	525	20	0.5	1662	9	US-09-938-842A-1014	Sequence 1014, Ap
	526	20	0.5	1662	11	US-09-938-842A-1014	Sequence 1014, Ap

	527	20	0.5	1680	12	US-10-424-599-50391	Sequence 50391, A
	528	20	0.5	1688	12	US-10-425-114-32113	Sequence 32113, A
c	529	20	0.5	1713	15	US-10-388-934-602	Sequence 602, App
	530	20	0.5	1722	12	US-10-425-114-27699	Sequence 27699, A
	531	20	0.5	1783	12	US-10-425-114-3835	Sequence 3835, Ap
	532	20	0.5	1785	14	US-10-148-662-5	Sequence 5, Appli
	533	20	0.5	1802	12	US-10-425-114-32170	Sequence 32170, A
	534	20	0.5	1831	13	US-10-108-605-160	Sequence 160, App
	535	20	0.5	1865	15	US-10-108-260A-2034	Sequence 2034, Ap
	536	20	0.5	1869	13	US-10-098-841-114	Sequence 114, App
	537	20	0.5	1874	13	US-10-005-057A-1	Sequence 1, Appli
	538	20	0.5	1927	12	US-10-425-114-34277	Sequence 34277, A
	539	20	0.5	1996	15	US-10-104-047-1035	Sequence 1035, Ap
	540	20	0.5	2028	14	US-10-148-662-3	Sequence 3, Appli
	541	20	0.5	2031	14	US-10-148-662-2	Sequence 2, Appli
	542	20	0.5	2037	15	US-10-369-493-27480	Sequence 27480, A
	543	20	0.5	2052	15	US-10-104-047-207	Sequence 207, App
	544	20	0.5	2076	12	US-10-424-599-101951	Sequence 101951,
c	545	20	0.5	2100	9	US-09-804-626-5	Sequence 5, Appli
c	546	20	0.5	2133	12	US-10-424-599-81204	Sequence 81204, A
c	547	20	0.5	2138	14	US-10-101-464A-462	Sequence 462, App
	548	20	0.5	2197	12	US-10-424-599-5275	Sequence 5275, Ap
	549	20	0.5	2223	15	US-10-259-194A-107	Sequence 107, App
c	550	20	0.5	2254	10	US-09-814-353-20066	Sequence 20066, A
	551	20	0.5	2261	15	US-10-108-260A-1861	Sequence 1861, Ap
	552	20	0.5	2314	15	US-10-027-632-103281	Sequence 103281,
	553	20	0.5	2314	15	US-10-027-632-103282	Sequence 103282,
	554	20	0.5	2333	15	US-10-108-260A-2386	Sequence 2386, Ap
	555	20	0.5	2337	14	US-10-148-662-1	Sequence 1, Appli
	556	20	0.5	2352	14	US-10-148-662-11	Sequence 11, Appl
c	557	20	0.5	2394	9	US-09-960-253-164	Sequence 164, App
	558	20	0.5	2404	15	US-10-104-047-1740	Sequence 1740, Ap
	559	20	0.5	2450	14	US-10-037-270-336	Sequence 336, App
	560	20	0.5	2450	15	US-10-117-722-336	Sequence 336, App
	561	20	0.5	2513	14	US-10-037-270-337	Sequence 337, App
	562	20	0.5	2513	15	US-10-117-722-337	Sequence 337, App
	563	20	0.5	2685	12	US-10-221-625-154	Sequence 154, App
c	564	20	0.5	2787	14	US-10-300-834-2	Sequence 2, Appli
	565	20	0.5	2807	14	US-10-317-835-9	Sequence 9, Appli
	566	20	0.5	2862	9	US-09-888-615-7	Sequence 7, Appli
	567	20	0.5	2897	14	US-10-317-835-6	Sequence 6, Appli
	568	20	0.5	2900	14	US-10-037-270-673	Sequence 673, App
	569	20	0.5	2900	15	US-10-117-722-673	Sequence 673, App
c	570	20	0.5	2995	14	US-10-225-567A-149	Sequence 149, App
	571	20	0.5	3032	15	US-10-352-684A-61	Sequence 61, Appl
	572	20	0.5	3067	16	US-10-311-035-42	Sequence 42, Appl
	573	20	0.5	3108	14	US-10-210-120-59	Sequence 59, Appl
c	574	20	0.5	3118	9	US-09-864-864-289	Sequence 289, App
	575	20	0.5	3120	14	US-10-207-655-106	Sequence 106, App
	576	20	0.5	3132	9	US-09-880-107-3721	Sequence 3721, Ap
	577	20	0.5	3132	9	US-09-736-457-320	Sequence 320, App
	578	20	0.5	3132	9	US-09-902-941-320	Sequence 320, App
	579	20	0.5	3132	9	US-09-849-626-320	Sequence 320, App
	580	20	0.5	3132	10	US-09-476-300-320	Sequence 320, App
	581	20	0.5	3132	10	US-09-960-706-1064	Sequence 1064, Ap
	582	20	0.5	3132	10	US-09-873-319-706	Sequence 706, App
	583	20	0.5	3132	10	US-09-873-367C-813	Sequence 813, App
	584	20	0.5	3132	14	US-10-017-754-320	Sequence 320, App
	585	20	0.5	3132	14	US-10-205-823-94	Sequence 94, Appl
	586	20	0.5	3132	14	US-10-251-661-5	Sequence 5, Appli
	587	20	0.5	3132	14	US-10-113-872-320	Sequence 320, App
	588	20	0.5	3132	15	US-10-341-434-183	Sequence 183, App
	589	20	0.5	3132	15	US-10-341-434-197	Sequence 197, App
	590	20	0.5	3132	15	US-10-085-117-167	Sequence 167, App
	591	20	0.5	3137	14	US-10-037-270-714	Sequence 714, App
	592	20	0.5	3137	15	US-10-117-722-714	Sequence 714, App
	593	20	0.5	3148	14	US-10-317-835-7	Sequence 7, Appli
	594	20	0.5	3148	14	US-10-317-835-15	Sequence 15, Appl
	595	20	0.5	3188	15	US-10-320-797-106	Sequence 106, App
c	596	20	0.5	3195	14	US-10-300-834-1	Sequence 1, Appli
	597	20	0.5	3231	15	US-10-375-592A-2	Sequence 2, Appli
	598	20	0.5	3238	10	US-09-870-133-1	Sequence 1, Appli
	599	20	0.5	3238	14	US-10-160-501-4	Sequence 4, Appli
	600	20	0.5	3243	10	US-09-814-353-19627	Sequence 19627, A
	601	20	0.5	3439	15	US-10-161-927-53	Sequence 53, Appl
	602	20	0.5	3609	9	US-09-917-800A-1715	Sequence 1715, Ap
	603	20	0.5	3611	9	US-09-836-392-3	Sequence 3, Appli
	604	20	0.5	3715	9	US-09-880-107-2300	Sequence 2300, Ap
	605	20	0.5	3715	15	US-10-375-592A-1	Sequence 1, Appli
	606	20	0.5	3758	12	US-10-425-114-10917	Sequence 10917, A
	607	20	0.5	3832	15	US-10-374-780A-2069	Sequence 2069, Ap
c	608	20	0.5	3886	13	US-10-124-800-37	Sequence 37, Appl
	609	20	0.5	3899	9	US-09-735-367B-5	Sequence 5, Appli
	610	20	0.5	3906	15	US-10-369-493-25331	Sequence 25331, A
	611	20	0.5	4021	13	US-10-002-600-40	Sequence 40, Appl
	612	20	0.5	4021	13	US-10-071-766-57	Sequence 57, Appl
	613	20	0.5	4034	14	US-10-240-965-161	Sequence 161, App
	614	20	0.5	4035	10	US-09-919-039-147	Sequence 147, App
	615	20	0.5	4035	14	US-10-101-510-349	Sequence 349, App
	616	20	0.5	4035	14	US-10-252-157-156	Sequence 156, App
c	617	20	0.5	4079	15	US-10-305-720-1208	Sequence 1208, Ap
	618	20	0.5	4188	14	US-10-317-835-8	Sequence 8, Appli
	619	20	0.5	4196	10	US-09-291-417-19	Sequence 19, Appl
c	620	20	0.5	4208	12	US-10-425-114-18477	Sequence 18477, A
c	621	20	0.5	4240	14	US-10-084-817-62	Sequence 62, Appl
	622	20	0.5	4296	15	US-10-445-735-3	Sequence 3, Appli
	623	20	0.5	4320	15	US-10-440-464-139	Sequence 139, App
	624	20	0.5	4321	12	US-10-058-270A-93	Sequence 93, Appl
	625	20	0.5	4321	14	US-10-205-823-35	Sequence 35, Appl
	626	20	0.5	4393	14	US-10-198-846-10819	Sequence 10819, A
c	627	20	0.5	4658	10	US-09-814-353-20101	Sequence 20101, A
c	628	20	0.5	4778	14	US-10-174-677-116	Sequence 116, App
c	629	20	0.5	4793	12	US-10-425-114-26834	Sequence 26834, A
c	630	20	0.5	4828	14	US-10-097-340-36	Sequence 36, Appl
c	631	20	0.5	4828	14	US-10-007-926A-328	Sequence 328, App
c	632	20	0.5	4828	15	US-10-439-388-38	Sequence 38, Appl
c	633	20	0.5	4895	14	US-10-198-846-11387	Sequence 11387, A
c	634	20	0.5	5312	10	US-09-764-891-9241	Sequence 9241, Ap
c	635	20	0.5	5312	14	US-10-091-572-817	Sequence 817, App
c	636	20	0.5	5445	14	US-10-371-474-10	Sequence 10, Appl
	637	20	0.5	6003	12	US-10-211-462-58	Sequence 58, Appl
c	638	20	0.5	6268	14	US-10-252-157-148	Sequence 148, App
c	639	20	0.5	6288	12	US-10-221-278-171	Sequence 171, App
c	640	20	0.5	6288	14	US-10-251-186-23	Sequence 23, Appl
c	641	20	0.5	6288	15	US-10-291-172-171	Sequence 171, App
	642	20	0.5	6504	9	US-09-969-347-171	Sequence 171, App
	643	20	0.5	6504	9	US-09-735-367B-9	Sequence 9, Appli
	644	20	0.5	6878	9	US-09-735-367B-1	Sequence 1, Appli
	645	20	0.5	8600	9	US-09-950-046A-1	Sequence 1, Appli
c	646	20	0.5	9090	13	US-10-000-789-1	Sequence 1, Appli
c	647	20	0.5	9090	14	US-10-171-581-305	Sequence 305, App
	648	20	0.5	12541	15	US-10-074-024-524	Sequence 524, App
	649	20	0.5	12541	15	US-10-074-024-525	Sequence 525, App
	650	20	0.5	12561	13	US-10-005-057A-41	Sequence 41, Appl
	651	20	0.5	12758	13	US-10-108-605-24	Sequence 24, Appl
	652	20	0.5	14536	11	US-09-970-944-3	Sequence 3, Appli
	653	20	0.5	14536	14	US-10-160-758-6	Sequence 6, Appli
	654	20	0.5	14536	14	US-10-160-758-7	Sequence 7, Appli
	655	20	0.5	23825	15	US-10-085-117-166	Sequence 166, App
c	656	20	0.5	52899	15	US-10-085-117-148	Sequence 148, App
c	657	20	0.5	77992	14	US-10-225-810-11	Sequence 11, Appl
c	658	20	0.5	78333	15	US-10-298-122-3	Sequence 3, Appli
	659	20	0.5	110096	9	US-09-880-107-1542	Sequence 1542, Ap
c	660	20	0.5	250000	14	US-10-225-810-26	Sequence 26, Appl
c	661	19	0.5	19	10	US-09-291-417-62	Sequence 62, Appl
	662	19	0.5	21	10	US-09-789-390-50	Sequence 50, Appl
c	663	19	0.5	22	13	US-10-028-415-27	Sequence 27, Appl
	664	19	0.5	49	15	US-10-148-835-23	Sequence 23, Appl
c	665	19	0.5	58	14	US-10-215-432-36	Sequence 36, Appl
	666	19	0.5	65	14	US-10-032-585-2138	Sequence 2138, Ap
	667	19	0.5	67	14	US-10-106-698-3325	Sequence 3325, Ap
c	668	19	0.5	97	9	US-09-864-761-22933	Sequence 22933, A
	669	19	0.5	102	9	US-09-864-761-22363	Sequence 22363, A
c	670	19	0.5	117	9	US-09-864-761-30735	Sequence 30735, A
	671	19	0.5	174	9	US-09-878-178-565	Sequence 565, App
	672	19	0.5	174	13	US-10-046-935-565	Sequence 565, App

	673	19	0.5	174	14	US-10-146-502-565	Sequence 565, App
	674	19	0.5	178	15	US-10-242-535A-1493	Sequence 1493, Ap
	675	19	0.5	184	14	US-10-029-386-22041	Sequence 22041, A
	676	19	0.5	201	14	US-10-029-386-14258	Sequence 14258, A
c	677	19	0.5	207	14	US-10-029-386-14184	Sequence 14184, A
	678	19	0.5	226	9	US-09-728-444-58	Sequence 58, Appl
	679	19	0.5	232	12	US-10-424-599-27481	Sequence 27481, A
	680	19	0.5	238	12	US-10-424-599-117404	Sequence 117404,
	681	19	0.5	252	9	US-09-783-590-6640	Sequence 6640, Ap
	682	19	0.5	259	14	US-10-029-386-19393	Sequence 19393, A
	683	19	0.5	262	12	US-10-424-599-23791	Sequence 23791, A
	684	19	0.5	272	14	US-10-029-386-18093	Sequence 18093, A
c	685	19	0.5	276	9	US-09-893-737-5	Sequence 5, Appli
c	686	19	0.5	279	15	US-10-242-535A-29517	Sequence 29517, A
c	687	19	0.5	292	9	US-09-864-761-27633	Sequence 27633, A
	688	19	0.5	305	9	US-09-864-761-31945	Sequence 31945, A
c	689	19	0.5	307	9	US-09-864-761-22970	Sequence 22970, A
c	690	19	0.5	309	14	US-10-029-386-19341	Sequence 19341, A
	691	19	0.5	320	9	US-09-960-352-2839	Sequence 2839, Ap
	692	19	0.5	320	12	US-10-424-599-139689	Sequence 139689,
	693	19	0.5	335	15	US-10-242-535A-9557	Sequence 9557, Ap
	694	19	0.5	368	9	US-09-815-343-59	Sequence 59, Appl
	695	19	0.5	376	9	US-09-864-761-3481	Sequence 3481, Ap
c	696	19	0.5	393	15	US-10-242-535A-12781	Sequence 12781, A
c	697	19	0.5	397	10	US-09-814-353-1381	Sequence 1381, Ap
c	698	19	0.5	397	10	US-09-814-353-7744	Sequence 7744, Ap
	699	19	0.5	398	12	US-10-424-599-61843	Sequence 61843, A
	700	19	0.5	399	15	US-10-242-535A-9531	Sequence 9531, Ap
c	701	19	0.5	402	9	US-09-864-761-14182	Sequence 14182, A
c	702	19	0.5	405	10	US-09-918-995-6775	Sequence 6775, Ap
	703	19	0.5	411	9	US-09-922-217-659	Sequence 659, App
	704	19	0.5	411	9	US-09-833-263-659	Sequence 659, App
c	705	19	0.5	411	10	US-09-918-995-33029	Sequence 33029, A
	706	19	0.5	411	13	US-10-025-380-659	Sequence 659, App
	707	19	0.5	419	15	US-10-369-493-30016	Sequence 30016, A
	708	19	0.5	427	9	US-09-864-761-89	Sequence 89, Appl
c	709	19	0.5	427	10	US-09-918-995-5941	Sequence 5941, Ap
c	710	19	0.5	428	10	US-09-918-995-34181	Sequence 34181, A
c	711	19	0.5	430	9	US-09-768-020-24	Sequence 24, Appl
c	712	19	0.5	438	9	US-09-893-737-247	Sequence 247, App
c	713	19	0.5	439	9	US-09-834-975-661	Sequence 661, App
	714	19	0.5	441	9	US-09-770-444-906	Sequence 906, App
c	715	19	0.5	441	9	US-09-893-737-39	Sequence 39, Appl
	716	19	0.5	441	9	US-09-924-035A-481	Sequence 481, App
	717	19	0.5	442	10	US-09-918-995-14168	Sequence 14168, A
c	718	19	0.5	448	10	US-09-764-891-7304	Sequence 7304, Ap
	719	19	0.5	448	10	US-09-764-891-8371	Sequence 8371, Ap
c	720	19	0.5	449	10	US-09-814-353-14129	Sequence 14129, A
	721	19	0.5	453	12	US-10-424-599-34147	Sequence 34147, A
	722	19	0.5	454	10	US-09-918-995-28259	Sequence 28259, A
	723	19	0.5	454	13	US-10-040-739-598	Sequence 598, App
c	724	19	0.5	455	9	US-09-864-761-10998	Sequence 10998, A
c	725	19	0.5	455	10	US-09-983-802-70	Sequence 70, Appl
c	726	19	0.5	455	10	US-09-918-995-23192	Sequence 23192, A
	727	19	0.5	459	10	US-09-918-995-36086	Sequence 36086, A
c	728	19	0.5	460	9	US-09-864-761-5797	Sequence 5797, Ap
	729	19	0.5	460	10	US-09-918-995-28523	Sequence 28523, A
c	730	19	0.5	461	9	US-09-864-761-11608	Sequence 11608, A
c	731	19	0.5	462	9	US-09-864-761-22557	Sequence 22557, A
c	732	19	0.5	463	14	US-10-106-698-806	Sequence 806, App
c	733	19	0.5	464	9	US-09-864-761-5988	Sequence 5988, Ap
	734	19	0.5	469	15	US-10-242-535A-38077	Sequence 38077, A
c	735	19	0.5	473	9	US-09-864-761-6213	Sequence 6213, Ap
	736	19	0.5	474	9	US-09-867-701-4802	Sequence 4802, Ap
	737	19	0.5	478	10	US-09-918-995-31189	Sequence 31189, A
c	738	19	0.5	478	10	US-09-918-995-31485	Sequence 31485, A
c	739	19	0.5	480	9	US-09-864-761-6250	Sequence 6250, Ap
c	740	19	0.5	487	12	US-10-425-114-13151	Sequence 13151, A
	741	19	0.5	491	9	US-09-864-761-5595	Sequence 5595, Ap
c	742	19	0.5	500	9	US-09-867-701-2973	Sequence 2973, Ap
c	743	19	0.5	503	10	US-09-918-995-32127	Sequence 32127, A
c	744	19	0.5	504	9	US-09-879-536-123	Sequence 123, App
	745	19	0.5	504	14	US-10-029-386-553	Sequence 553, App
c	746	19	0.5	504	15	US-10-027-632-135579	Sequence 135579,
c	747	19	0.5	504	15	US-10-027-632-135580	Sequence 135580,
c	748	19	0.5	514	9	US-09-768-020-23	Sequence 23, Appl
	749	19	0.5	515	14	US-10-029-386-4393	Sequence 4393, Ap
	750	19	0.5	534	14	US-10-029-386-8341	Sequence 8341, Ap
c	751	19	0.5	538	10	US-09-918-995-30418	Sequence 30418, A
c	752	19	0.5	538	15	US-10-027-632-273922	Sequence 273922,
	753	19	0.5	539	12	US-10-424-599-104452	Sequence 104452,
	754	19	0.5	540	14	US-10-029-386-5637	Sequence 5637, Ap
c	755	19	0.5	548	14	US-10-029-386-5585	Sequence 5585, Ap
c	756	19	0.5	549	14	US-10-029-386-479	Sequence 479, App
c	757	19	0.5	549	15	US-10-260-238-5568	Sequence 5568, Ap
c	758	19	0.5	555	10	US-09-764-891-7305	Sequence 7305, Ap
	759	19	0.5	555	10	US-09-764-891-8372	Sequence 8372, Ap
c	760	19	0.5	561	12	US-10-425-114-22982	Sequence 22982, A
c	761	19	0.5	562	15	US-10-264-237-1032	Sequence 1032, Ap
	762	19	0.5	566	12	US-10-424-599-88696	Sequence 88696, A
	763	19	0.5	580	12	US-10-424-599-18726	Sequence 18726, A
c	764	19	0.5	590	9	US-09-745-288-67	Sequence 67, Appl
c	765	19	0.5	590	12	US-10-453-919-67	Sequence 67, Appl
c	766	19	0.5	591	9	US-09-738-973-303	Sequence 303, App
c	767	19	0.5	591	9	US-09-854-133-303	Sequence 303, App
c	768	19	0.5	591	14	US-10-144-649A-303	Sequence 303, App
	769	19	0.5	594	14	US-10-029-386-10236	Sequence 10236, A
	770	19	0.5	607	12	US-10-424-599-120671	Sequence 120671,
	771	19	0.5	608	12	US-10-240-425-150	Sequence 150, App
c	772	19	0.5	608	14	US-10-255-536-247	Sequence 247, App
c	773	19	0.5	611	15	US-10-027-632-224608	Sequence 224608,
c	774	19	0.5	611	15	US-10-027-632-224609	Sequence 224609,
	775	19	0.5	611	15	US-10-027-632-240573	Sequence 240573,
c	776	19	0.5	613	12	US-10-425-114-22102	Sequence 22102, A
	777	19	0.5	616	15	US-10-242-535A-1932	Sequence 1932, Ap
	778	19	0.5	618	15	US-10-062-674-1774	Sequence 1774, Ap
	779	19	0.5	621	9	US-09-950-933A-5	Sequence 5, Appli
	780	19	0.5	629	9	US-09-764-855-59	Sequence 59, Appl
	781	19	0.5	629	14	US-10-072-349-59	Sequence 59, Appl
c	782	19	0.5	635	15	US-10-027-632-14842	Sequence 14842, A
	783	19	0.5	642	12	US-10-424-599-13907	Sequence 13907, A
	784	19	0.5	645	15	US-10-027-632-113146	Sequence 113146,
	785	19	0.5	645	15	US-10-027-632-113147	Sequence 113147,
	786	19	0.5	645	15	US-10-027-632-113148	Sequence 113148,
c	787	19	0.5	650	12	US-10-424-599-30365	Sequence 30365, A
c	788	19	0.5	654	15	US-10-260-238-5696	Sequence 5696, Ap
c	789	19	0.5	656	15	US-10-027-632-115617	Sequence 115617,
	790	19	0.5	658	14	US-10-198-846-9119	Sequence 9119, Ap
	791	19	0.5	672	9	US-09-864-761-16927	Sequence 16927, A
	792	19	0.5	692	9	US-09-954-973-5	Sequence 5, Appli
c	793	19	0.5	698	9	US-09-834-975-992	Sequence 992, App
c	794	19	0.5	710	15	US-10-027-632-21966	Sequence 21966, A
c	795	19	0.5	713	15	US-10-027-632-27620	Sequence 27620, A
	796	19	0.5	718	12	US-10-424-599-56571	Sequence 56571, A
	797	19	0.5	718	14	US-10-029-386-22967	Sequence 22967, A
	798	19	0.5	721	15	US-10-264-049-1106	Sequence 1106, Ap
	799	19	0.5	723	12	US-10-424-599-122849	Sequence 122849,
	800	19	0.5	731	15	US-10-027-632-164297	Sequence 164297,
	801	19	0.5	732	15	US-10-027-632-148086	Sequence 148086,
	802	19	0.5	735	12	US-10-425-114-12188	Sequence 12188, A
	803	19	0.5	738	8	US-08-722-570-13	Sequence 13, Appl
c	804	19	0.5	742	13	US-10-124-591-2	Sequence 2, Appli
c	805	19	0.5	747	14	US-10-032-585-6542	Sequence 6542, Ap
	806	19	0.5	758	14	US-10-029-386-25015	Sequence 25015, A
c	807	19	0.5	771	12	US-10-424-599-63555	Sequence 63555, A
	808	19	0.5	788	12	US-10-424-599-38379	Sequence 38379, A
	809	19	0.5	792	13	US-10-029-180-29	Sequence 29, Appl
c	810	19	0.5	795	9	US-09-884-441-86	Sequence 86, Appl
c	811	19	0.5	795	10	US-09-907-969-86	Sequence 86, Appl
c	812	19	0.5	795	10	US-09-827-271-86	Sequence 86, Appl
c	813	19	0.5	795	14	US-10-198-053-86	Sequence 86, Appl
c	814	19	0.5	804	15	US-10-027-632-173765	Sequence 173765,
c	815	19	0.5	805	12	US-10-424-599-48951	Sequence 48951, A
	816	19	0.5	805	15	US-10-027-632-172202	Sequence 172202,
c	817	19	0.5	808	12	US-10-424-599-101439	Sequence 101439,
	818	19	0.5	810	12	US-10-425-114-31528	Sequence 31528, A

c	819	19	0.5	813	9	US-09-910-664-21	Sequence 21, Appl
	820	19	0.5	813	12	US-10-424-599-89934	Sequence 89934, A
c	821	19	0.5	820	15	US-10-027-632-172203	Sequence 172203,
c	822	19	0.5	827	12	US-10-424-599-107476	Sequence 107476,
	823	19	0.5	830	12	US-10-424-599-43992	Sequence 43992, A
	824	19	0.5	837	14	US-10-198-846-4998	Sequence 4998, Ap
	825	19	0.5	843	10	US-09-814-353-19793	Sequence 19793, A
	826	19	0.5	843	12	US-10-425-114-18553	Sequence 18553, A
c	827	19	0.5	843	15	US-10-027-632-137886	Sequence 137886,
	828	19	0.5	853	12	US-10-425-114-26049	Sequence 26049, A
	829	19	0.5	899	12	US-10-425-114-13318	Sequence 13318, A
c	830	19	0.5	900	14	US-10-029-386-22787	Sequence 22787, A
c	831	19	0.5	904	12	US-10-425-114-11751	Sequence 11751, A
c	832	19	0.5	910	12	US-10-425-114-19407	Sequence 19407, A
	833	19	0.5	916	9	US-09-790-099-6	Sequence 6, Appli
	834	19	0.5	921	14	US-10-198-846-5051	Sequence 5051, Ap
c	835	19	0.5	942	12	US-10-424-599-43501	Sequence 43501, A
	836	19	0.5	985	12	US-10-424-599-41450	Sequence 41450, A
	837	19	0.5	994	12	US-10-425-114-20545	Sequence 20545, A
c	838	19	0.5	1002	12	US-10-425-114-21637	Sequence 21637, A
	839	19	0.5	1008	15	US-10-374-780A-1092	Sequence 1092, Ap
	840	19	0.5	1014	14	US-10-279-029-13	Sequence 13, Appl
	841	19	0.5	1014	14	US-10-279-029-14	Sequence 14, Appl
	842	19	0.5	1021	15	US-10-023-339-7	Sequence 7, Appli
	843	19	0.5	1036	14	US-10-180-375-111	Sequence 111, App
c	844	19	0.5	1042	12	US-10-424-599-132279	Sequence 132279,
c	845	19	0.5	1044	12	US-10-424-599-13628	Sequence 13628, A
	846	19	0.5	1053	15	US-10-260-238-3813	Sequence 3813, Ap
	847	19	0.5	1056	14	US-10-029-386-25103	Sequence 25103, A
c	848	19	0.5	1062	12	US-10-425-114-17508	Sequence 17508, A
	849	19	0.5	1063	15	US-10-374-780A-1091	Sequence 1091, Ap
	850	19	0.5	1114	15	US-10-259-194A-43	Sequence 43, Appl
	851	19	0.5	1123	12	US-10-425-114-15938	Sequence 15938, A
c	852	19	0.5	1146	12	US-10-425-114-10516	Sequence 10516, A
	853	19	0.5	1160	13	US-10-062-254-285	Sequence 285, App
	854	19	0.5	1167	10	US-09-814-353-21067	Sequence 21067, A
c	855	19	0.5	1218	15	US-10-320-797-2146	Sequence 2146, Ap
	856	19	0.5	1225	10	US-09-822-846-198	Sequence 198, App
c	857	19	0.5	1233	12	US-10-424-599-30274	Sequence 30274, A
c	858	19	0.5	1254	12	US-10-425-114-3532	Sequence 3532, Ap
	859	19	0.5	1260	15	US-10-085-117-45	Sequence 45, Appl
c	860	19	0.5	1287	12	US-10-282-122A-28283	Sequence 28283, A
	861	19	0.5	1291	14	US-10-102-806-60	Sequence 60, Appl
	862	19	0.5	1294	12	US-10-425-114-17909	Sequence 17909, A
	863	19	0.5	1310	9	US-09-849-243-13	Sequence 13, Appl
c	864	19	0.5	1332	14	US-10-084-817-107	Sequence 107, App
	865	19	0.5	1337	12	US-10-425-114-7688	Sequence 7688, Ap
	866	19	0.5	1344	9	US-09-738-626-3295	Sequence 3295, Ap
c	867	19	0.5	1356	15	US-10-264-049-703	Sequence 703, App
	868	19	0.5	1381	14	US-10-198-846-10587	Sequence 10587, A
	869	19	0.5	1395	12	US-10-424-599-35498	Sequence 35498, A
c	870	19	0.5	1407	15	US-10-158-057-102	Sequence 102, App
c	871	19	0.5	1430	15	US-10-320-797-1146	Sequence 1146, Ap
	872	19	0.5	1435	12	US-10-424-599-135175	Sequence 135175,
	873	19	0.5	1440	12	US-10-627-476-513	Sequence 513, App
c	874	19	0.5	1441	15	US-10-310-154-176	Sequence 176, App
	875	19	0.5	1445	12	US-10-425-114-22710	Sequence 22710, A
	876	19	0.5	1462	15	US-10-260-238-914	Sequence 914, App
	877	19	0.5	1467	14	US-10-037-270-662	Sequence 662, App
	878	19	0.5	1467	15	US-10-117-722-662	Sequence 662, App
c	879	19	0.5	1472	15	US-10-443-201-17	Sequence 17, Appl
	880	19	0.5	1479	14	US-10-032-585-6836	Sequence 6836, Ap
c	881	19	0.5	1510	12	US-10-425-114-10459	Sequence 10459, A
	882	19	0.5	1521	12	US-10-424-599-103760	Sequence 103760,
	883	19	0.5	1522	12	US-10-425-114-20829	Sequence 20829, A
c	884	19	0.5	1525	12	US-10-425-114-20759	Sequence 20759, A
	885	19	0.5	1529	9	US-09-925-302-212	Sequence 212, App
	886	19	0.5	1534	12	US-10-425-114-862	Sequence 862, App
c	887	19	0.5	1590	9	US-09-888-615-3	Sequence 3, Appli
	888	19	0.5	1602	14	US-10-156-761-6647	Sequence 6647, Ap
	889	19	0.5	1611	14	US-10-260-046-7	Sequence 7, Appli
c	890	19	0.5	1613	12	US-10-425-114-20950	Sequence 20950, A
	891	19	0.5	1640	14	US-10-237-852-6	Sequence 6, Appli
	892	19	0.5	1646	14	US-10-278-173-135	Sequence 135, App
	893	19	0.5	1664	15	US-10-426-776-33	Sequence 33, Appl
	894	19	0.5	1665	12	US-10-425-114-19288	Sequence 19288, A
	895	19	0.5	1666	15	US-10-374-780A-2835	Sequence 2835, Ap
	896	19	0.5	1673	14	US-10-260-046-5	Sequence 5, Appli
c	897	19	0.5	1679	12	US-10-425-114-25109	Sequence 25109, A
	898	19	0.5	1692	15	US-10-027-632-97417	Sequence 97417, A
c	899	19	0.5	1718	12	US-10-424-599-30208	Sequence 30208, A
c	900	19	0.5	1743	10	US-09-822-846-459	Sequence 459, App
	901	19	0.5	1756	12	US-10-424-599-21459	Sequence 21459, A
	902	19	0.5	1758	9	US-09-880-107-2157	Sequence 2157, Ap
c	903	19	0.5	1761	12	US-10-424-599-20866	Sequence 20866, A
	904	19	0.5	1765	12	US-10-424-599-42903	Sequence 42903, A
	905	19	0.5	1778	15	US-10-094-749-1542	Sequence 1542, Ap
	906	19	0.5	1849	14	US-10-215-224-1	Sequence 1, Appli
	907	19	0.5	1849	14	US-10-225-060-9	Sequence 9, Appli
	908	19	0.5	1854	12	US-10-425-114-8463	Sequence 8463, Ap
c	909	19	0.5	1880	15	US-10-027-632-98074	Sequence 98074, A
	910	19	0.5	1905	14	US-10-087-887-11	Sequence 11, Appl
	911	19	0.5	1909	12	US-10-425-114-20633	Sequence 20633, A
c	912	19	0.5	1926	13	US-10-024-632-5	Sequence 5, Appli
	913	19	0.5	1975	15	US-10-027-632-97507	Sequence 97507, A
c	914	19	0.5	1975	15	US-10-027-632-99279	Sequence 99279, A
	915	19	0.5	2019	15	US-10-426-776-18	Sequence 18, Appl
c	916	19	0.5	2025	15	US-10-108-260A-80	Sequence 80, Appl
	917	19	0.5	2034	13	US-10-044-090-209	Sequence 209, App
	918	19	0.5	2045	12	US-10-425-114-26238	Sequence 26238, A
	919	19	0.5	2095	15	US-10-094-749-543	Sequence 543, App
	920	19	0.5	2097	15	US-10-085-117-44	Sequence 44, Appl
	921	19	0.5	2108	12	US-10-425-114-13067	Sequence 13067, A
c	922	19	0.5	2143	12	US-10-425-114-29372	Sequence 29372, A
	923	19	0.5	2149	9	US-09-880-107-3031	Sequence 3031, Ap
	924	19	0.5	2149	14	US-10-171-581-103	Sequence 103, App
	925	19	0.5	2149	14	US-10-007-926A-460	Sequence 460, App
	926	19	0.5	2149	15	US-10-439-703-63	Sequence 63, Appl
	927	19	0.5	2177	15	US-10-161-493-75	Sequence 75, Appl
	928	19	0.5	2239	15	US-10-104-047-1816	Sequence 1816, Ap
c	929	19	0.5	2249	12	US-10-424-599-101437	Sequence 101437,
c	930	19	0.5	2268	15	US-10-094-749-842	Sequence 842, App
	931	19	0.5	2277	14	US-10-114-153-7	Sequence 7, Appli
	932	19	0.5	2294	10	US-09-946-374-152	Sequence 152, App
	933	19	0.5	2294	12	US-10-206-915-283	Sequence 283, App
	934	19	0.5	2294	12	US-10-199-670-283	Sequence 283, App
	935	19	0.5	2294	13	US-10-052-586-283	Sequence 283, App
	936	19	0.5	2294	14	US-10-174-590-283	Sequence 283, App
	937	19	0.5	2294	14	US-10-176-758-283	Sequence 283, App
	938	19	0.5	2294	14	US-10-175-737-283	Sequence 283, App
	939	19	0.5	2294	14	US-10-173-706-283	Sequence 283, App
	940	19	0.5	2294	14	US-10-175-738-283	Sequence 283, App
	941	19	0.5	2294	14	US-10-175-752-283	Sequence 283, App
	942	19	0.5	2294	14	US-10-176-482-283	Sequence 283, App
	943	19	0.5	2294	14	US-10-176-757-283	Sequence 283, App
	944	19	0.5	2294	14	US-10-176-913-283	Sequence 283, App
	945	19	0.5	2294	14	US-10-180-552-283	Sequence 283, App
	946	19	0.5	2294	14	US-10-180-557-283	Sequence 283, App
	947	19	0.5	2294	14	US-10-173-700-283	Sequence 283, App
	948	19	0.5	2294	14	US-10-174-572-283	Sequence 283, App
	949	19	0.5	2294	14	US-10-174-579-283	Sequence 283, App
	950	19	0.5	2294	14	US-10-174-582-283	Sequence 283, App
	951	19	0.5	2294	14	US-10-174-588-283	Sequence 283, App
	952	19	0.5	2294	14	US-10-175-739-283	Sequence 283, App
	953	19	0.5	2294	14	US-10-175-740-283	Sequence 283, App
	954	19	0.5	2294	14	US-10-175-743-283	Sequence 283, App
	955	19	0.5	2294	14	US-10-176-488-283	Sequence 283, App
	956	19	0.5	2294	14	US-10-176-492-283	Sequence 283, App
	957	19	0.5	2294	14	US-10-176-747-283	Sequence 283, App
	958	19	0.5	2294	14	US-10-176-750-283	Sequence 283, App
	959	19	0.5	2294	14	US-10-176-985-283	Sequence 283, App
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 991      19     0.5     2294   14   US-10-183-010-283            Sequence 283, App
 992      19     0.5     2294   14   US-10-183-012-283            Sequence 283, App
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 994      19     0.5     2294   14   US-10-184-623-283            Sequence 283, App
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 996      19     0.5     2294   14   US-10-184-637-283            Sequence 283, App
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ALIGNMENTS

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RESULT 1
US-10-029-115-1
; Sequence 1, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Ying
;  APPLICANT:  Fu, Alan C
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION: No. US20030077597A1el Germinal Center Kinase Cell Cycle Protiens,
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: A-70229/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/10/029,115
;  CURRENT FILING DATE:  2001-10-19
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 3951
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-1

  Query Match             100.0%;  Score 3951;  DB 14;  Length 3951;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3951;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAG 120
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Qy        181 ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC 240
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Qy       3601 CCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC 3660
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Qy       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT 3780

Qy       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC 3840

Qy       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA 3900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA 3900

Qy       3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC 3951


RESULT 2
US-10-029-115-5
; Sequence 5, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Ying
;  APPLICANT:  Fu, Alan C
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION: No. US20030077597A1el Germinal Center Kinase Cell Cycle Protiens,
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: A-70229/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/10/029,115
;  CURRENT FILING DATE:  2001-10-19
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 4033
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-5

  Query Match             48.3%;  Score 1907;  DB 14;  Length 4033;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2197;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy       1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1836 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1895

Qy       1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1896 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1955

Qy       1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1956 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 2015

Qy       1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2016 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2075

Qy       1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2076 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2135

Qy       2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2136 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2195

Qy       2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2196 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2255

Qy       2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2256 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2315

Qy       2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2316 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2375

Qy       2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2376 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2435

Qy       2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2436 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2495

Qy       2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2496 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2555

Qy       2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
              |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       2556 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2612

Qy       2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2613 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2672

Qy       2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2673 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2732

Qy       2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2733 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2792

Qy       2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2793 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2852

Qy       2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2853 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2912

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2913 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2972

Qy       2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2973 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 3032

Qy       2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3033 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3092

Qy       3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3093 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3152

Qy       3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3153 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3212

Qy       3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3213 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3272

Qy       3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3273 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3332

Qy       3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3333 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3392

Qy       3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3393 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3452

Qy       3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3453 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3512

Qy       3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3513 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3572

Qy       3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       3573 TCTATGGCTCCAGTGCTGGCTTCCATGCTGCGGATGTCGACTCGGGGAACAGCTATGACA 3632

Qy       3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3633 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3692

Qy       3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3693 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3752

Qy       3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3753 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3812

Qy       3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3813 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3872

Qy       3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3873 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3932

Qy       3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3933 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTT 3992

Qy       3905 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||||
Db       3993 ACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 4033
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RESULT 3
US-09-291-417-11
; Sequence 11, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT: MARTINEZ, RICARDO
;  APPLICANT: WHYTE, DAVID
;  TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;  FILE REFERENCE: 240/300
;  CURRENT APPLICATION NUMBER: US/09/291,417A
;  CURRENT FILING DATE: 1999-04-13
;  EARLIER APPLICATION NUMBER: US 60/081,784
;  EARLIER FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 4133
;   TYPE: DNA
;   ORGANISM: Mammalian (Human) ZC3
US-09-291-417-11

  Query Match             45.2%;  Score 1787;  DB 10;  Length 4133;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2177;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy       1745 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1784 AGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCG 1843

Qy       1805 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1844 ACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGA 1903

Qy       1865 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1904 ATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTCCGCC 1963

Qy       1925 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 1984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1964 CAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTA 2023

Qy       1985 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2024 ACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCA 2083

Qy       2045 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2084 ACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAG 2143

Qy       2105 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2144 GGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCGACCTCAGGAGGA 2203

Qy       2165 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2204 GCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCC 2263

Qy       2225 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCCCCTG 2284
              ||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||
Db       2264 AGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTG 2323

Qy       2285 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2324 TGCTCTCCCCTGGGAATAAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCG 2383

Qy       2345 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2384 CAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGG 2443

Qy       2405 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2444 CCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAG 2503

Qy       2465 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATA 2524
              |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       2504 GCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCC---GCGATGGGGATA 2560

Qy       2525 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2584
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2561 CAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCC 2620

Qy       2585 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2621 CATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGC 2680

Qy       2645 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2681 ATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCA 2740

Qy       2705 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2741 CCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTC 2800

Qy       2765 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2824
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2801 GTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCT 2860

Qy       2825 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2861 ACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCA 2920

Qy       2885 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2921 CTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCA 2980

Qy       2945 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2981 CCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACT 3040

Qy       3005 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3041 CCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGC 3100

Qy       3065 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3101 TGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCT 3160

Qy       3125 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3161 TCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGA 3220

Qy       3185 ACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3244
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       3221 ACAAACTGCGGGTGTATTACTTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAG 3280

Qy       3245 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3281 AAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACC 3340

Qy       3305 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3341 GTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGG 3400

Qy       3365 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3401 TGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACC 3460

Qy       3425 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3461 TCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCA 3520

Qy       3485 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3521 TCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACA 3580

Qy       3545 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3581 TCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCA 3640

Qy       3605 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3641 ACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGT 3700

Qy       3665 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3701 ACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCT 3760

Qy       3725 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3761 ACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG 3820

Qy       3785 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3821 AGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3880

Qy       3845 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTT 3904
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3881 GTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTT 3940

Qy       3905 ACTTCATGACTCTGAACCGTAAC 3927
              |||||||||||||||||||||||
Db       3941 ACTTCATGACTCTGAACCGTAAC 3963
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RESULT 4
US-10-441-281-30
; Sequence 30, Application US/10441281
; Publication No. US20030228618A1
; GENERAL INFORMATION:
;  APPLICANT: Levanon Erez, et al.
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING NATURALLY OCCURRING ANTISENSE
;  TITLE OF INVENTION:  TRANSCRIPTS AND METHODS AND KITS UTILIZING SAME
;  FILE REFERENCE: 02/26133
;  CURRENT APPLICATION NUMBER: US/10/441,281
;  CURRENT FILING DATE:  2003-05-20
;  PRIOR APPLICATION NUMBER: US 09/718,407
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: US 09/732,938
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/785,439
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: US 09/907,923
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 009/993,398
;  PRIOR FILING DATE: 2001-11-06
;  PRIOR APPLICATION NUMBER: US 10/201,605
;  PRIOR FILING DATE: 2002-07-24
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 4863
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-441-281-30

  Query Match             42.7%;  Score 1689;  DB 15;  Length 4863;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1739;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 244

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 304

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 364

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 424
```

```
Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 484

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 544

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 604

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 664

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 724

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 784

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        785 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 844

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        845 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 904

Qy        727 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 GCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAG 964

Qy        787 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        965 AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACG 1024

Qy        847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATC 1084

Qy        907 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1085 CAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAA 1144

Qy        967 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1145 TATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGC 1204

Qy       1027 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1205 TCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAG 1264

Qy       1087 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1265 GAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG 1324

Qy       1147 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 CGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAG 1384

Qy       1207 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1385 CAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAG 1444

Qy       1267 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1445 CTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAG 1504

Qy       1327 GAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1386
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1505 GAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGG 1564

Qy       1387 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1565 CAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAG 1624

Qy       1447 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1625 CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGGGAC 1684

Qy       1507 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1685 AGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCC 1744

Qy       1567 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1745 CGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGC 1804

Qy       1627 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1805 AAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGA 1864

Qy       1687 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1865 CCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAG 1924


RESULT 5
US-10-029-115-3
; Sequence 3, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Ying
;  APPLICANT:  Fu, Alan C
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION: No. US20030077597A1el Germinal Center Kinase Cell Cycle Protiens,
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: A-70229/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/10/029,115
;  CURRENT FILING DATE:  2001-10-19
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 4414
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-029-115-3

  Query Match             42.6%;  Score 1683;  DB 14;  Length 4414;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1683;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         64 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 GACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTG 160

Qy        124 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACG 220

Qy        184 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 GAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCAC 280

Qy        244 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 CGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGAC 340

Qy        304 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAAC 400
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Qy        364 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGG 460

Qy        424 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 GGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTG 520

Qy        484 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 CTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGAC 580

Qy        544 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 CGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTC 640

Qy        604 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 ATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTA 700

Qy        664 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 GGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATG 760

Qy        724 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 CGAGCCCTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCT 820

Qy        784 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCC 880

Qy        844 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGC 940

Qy        904 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 963
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 ATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACA 1000

Qy        964 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1001 GAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCA 1060

Qy       1024 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1083
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 AGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAG 1120

Qy       1084 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 CAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG 1180

Qy       1144 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 CAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAG 1240

Qy       1204 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1241 GAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGG 1300

Qy       1264 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 AAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAG 1360

Qy       1324 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 GAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAGCAG 1420

Qy       1384 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1421 CGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTG 1480

Qy       1444 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1481 CAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCTGGG 1540

Qy       1504 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1541 GACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGG 1600

Qy       1564 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1601 GCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAG 1660

Qy       1624 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1661 AGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCCATCCCCCAGGCCTCCCCAGGGCCCCCA 1720

Qy       1684 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1721 GGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCAC 1780

Qy       1744 AAG 1746
              |||
Db       1781 AAG 1783


RESULT 6
US-09-789-390-12
; Sequence 12, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 3735
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3732)
US-09-789-390-12

  Query Match             40.5%;  Score 1599;  DB 10;  Length 3735;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2137 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2196

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2197 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2256

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2257 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2316

Qy          2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2317 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2376

Qy          2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2377 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2436

Qy          2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2437 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2496

Qy          2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2497 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2556

Qy          2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2557 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2616

Qy          2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
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Db          2617 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2676

Qy          2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
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Db          2677 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2736

Qy          2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
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Db          2737 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 2796

Qy          3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
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Db          2797 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 2856

Qy          3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2857 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 2916

Qy          3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2917 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 2976

Qy          3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2977 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3036

Qy          3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3037 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3096

Qy          3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3097 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3156

Qy          3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3157 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3216

Qy          3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3217 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3276

Qy          3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3277 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3336

Qy          3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3337 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3396

Qy          3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3397 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3456

Qy          3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3457 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3516

Qy          3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3517 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3576

Qy          3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
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Db          3577 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3636

Qy          3847 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
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Db          3637 GAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3696

Qy          3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
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Db          3697 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3735
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RESULT 7
US-09-789-390-10
; Sequence 10, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 3822
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3819)
US-09-789-390-10

  Query Match             40.5%;  Score 1599;  DB 10;  Length 3822;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2224 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2283

Qy          2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2284 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2343
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Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
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Db       2344 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2403

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2404 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2463

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2464 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2523

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2524 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2583

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2584 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2643

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2644 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2703

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2704 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2763

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2764 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2823

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2824 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 2883

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2884 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 2943

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2944 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3003

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3004 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3063

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3064 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3123

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3124 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3183

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3184 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3243

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3244 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3303

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3304 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3363

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3364 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3423

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3424 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3483

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3484 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3543

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3544 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3603

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3604 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3663

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3664 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3723

Qy       3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3724 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3783

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
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Db       3784 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3822
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RESULT 8
US-09-789-390-8
; Sequence 8, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 3912
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3909)
US-09-789-390-8

  Query Match             40.5%;  Score 1599;  DB 10;  Length 3912;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
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Db       2314 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2373

Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2433

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2493

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2553

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2613

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
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Db       2614 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2673

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2733

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2793

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
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Db       2794 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2853

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
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Db       2854 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2913

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
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Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
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Db       2974 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3033

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
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Db       3034 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3093

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
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Db       3094 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3153

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3213

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3273

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3333

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3393

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3453

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3513

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3573

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3574 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3633

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3634 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3693

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3694 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3753

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3754 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3813

Qy       3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3814 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3873

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||
Db       3874 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3912
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RESULT 9
US-09-789-390-6
; Sequence 6, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 3999
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3996)
US-09-789-390-6

  Query Match             40.5%;  Score 1599;  DB 10;  Length 3999;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2347 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCC 2460
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Qy       2407 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGC 2520

Qy       2467 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGCAGCGATGGGGATACA 2580

Qy       2527 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCA 2640

Qy       2587 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCAT 2700

Qy       2647 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACC 2760

Qy       2707 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGT 2820

Qy       2767 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTAC 2880

Qy       2827 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACT 2940

Qy       2887 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACC 3000

Qy       2947 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCC 3060

Qy       3007 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 GAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTG 3120

Qy       3067 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 ATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTC 3180

Qy       3127 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAAC 3240

Qy       3187 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 AAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3300

Qy       3247 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGT 3360

Qy       3307 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3420

Qy       3367 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 TATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTC 3480

Qy       3427 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATC 3540

Qy       3487 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATC 3600

Qy       3547 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 TACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAAC 3660

Qy       3607 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 ACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTAC 3720

Qy       3667 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTAC 3780

Qy       3727 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 ATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAG 3840

Qy       3787 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 ACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGT 3900

Qy       3847 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTAC 3960

Qy       3907 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||||||||
Db       3961 TTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3999
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RESULT 10
US-09-789-390-64
; Sequence 64, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
;   LENGTH: 1482
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-789-390-64

  Query Match             33.8%;  Score 1337;  DB 10;  Length 1482;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60
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Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy        370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy        430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy        490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy       1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy       1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy       1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy       1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy       1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy       1330 CGGCGGCAGGCGGAGCG 1346
              |||||||||||||||||
Db       1321 CGGCGGCAGGCGGAGCG 1337

RESULT 11
US-09-789-390-62
; Sequence 62, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
;   LENGTH: 1649
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-789-390-62

  Query Match             33.8%;  Score 1337;  DB 10;  Length 1649;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy          370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy          430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy          490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy          550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy          610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy          670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy          730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy          790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy          850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy          910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy          970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy         1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy         1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy         1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
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Db         1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy         1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy         1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy         1330 CGGCGGCAGGCGGAGCG 1346
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Db         1321 CGGCGGCAGGCGGAGCG 1337
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RESULT 12

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US-09-789-390-69
; Sequence 69, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
;   LENGTH: 1717
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-789-390-69

  Query Match             33.8%;  Score 1337;  DB 10;  Length 1717;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy           70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy          130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy          190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
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Db          181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy          250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy          310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy          370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy          430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy          490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy          550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840

Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy       1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy       1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy       1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
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Db       1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy       1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy       1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy       1330 CGGCGGCAGGCGGAGCG 1346
              |||||||||||||||||
Db       1321 CGGCGGCAGGCGGAGCG 1337
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RESULT 13
US-09-789-390-66
; Sequence 66, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Spaderna, Steven K
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-692
;  CURRENT APPLICATION NUMBER: US/09/789,390
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185,548
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/199,957
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/184,951
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 60/185,967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 60/197,723
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 1787
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-789-390-66

  Query Match             33.8%;  Score 1337;  DB 10;  Length 1787;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGACCCT 60

Qy         70 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTACAAG 120

Qy        130 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGAC 180

Qy        190 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGCAAC 240

Qy        250 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAGCTC 300

Qy        310 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACAAAA 360

Qy        370 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTG 420

Qy        430 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTG 480

Qy        490 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGCACC 540

Qy        550 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATCGCC 600

Qy        610 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGAATC 660

Qy        670 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGAGCC 720

Qy        730 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 789
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Db        721 CTCTTCCTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTAAGAAG 780

Qy        790 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCACCCACGGAG 840
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Qy        850 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTCCGCATCCAG 900

Qy        910 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAATAT 960

Qy        970 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAGCCAAGCTCC 1020

Qy       1030 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTCCAGCAGGAA 1080

Qy       1090 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1149
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Db       1081 AATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGA 1140

Qy       1150 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAG 1200

Qy       1210 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTG 1260

Qy       1270 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGGGAGGAGGAG 1320

Qy       1330 CGGCGGCAGGCGGAGCG 1346
              |||||||||||||||||
Db       1321 CGGCGGCAGGCGGAGCG 1337
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RESULT 14
US-09-925-297-137
; Sequence 137, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA105
;  CURRENT APPLICATION NUMBER: US/09/925,297
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05989
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 928
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
;   LENGTH: 2345
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (184)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (339)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (1805)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (1887)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (2325)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (2339)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-137

  Query Match             26.1%;  Score 1030;  DB 9;  Length 2345;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1180;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2763 TCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGAT 2822
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Db        351 TCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGAT 410

Qy       2823 CTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGG 2882
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Db        411 TTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGG 470

Qy       2883 CACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCC 2942
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Db        471 CACTCGGTTCGACCAGCTGCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCC 530

Qy       2943 CACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAA 3002
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Db        531 CACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAA 590

Qy       3003 CTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGG 3062
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Db        591 CTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGG 650

Qy       3063 GCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACG 3122
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Db        651 GCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACG 710

Qy       3123 CTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAG 3182
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Db        711 CTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAG 770

Qy       3183 GAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCC 3242
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Qy       3243 AGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTA 3302
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Qy       3303 CCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGA 3362
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Qy       3363 GGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGA 3422
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Db        951 GGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGA 1010

Qy       3423 CCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGT 3482
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Db       1011 CCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGT 1070

Qy       3483 CATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGA 3542
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Db       1071 CATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGA 1130

Qy       3543 CATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCC 3602
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Qy       3603 CAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACAC 3662
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Qy       3663 GTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGC 3722
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Qy       3723 CTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGT 3782
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Qy       3783 GGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCT 3842
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Qy       3903 TTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
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Db       1491 TTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGA 1533

RESULT 15
US-10-108-260A-1388
; Sequence 1388, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20040005560A1el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1388
;   LENGTH: 3152
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-108-260A-1388

  Query Match             14.0%;  Score 555;  DB 15;  Length 3152;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-258;
  Matches  555;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       3370 GCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCC 3429
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Qy       3430 CACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTAT 3489
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Qy       3790 GGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAG 3849
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Qy       3850 CGGAATGACAAGGTG 3864
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Db       1892 CGGAATGACAAGGTG 1906

Search completed: March  3, 2004, 05:43:51
Job time : 907 secs
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OM nucleic - nucleic search, using sw model

Run on:         March  2, 2004, 17:02:58 ; Search time 6279 Seconds
                                           (without alignments)
                                           18790.488 Million cell updates/sec

Title:          US-10-029-115-1
Perfect score:  3951
Sequence:       1 gcccttatgggcgacccagc..........tcatgaactggtgaaagggc 3951

Scoring table:  OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched:       27513289 seqs, 14931090276 residues

Word size :     0

Total number of hits satisfying chosen parameters:      55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :       EST:*
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                 29:  gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	786	19.9	907	13	BQ684810	BQ684810 AGENCOURT
	2	779	19.7	908	13	BU542554	BU542554 AGENCOURT
	3	757	19.2	969	13	BU838349	BU838349 AGENCOURT
	4	735	18.6	1201	9	AL551911	AL551911 AL551911
	5	730	18.5	881	13	BU542006	BU542006 AGENCOURT
	6	727	18.4	910	14	CD557991	CD557991 AGENCOURT
	7	724	18.3	1515	11	BC028888	BC028888 Homo sapi
	8	720	18.2	1026	12	BM541693	BM541693 AGENCOURT
	9	714	18.1	1022	13	BQ073811	BQ073811 AGENCOURT
	10	697	17.6	936	12	BM451246	BM451246 AGENCOURT
	11	693	17.5	951	13	BQ706178	BQ706178 AGENCOURT
	12	638	16.1	1167	13	BX359762	BX359762 BX359762
	13	633	16.0	727	12	BI000010	BI000010 MR3-HN006
	14	621	15.7	1037	12	BM800664	BM800664 AGENCOURT
	15	616	15.6	629	12	BI916276	BI916276 603178186
	16	613	15.5	1047	12	BG331648	BG331648 602432668
	17	611	15.5	999	12	BM477724	BM477724 AGENCOURT
	18	593	15.0	811	13	BU527825	BU527825 AGENCOURT
	19	582	14.7	582	14	CB132954	CB132954 K-EST0183
	20	568	14.4	903	13	BU527220	BU527220 AGENCOURT
	21	564	14.3	1040	13	BQ072284	BQ072284 AGENCOURT
	22	563	14.2	1041	12	BM906355	BM906355 AGENCOURT
	23	551	13.9	805	10	BE312777	BE312777 601149545
	24	529	13.4	866	12	BI756763	BI756763 603024432
	25	527	13.3	527	10	BF724524	BF724524 bx05h04.y
	26	519	13.1	828	14	CD108219	CD108219 AGENCOURT
c	27	517	13.1	541	14	CB853199	CB853199 UI-CF-FN0
	28	504	12.8	652	12	BG821758	BG821758 602727782
	29	500	12.7	947	12	BG327623	BG327623 602426617
	30	496	12.6	744	12	BG755560	BG755560 602716243
	31	495	12.5	705	10	BE940486	BE940486 RC1-UT006
	32	492	12.5	492	14	CB144863	CB144863 K-EST0199
	33	492	12.5	492	14	CB145533	CB145533 K-EST0200
	34	473	12.0	873	13	BQ717112	BQ717112 AGENCOURT
	35	472	11.9	472	9	AA780425	AA780425 ae93c06.s
	36	468	11.8	1058	12	BM464994	BM464994 AGENCOURT
	37	467	11.8	1205	12	BM806023	BM806023 AGENCOURT
	38	466	11.8	534	12	BG419855	BG419855 602453316
	39	459	11.6	918	13	BQ945934	BQ945934 AGENCOURT
	40	451	11.4	971	13	BU173419	BU173419 AGENCOURT
	41	439	11.1	1218	12	BM548024	BM548024 AGENCOURT
	42	432	10.9	881	14	CA454128	CA454128 AGENCOURT
	43	432	10.9	939	13	BQ931753	BQ931753 AGENCOURT
	44	425	10.8	666	14	CF135957	CF135957 UI-HF-BN0
	45	423	10.7	423	10	AW239077	AW239077 xb36c06.y
	46	423	10.7	633	12	BI771641	BI771641 603058774
	47	421	10.7	924	14	CA488783	CA488783 AGENCOURT
	48	418	10.6	434	10	BF882128	BF882128 QV1-ET017
	49	415	10.5	706	12	BG761039	BG761039 602717549
	50	408	10.3	408	14	CA391844	CA391844 cs19e06.y
	51	407	10.3	477	10	BF881056	BF881056 QV1-ET018
	52	406	10.3	715	12	BI195766	BI195766 602754145
	53	400	10.1	702	10	BE271987	BE271987 601141142
	54	397	10.0	923	10	BE965592	BE965592 601659629
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	56	382	9.7	917	12	BG106177	BG106177 602289510
	57	381	9.6	438	14	CF142044	CF142044 UI-HF-CB0
	58	371	9.4	696	12	BM020958	BM020958 603646206
	59	371	9.4	708	12	BI117656	BI117656 602867049
c	60	360	9.1	422	10	BF893960	BF893960 QV1-MT016
c	61	350	8.9	637	12	BI009982	BI009982 MR4-RT004
c	62	337	8.5	617	10	AW973784	AW973784 EST385885
	63	324	8.2	391	10	BF998490	BF998490 CM2-GN016
	64	324	8.2	849	10	BE898845	BE898845 601682136
	65	324	8.2	977	13	BQ675474	BQ675474 AGENCOURT
	66	322	8.1	626	12	BG826212	BG826212 602750606
	67	320	8.1	640	12	BG769421	BG769421 602742533
	68	318	8.0	630	10	BE882515	BE882515 601507257
	69	314	7.9	329	10	BF849628	BF849628 IL5-EN008
	70	311	7.9	353	14	CF139311	CF139311 UI-HF-CB0
	71	310	7.8	311	10	BF873626	BF873626 IL5-ET011
	72	309	7.8	767	12	BG680567	BG680567 602628396
	73	308	7.8	632	12	BI819914	BI819914 603035459
	74	302	7.6	442	9	AI125161	AI125161 am55f06.x
	75	301	7.6	818	12	BG113745	BG113745 602284267
	76	300	7.6	882	14	CD358179	CD358179 AGENCOURT
	77	300	7.6	901	13	BX390479	BX390479 BX390479

	78	289	7.3	906	10	BG031081	BG031081 602298934
	79	285	7.2	420	9	AI372794	AI372794 EST175337
	80	283	7.2	867	12	BG421677	BG421677 602449775
	81	281	7.1	1043	10	BE778941	BE778941 601465044
	82	279	7.1	1178	12	BM910742	BM910742 AGENCOURT
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	84	271	6.9	586	12	BI199531	BI199531 602758664
c	85	270	6.8	434	9	AI372793	AI372793 EST175336
c	86	268	6.8	467	12	BG945851	BG945851 MR3-KT005
c	87	262	6.6	279	10	BF946368	BF946368 RC6-NN117
c	88	259	6.6	394	9	AA557573	AA557573 nl45a04.s
	89	258	6.5	1262	13	BQ058598	BQ058598 AGENCOURT
c	90	253	6.4	273	10	AW885288	AW885288 QV4-OT006
	91	253	6.4	286	10	BF988086	BF988086 CM0-GN016
	92	253	6.4	787	12	BM051265	BM051265 603634236
	93	252	6.4	749	12	BG757547	BG757547 602714720
	94	242	6.1	327	9	AA295021	AA295021 EST100479
	95	241	6.1	535	12	BM739040	BM739040 K-EST0008
	96	239	6.0	258	14	R10658	R10658 yf31e12.r1
	97	238	6.0	1114	14	CD558642	CD558642 AGENCOURT
	98	236	6.0	353	10	BF091038	BF091038 MR3-SN003
	99	232	5.9	725	10	BE536499	BE536499 601067444
c	100	227	5.7	270	10	AW885349	AW885349 QV4-OT006
c	101	224	5.7	398	12	BG984025	BG984025 IL5-CN006
	102	223	5.6	491	9	AA434299	AA434299 zw30g06.r
	103	221	5.6	256	12	BM823989	BM823989 K-EST0095
	104	221	5.6	443	14	R18578	R18578 yf95f12.r1
c	105	221	5.6	512	13	BQ327795	BQ327795 MR4-RT003
	106	221	5.6	800	12	BI754257	BI754257 603025559
c	107	219	5.5	432	12	BG994275	BG994275 CM3-HT115
c	108	211	5.3	454	12	BI052005	BI052005 RC3-GN026
	109	210	5.3	360	10	BF924542	BF924542 IL5-NT022
	110	207	5.2	524	10	BF920346	BF920346 QV2-NT014
	111	206	5.2	550	14	CB119344	CB119344 K-EST0166
	112	202	5.1	250	10	AW843642	AW843642 CM0-CN004
	113	198	5.0	198	14	CB117740	CB117740 K-EST0163
	114	198	5.0	625	12	BI772266	BI772266 603055847
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	116	193	4.9	1036	12	BM044589	BM044589 603622248
	117	185	4.7	203	10	AW366519	AW366519 CM3-HT014
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	121	178	4.5	606	12	BM047589	BM047589 603628918
	122	174	4.4	289	9	AI905357	AI905357 IL-BT086-
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	124	172	4.4	719	10	BG032073	BG032073 602300589
	125	170	4.3	288	10	BF752910	BF752910 RC4-BN022
c	126	170	4.3	528	10	BE932268	BE932268 IL3-HT061
	127	169	4.3	283	10	BF898266	BF898266 QV1-MT022
	128	163	4.1	269	10	BF088961	BF088961 PM4-HT090
	129	161	4.1	189	14	Z42685	Z42685 HSC0RA101 n
	130	160	4.0	959	13	BQ716738	BQ716738 AGENCOURT
c	131	158	4.0	508	10	BF086296	BF086296 QV1-GN006
	132	156	3.9	473	9	AA233207	AA233207 zr69b04.r
	133	155	3.9	337	10	BF868921	BF868921 IL5-ET011
c	134	154	3.9	362	13	BQ334589	BQ334589 QV1-MT023
	135	151	3.8	399	9	AA349349	AA349349 EST55972
	136	151	3.8	451	13	BQ367113	BQ367113 RC1-GN019
c	137	150	3.8	360	9	AA788891	AA788891 ae93f02.s
	138	145	3.7	349	10	BF087135	BF087135 PM1-HT045
c	139	143	3.6	1201	9	AL575366	AL575366 AL575366
	140	139	3.5	424	10	BF805131	BF805131 QV1-CI017
c	141	137	3.5	351	13	BQ346024	BQ346024 PM3-NT031
	142	135	3.4	251	14	R00019	R00019 ye69h10.r1
c	143	135	3.4	387	10	BG014371	BG014371 CM3-GN029
c	144	134	3.4	303	13	BQ364055	BQ364055 MR4-ST024
	145	131	3.3	180	10	BG011162	BG011162 IL5-GN024
	146	130	3.3	387	9	AA325902	AA325902 EST28976
	147	129	3.3	298	10	BF946362	BF946362 RC6-NN117
	148	125	3.2	557	10	BF926778	BF926778 MR2-NT013
	149	119	3.0	376	12	BI021730	BI021730 CM3-MT018
	150	118	3.0	179	9	AA325971	AA325971 EST29058

c	151	117	3.0	231	13	BQ368123	BQ368123 PM3-GN051
	152	116	2.9	176	10	BF924939	BF924939 IL2-NT020
	153	115	2.9	1712	12	BM918883	BM918883 AGENCOURT
c	154	114	2.9	356	12	BI011871	BI011871 PM1-EN006
c	155	113	2.9	143	10	BF742906	BF742906 CM0-BT086
	156	113	2.9	629	12	BG910247	BG910247 602805744
c	157	112	2.8	299	13	BQ326905	BQ326905 RC4-CN020
	158	111	2.8	351	14	R54563	R54563 yg81b12.r1
c	159	109	2.8	408	9	AA701376	AA701376 zi63g12.s
c	160	109	2.8	477	9	AA777771	AA777771 zi95h04.s
c	161	108	2.7	342	9	AI040133	AI040133 ox08h05.x
c	162	107	2.7	341	10	AW751287	AW751287 IL2-CT003
	163	104	2.6	463	14	R20150	R20150 yg18h06.r1
	164	102	2.6	293	14	R02058	R02058 ye86b11.r1
	165	102	2.6	363	10	BF851235	BF851235 IL5-EN008
	166	101	2.6	223	10	BF851327	BF851327 IL5-EN008
	167	101	2.6	405	10	BE937980	BE937980 MR1-TN004
c	168	98	2.5	451	13	BQ367113	BQ367113 RC1-GN019
	169	97	2.5	290	10	BF229406	BF229406 MR1-CI002
	170	95	2.4	490	13	BX476452	BX476452 DKFZp686D
	171	94	2.4	212	13	BQ326990	BQ326990 RC4-CN020
	172	94	2.4	303	12	BI051567	BI051567 CM4-GN036
c	173	94	2.4	450	13	BQ300059	BQ300059 MR3-KT005
	174	93	2.4	276	10	AW368321	AW368321 CM2-HT018
c	175	93	2.4	281	10	AW368328	AW368328 CM3-HT018
	176	92	2.3	390	28	AZ301117	AZ301117 UP_305-1G
	177	92	2.3	934	14	CB990560	CB990560 AGENCOURT
c	178	91	2.3	170	10	BF931929	BF931929 PM1-NT023
c	179	88	2.2	236	10	AW298772	AW298772 UI-H-BW0-
c	180	86	2.2	219	13	BQ327059	BQ327059 RC4-CN020
	181	86	2.2	564	12	BM967105	BM967105 ij30e04.y
	182	86	2.2	657	12	BM722585	BM722585 UI-E-EO0-
	183	85	2.2	507	10	BE485510	BE485510 172555 BA
	184	81	2.1	345	13	BQ300043	BQ300043 PM1-KT004
c	185	80	2.0	330	9	AI905697	AI905697 IL-BT096-
	186	79	2.0	297	14	R88464	R88464 ym92h01.r1
	187	72	1.8	304	14	T32148	T32148 EST44087 Hu
	188	72	1.8	563	10	BE751204	BE751204 203083 MA
	189	70	1.8	320	10	BF765603	BF765603 RC0-CS004
c	190	67	1.7	161	10	BF880445	BF880445 QV3-ET019
	191	66	1.7	191	10	BF879175	BF879175 QV3-ET017
	192	66	1.7	658	10	BF821438	BF821438 MR1-RT003
	193	65	1.6	467	10	BF603813	BF603813 269407 MA
	194	64	1.6	453	12	BI012190	BI012190 PM1-EN006
	195	59	1.5	114	10	BF924940	BF924940 IL2-NT020
c	196	56	1.4	136	10	BF373997	BF373997 CM2-SN002
c	197	54	1.4	96	9	AI905698	AI905698 IL-BT096-
	198	53	1.3	155	10	BF886565	BF886565 RC6-TN007
	199	53	1.3	427	10	AW762248	AW762248 ur55e07.y
	200	53	1.3	434	14	CB793477	CB793477 AMGNNUC:N
	201	53	1.3	434	14	CB793690	CB793690 AMGNNUC:N
	202	53	1.3	456	10	AW258584	AW258584 uq37a10.y
	203	53	1.3	567	14	CB616524	CB616524 AMGNNUC:N
	204	53	1.3	595	14	CB584150	CB584150 AMGNNUC:N
	205	53	1.3	600	12	BI991507	BI991507 4101-82 M
	206	53	1.3	696	12	BM932728	BM932728 UI-M-CG0p
	207	53	1.3	696	14	CB244053	CB244053 UI-M-FY0-
	208	53	1.3	698	12	BG665574	BG665574 DRACEH03
	209	53	1.3	709	12	BG975412	BG975412 602843063
	210	53	1.3	709	14	CA316178	CA316178 UI-M-FW0-
	211	53	1.3	790	14	CF733432	CF733432 UI-M-HB0-
	212	53	1.3	794	12	BI409187	BI409187 602961334
	213	53	1.3	832	13	BU558574	BU558574 AGENCOURT
	214	50	1.3	297	9	AI007546	AI007546 EST108048
	215	50	1.3	425	14	CB696067	CB696067 AMGNNUC:N
	216	50	1.3	538	10	BF450846	BF450846 uz71f01.y
	217	50	1.3	628	10	BE569708	BE569708 601332311
	218	50	1.3	640	9	AU296392	AU296392 AU296392
	219	50	1.3	721	13	BU707794	BU707794 UI-M-FR0-
	220	49	1.2	219	13	BQ368422	BQ368422 PM3-GN051
	221	49	1.2	428	14	CB793968	CB793968 AMGNNUC:N
	222	47	1.2	247	9	AA673268	AA673268 vn36a04.r
	223	47	1.2	331	9	AI641825	AI641825 vq32d10.y

	224	47	1.2	388	14	W64920	W64920 me02a11.r1
	225	47	1.2	396	10	AW742571	AW742571 up59e05.y
	226	47	1.2	411	10	BE226541	BE226541 ia22b12.y
	227	47	1.2	448	14	W88105	W88105 mf70b04.r1
	228	47	1.2	452	9	AA871207	AA871207 vq32d10.r
	229	47	1.2	506	13	BU694525	BU694525 LL2in1065
	230	47	1.2	514	10	BF233525	BF233525 602024122
	231	47	1.2	635	14	CD351693	CD351693 UI-M-GI0-
	232	47	1.2	643	10	BF167402	BF167402 601773690
	233	47	1.2	679	12	BM947633	BM947633 UI-M-EG0p
	234	47	1.2	714	12	BG294704	BG294704 602392074
	235	47	1.2	771	12	BI646294	BI646294 603276438
	236	47	1.2	778	14	CB245214	CB245214 UI-M-FY0-
	237	47	1.2	786	12	BI737039	BI737039 603360892
	238	47	1.2	791	12	BI852403	BI852403 603378228
	239	47	1.2	835	12	BI430479	BI430479 UMN41C01
	240	47	1.2	898	13	BQ885202	BQ885202 AGENCOURT
	241	47	1.2	956	12	BG297263	BG297263 602394974
	242	46	1.2	372	10	BF847314	BF847314 CM3-EN004
	243	46	1.2	524	10	BE369969	BE369969 601221191
	244	46	1.2	652	10	BB034168	BB034168 BB034168
	245	46	1.2	916	13	BQ922876	BQ922876 AGENCOURT
	246	44	1.1	168	14	CF171538	CF171538 B0843G02-
	247	44	1.1	341	10	AW231063	AW231063 uo70d04.y
	248	44	1.1	347	13	BY151323	BY151323 BY151323
	249	44	1.1	395	9	AA646811	AA646811 vn37b07.r
	250	44	1.1	455	14	CB741202	CB741202 AMGNNUC:N
	251	44	1.1	459	9	AA921243	AA921243 vy54g09.r
	252	44	1.1	508	14	CB518343	CB518343 UI-M-GH0-
	253	44	1.1	593	12	BI664323	BI664323 603289080
	254	44	1.1	607	13	BQ554558	BQ554558 H4028G09-
	255	44	1.1	635	14	CF171784	CF171784 B0847D08-
	256	44	1.1	641	10	BB620167	BB620167 BB620167
	257	44	1.1	663	14	CF533672	CF533672 UI-M-FY0-
	258	44	1.1	692	13	BU611352	BU611352 UI-M-FI0-
	259	44	1.1	720	14	CB249067	CB249067 UI-M-EX0-
	260	44	1.1	724	14	CF531764	CF531764 UI-M-FY0-
	261	44	1.1	757	14	CB519879	CB519879 UI-M-GH0-
	262	44	1.1	764	13	BQ180764	BQ180764 UI-M-EX0-
	263	44	1.1	827	10	BE295363	BE295363 601175870
	264	44	1.1	838	12	BI104781	BI104781 602891326
	265	44	1.1	844	13	BQ443922	BQ443922 UI-M-EW0-
	266	44	1.1	1490	10	BF539764	BF539764 602049976
	267	44	1.1	3585	29	AY400358	AY400358 Mus muscu
	268	42	1.1	593	12	BI372041	BI372041 RE57474.5
	269	42	1.1	599	12	BI234317	BI234317 RE30007.5
	270	42	1.1	611	12	BI232730	BI232730 RE28851.5
	271	42	1.1	618	12	BI235813	BI235813 RE31748.5
	272	42	1.1	624	12	BI365867	BI365867 RE51260.5
	273	42	1.1	657	12	BI231531	BI231531 RE22407.5
	274	42	1.1	668	12	BG637447	BG637447 SD15452.5
	275	42	1.1	705	13	BQ180518	BQ180518 UI-M-EX0-
	276	42	1.1	710	9	AA979568	AA979568 LD34191.5
	277	41	1.0	140	28	BH067865	BH067865 RPCI-24-3
	278	41	1.0	267	9	AA930283	AA930283 vs58c07.r
	279	41	1.0	393	14	CB777351	CB777351 AMGNNUC:N
	280	41	1.0	405	14	CB808584	CB808584 AMGNNUC:N
	281	41	1.0	479	14	CB546650	CB546650 AMGNNUC:N
	282	41	1.0	624	28	BH068131	BH068131 RPCI-24-3
c	283	41	1.0	847	13	BU935745	BU935745 AGENCOURT
	284	41	1.0	988	12	BG679244	BG679244 602627326
	285	40	1.0	316	10	BE929101	BE929101 PM3-GN001
	286	39	1.0	821	12	BI217509	BI217509 602933930
	287	38	1.0	272	14	Z44886	Z44886 HSC2BH081 n
	288	38	1.0	290	10	BF947862	BF947862 CM2-NN021
	289	38	1.0	301	10	AW480426	AW480426 31229 MAR
	290	38	1.0	563	10	BF385542	BF385542 602047087
	291	38	1.0	577	14	CD350084	CD350084 UI-M-FY0-
	292	38	1.0	646	12	BI103781	BI103781 602887788
	293	38	1.0	751	14	CF736764	CF736764 UI-M-HD0-
	294	38	1.0	941	10	BE573180	BE573180 601332853
c	295	38	1.0	1143	29	CNS03KWS	AL248725 Tetraodon
	296	38	1.0	1570	13	BQ885190	BQ885190 AGENCOURT
	297	37	0.9	212	12	BG865361	BG865361 602783968
	298	36	0.9	136	10	BE174066	BE174066 QV1-HT057
c	299	36	0.9	283	10	BF850781	BF850781 CM3-EN011
	300	36	0.9	440	14	CB749027	CB749027 AMGNNUC:C
	301	36	0.9	442	10	BE198798	BE198798 ug82f10.y
	302	36	0.9	455	14	CB741237	CB741237 AMGNNUC:N
	303	36	0.9	501	10	BE863915	BE863915 UI-M-BH0-
	304	36	0.9	582	28	AZ860896	AZ860896 2M0167C08
	305	36	0.9	617	12	BI108465	BI108465 602902176
	306	36	0.9	969	14	CB590530	CB590530 AGENCOURT
c	307	35	0.9	406	9	AL913187	AL913187 AL913187
	308	35	0.9	482	10	BF230263	BF230263 251785 BA
c	309	35	0.9	557	29	CE066918	CE066918 tigr-gss-
	310	35	0.9	584	9	AA497295	AA497295 fa03e11.r
	311	35	0.9	628	28	AZ937732	AZ937732 2M0196H04
	312	35	0.9	646	10	BE303496	BE303496 601086375
	313	35	0.9	652	12	BJ000404	BJ000404 BJ000404
	314	35	0.9	813	12	BI104219	BI104219 602889769
	315	34	0.9	506	12	BI895322	BI895322 EtESTea30
	316	34	0.9	574	9	AI533382	AI533382 SD05170.5
	317	34	0.9	800	12	BI649693	BI649693 603276611
	318	33	0.8	480	12	BI232278	BI232278 RE28324.5
	319	33	0.8	778	12	BG766518	BG766518 602739280
	320	33	0.8	978	13	BQ675493	BQ675493 AGENCOURT
	321	32	0.8	330	12	BG834273	BG834273 352430 MA
	322	32	0.8	361	12	BI895643	BI895643 EtESTeb01
	323	32	0.8	362	12	BI895650	BI895650 EtESTeb02
	324	32	0.8	385	10	BF079670	BF079670 230334 MA
	325	32	0.8	404	14	CB811652	CB811652 AMGNNUC:S
	326	32	0.8	407	14	CD343746	CD343746 EtESTee79
c	327	32	0.8	424	12	BI895715	BI895715 EtESTed27
	328	32	0.8	461	10	BE751193	BE751193 203072 MA
	329	32	0.8	560	14	CD344531	CD344531 EtESTee80
	330	32	0.8	581	14	CD344526	CD344526 EtESTee80
c	331	31	0.8	228	12	BJ488644	BJ488644 BJ488644
	332	31	0.8	282	12	BI042331	BI042331 MR4-NT014
	333	31	0.8	297	12	BI895975	BI895975 EtESTed84
	334	31	0.8	319	9	AI676744	AI676744 etmEST052
c	335	31	0.8	368	12	BI895096	BI895096 EtESTea10
	336	31	0.8	370	14	CD658393	CD658393 EtESTeg22
	337	31	0.8	373	14	CD345428	CD345428 EtESTef93
	338	31	0.8	376	9	AI371500	AI371500 qy07b02.x
	339	31	0.8	379	12	BI896060	BI896060 EtESTee02
c	340	31	0.8	390	12	BI895228	BI895228 EtESTea22
	341	31	0.8	397	12	BI895395	BI895395 EtESTea36
	342	31	0.8	423	12	BI895942	BI895942 EtESTed77
	343	31	0.8	434	9	AV625698	AV625698 AV625698
	344	31	0.8	435	12	BI895247	BI895247 EtESTea22
	345	31	0.8	443	12	BI895849	BI895849 EtESTed55
	346	31	0.8	448	12	BG561587	BG561587 EtESTee01
c	347	31	0.8	472	12	BI895246	BI895246 EtESTea22
c	348	31	0.8	489	14	CD345681	CD345681 EtESTef81
	349	31	0.8	525	12	BG929650	BG929650 etsHEST00
	350	31	0.8	547	10	BF821712	BF821712 MR1-RT007
	351	31	0.8	550	14	CD658484	CD658484 EtESTeg23
	352	31	0.8	552	12	BM306701	BM306701 EtESTee34
	353	31	0.8	561	12	BM306709	BM306709 EtESTee34
	354	31	0.8	576	12	BM306708	BM306708 EtESTee34
	355	31	0.8	582	14	CD661353	CD661353 EtESTeg46
	356	31	0.8	704	12	BJ015692	BJ015692 BJ015692
c	357	31	0.8	808	29	CNS02NGR	AL205380 Tetraodon
	358	31	0.8	816	14	CA326779	CA326779 UI-M-FY0-
	359	31	0.8	857	13	BQ686424	BQ686424 AGENCOURT
	360	31	0.8	881	12	BI868319	BI868319 603392278
	361	31	0.8	906	14	CF411097	CF411097 CH3#071_E
c	362	31	0.8	925	29	CNS0381E	AL232043 Tetraodon
	363	31	0.8	1007	12	BM458161	BM458161 AGENCOURT
	364	31	0.8	1201	13	BX366767	BX366767 BX366767
	365	31	0.8	1201	13	BX378991	BX378991 BX378991
	366	31	0.8	1201	13	BX420108	BX420108 BX420108
	367	31	0.8	1383	13	BU766484	BU766484 SJEAEF09
	368	31	0.8	2309	29	AY411306	AY411306 Homo sapi
	369	30	0.8	125	14	CF540002	CF540002 UI-M-EX0-

	370	30	0.8	297	10	AW346522	AW346522 28332 MAR
	371	30	0.8	308	12	BG516537	BG516537 EtESTed67
	372	30	0.8	397	12	BI895688	BI895688 EtESTed15
	373	30	0.8	401	12	BI895693	BI895693 EtESTed18
	374	30	0.8	428	12	BI895872	BI895872 EtESTed58
	375	30	0.8	428	14	CB794209	CB794209 AMGNNUC:N
	376	30	0.8	440	10	AW436887	AW436887 77454 MAR
	377	30	0.8	441	12	BI895586	BI895586 EtESTea84
	378	30	0.8	451	12	BI895833	BI895833 EtESTed52
	379	30	0.8	501	14	CD345170	CD345170 EtESTef86
	380	30	0.8	508	12	BI895774	BI895774 EtESTed43
	381	30	0.8	532	12	BI895372	BI895372 EtESTea34
	382	30	0.8	538	14	CD665292	CD665292 EtESTeg40
	383	30	0.8	547	14	CD665558	CD665558 EtESTeg45
	384	30	0.8	566	14	CD665296	CD665296 EtESTeg40
	385	30	0.8	571	14	CD345341	CD345341 EtESTef88
	386	30	0.8	571	14	CD665644	CD665644 EtESTeg33
	387	30	0.8	577	14	CB606109	CB606109 AMGNNUC:N
	388	30	0.8	583	14	CD570032	CD570032 EtESTeg10
c	389	30	0.8	670	29	CC572946	CC572946 CH240_449
	390	30	0.8	712	12	BI733567	BI733567 603352447
	391	30	0.8	728	12	BJ536233	BJ536233 BJ536233
	392	29	0.7	160	10	BF599374	BF599374 263132 MA
	393	29	0.7	176	10	BB606636	BB606636 BB606636
c	394	29	0.7	204	12	BG945838	BG945838 MR3-KT005
c	395	29	0.7	225	12	BG950812	BG950812 CM4-CT066
	396	29	0.7	281	12	BI895553	BI895553 EtESTea79
	397	29	0.7	290	13	BY356663	BY356663 BY356663
	398	29	0.7	309	13	BY355786	BY355786 BY355786
	399	29	0.7	313	10	AW417152	AW417152 53132 MAR
	400	29	0.7	316	12	BI895455	BI895455 EtESTea46
c	401	29	0.7	322	14	CD343484	CD343484 EtESTee71
	402	29	0.7	330	14	CD344805	CD344805 EtESTee73
	403	29	0.7	340	14	CD660081	CD660081 EtESTef38
	404	29	0.7	342	14	CD570299	CD570299 EtESTeg14
	405	29	0.7	402	12	BM305750	BM305750 EtESTee40
c	406	29	0.7	404	10	BB848390	BB848390 BB848390
	407	29	0.7	408	12	BI895447	BI895447 EtESTea43
	408	29	0.7	411	12	BI895541	BI895541 EtESTea78
	409	29	0.7	415	12	BM321582	BM321582 EtESTee13
c	410	29	0.7	417	10	BB848238	BB848238 BB848238
	411	29	0.7	417	12	BG466220	BG466220 EtESTed50
	412	29	0.7	418	12	BM321570	BM321570 EtESTee13
	413	29	0.7	425	12	BI895456	BI895456 EtESTea46
c	414	29	0.7	425	13	BY259515	BY259515 BY259515
	415	29	0.7	426	14	CD665730	CD665730 EtESTef13
	416	29	0.7	427	12	BI895104	BI895104 EtESTea11
	417	29	0.7	429	12	BI895111	BI895111 EtESTea12
c	418	29	0.7	437	13	BY246545	BY246545 BY246545
	419	29	0.7	440	10	AW481298	AW481298 35306 MAR
	420	29	0.7	441	14	CB546776	CB546776 AMGNNUC:N
	421	29	0.7	443	12	BI895285	BI895285 EtESTea26
	422	29	0.7	445	14	CB744466	CB744466 AMGNNUC:M
	423	29	0.7	446	12	BG929838	BG929838 etsHEST02
	424	29	0.7	450	10	BE851514	BE851514 uw97b02.y
c	425	29	0.7	450	14	CD664705	CD664705 EtESTeg35
	426	29	0.7	453	9	AI759230	AI759230 EtESTea26
	427	29	0.7	454	12	BI342913	BI342913 370893 MA
	428	29	0.7	454	12	BM305567	BM305567 EtESTee37
c	429	29	0.7	457	10	BB856190	BB856190 BB856190
	430	29	0.7	470	12	BI895549	BI895549 EtESTea79
	431	29	0.7	475	12	BM701243	BM701243 UI-E-EJ0-
	432	29	0.7	476	12	BI896023	BI896023 EtESTed94
	433	29	0.7	484	12	BI895470	BI895470 EtESTea48
c	434	29	0.7	484	14	CD661175	CD661175 EtESTef49
	435	29	0.7	485	10	BE851360	BE851360 uw95b02.y
	436	29	0.7	487	12	BM258980	BM258980 523961 MA
	437	29	0.7	518	14	CD569083	CD569083 EtESTef98
	438	29	0.7	518	28	AZ357021	AZ357021 1M0098A24
	439	29	0.7	527	14	CD657839	CD657839 EtESTef57
	440	29	0.7	541	14	CF103583	CF103583 EtESTeg73
	441	29	0.7	543	14	CD342339	CD342339 EtESTee51
	442	29	0.7	558	9	AI878252	AI878252 fc52d11.y

	443	29	0.7	559	28	AZ661862	AZ661862 1M0540H08
	444	29	0.7	573	14	CD660303	CD660303 EtESTef33
	445	29	0.7	574	14	CF103526	CF103526 EtESTeg72
	446	29	0.7	589	14	CD660432	CD660432 EtESTef40
	447	29	0.7	600	9	AV616533	AV616533 AV616533
c	448	29	0.7	601	28	AZ357375	AZ357375 1M0098A24
c	449	29	0.7	604	12	BM024735	BM024735 fu72b02.x
c	450	29	0.7	614	12	BI981369	BI981369 fu51h11.x
c	451	29	0.7	629	12	BM024223	BM024223 fu47g09.x
c	452	29	0.7	633	13	BY749990	BY749990 BY749990
	453	29	0.7	634	12	BG634231	BG634231 AT30371.5
c	454	29	0.7	635	10	BB654214	BB654214 BB654214
c	455	29	0.7	650	13	BY727248	BY727248 BY727248
	456	29	0.7	653	10	BB630275	BB630275 BB630275
	457	29	0.7	673	28	BH067947	BH067947 RPCI-24-3
c	458	29	0.7	679	28	CC321178	CC321178 TAM32-5O5
c	459	29	0.7	686	13	BY747575	BY747575 BY747575
	460	29	0.7	690	9	AL585202	AL585202 AL585202
c	461	29	0.7	704	9	AW076957	AW076957 fj33a09.x
c	462	29	0.7	720	13	BY720619	BY720619 BY720619
	463	29	0.7	724	12	BM715816	BM715816 UI-E-EJ0-
	464	29	0.7	732	12	BG633803	BG633803 AT29732.5
c	465	29	0.7	732	14	CB170818	CB170818 BKV603001
	466	29	0.7	747	10	BF506735	BF506735 AT09292.5
	467	29	0.7	775	10	BF489425	BF489425 AT25543.5
	468	29	0.7	779	28	CC320252	CC320252 TAM32-4M1
	469	29	0.7	857	14	CA321177	CA321177 UI-M-FW0-
	470	29	0.7	904	14	CA475635	CA475635 AGENCOURT
	471	29	0.7	910	29	CNS041O4	AL270445 Tetraodon
	472	29	0.7	1243	11	BC034882	BC034882 Mus muscu
	473	29	0.7	1246	11	AK037155	AK037155 Mus muscu
c	474	29	0.7	3227	11	AK083309	AK083309 Mus muscu
c	475	28	0.7	168	12	BI895635	BI895635 EtESTea99
	476	28	0.7	232	14	CD518840	CD518840 AGENCOURT
c	477	28	0.7	234	9	AA627411	AA627411 nq49d07.s
c	478	28	0.7	239	12	BI793012	BI793012 ie50f07.x
c	479	28	0.7	251	10	BE504942	BE504942 hz37e11.x
	480	28	0.7	259	12	BI895605	BI895605 EtESTea86
	481	28	0.7	269	12	BI793314	BI793314 ie50f07.y
	482	28	0.7	274	13	BX610827	BX610827 BX610827
	483	28	0.7	336	12	BI895725	BI895725 EtESTed32
	484	28	0.7	406	14	CB808295	CB808295 AMGNNUC:S
	485	28	0.7	408	14	CB771221	CB771221 AMGNNUC:S
	486	28	0.7	418	12	BI895103	BI895103 EtESTea11
	487	28	0.7	434	12	BI895077	BI895077 EtESTea09
	488	28	0.7	436	12	BJ271085	BJ271085 BJ271085
	489	28	0.7	443	14	CB788577	CB788577 AMGNNUC:N
c	490	28	0.7	449	13	BY291744	BY291744 BY291744
	491	28	0.7	452	9	AI759506	AI759506 EtESTea28
	492	28	0.7	453	14	CD659409	CD659409 EtESTef41
c	493	28	0.7	464	12	BM306489	BM306489 EtESTee43
c	494	28	0.7	472	14	CB730426	CB730426 AMGNNUC:N
	495	28	0.7	485	12	BI896074	BI896074 EtESTee04
	496	28	0.7	487	12	BI895049	BI895049 EtESTea06
	497	28	0.7	499	28	AZ325941	AZ325941 1M0048E06
	498	28	0.7	514	14	CB968416	CB968416 EtESTef74
	499	28	0.7	518	14	CD661382	CD661382 EtESTeg46
	500	28	0.7	526	14	CB118612	CB118612 K-EST0165
c	501	28	0.7	543	14	CD342339	CD342339 EtESTee51
	502	28	0.7	550	14	CD661226	CD661226 EtESTef50
	503	28	0.7	554	14	CD343941	CD343941 EtESTee89
	504	28	0.7	563	12	BG326499	BG326499 602425344
	505	28	0.7	564	14	CD658353	CD658353 EtESTef20
	506	28	0.7	575	14	CD665884	CD665884 EtESTeg38
	507	28	0.7	577	14	CD666062	CD666062 EtESTeg28
	508	28	0.7	579	14	CD658994	CD658994 EtESTef45
c	509	28	0.7	583	29	CNS04JHZ	AL293552 Tetraodon
	510	28	0.7	586	29	CNS03TJV	AL259924 Tetraodon
c	511	28	0.7	589	14	CD660432	CD660432 EtESTef40
	512	28	0.7	591	14	CF103543	CF103543 EtESTeg72
	513	28	0.7	593	14	CD666237	CD666237 EtESTef22
	514	28	0.7	611	14	CD658342	CD658342 EtESTef20
	515	28	0.7	683	14	CA340866	CA340866 NISC_lz08

	516	28	0.7	709	14	CA501370	CA501370 WHE4032_G
	517	28	0.7	709	14	CF994655	CF994655 AGENCOURT
c	518	28	0.7	728	13	BU611085	BU611085 UI-M-FC0-
	519	28	0.7	734	12	BM009770	BM009770 603630414
	520	28	0.7	736	10	BE565585	BE565585 601338358
	521	28	0.7	769	14	CB234590	CB234590 AGENCOURT
	522	28	0.7	800	13	BU505482	BU505482 AGENCOURT
	523	28	0.7	827	13	BU376059	BU376059 603813931
	524	28	0.7	843	13	BX353115	BX353115 BX353115
	525	28	0.7	894	14	CB849227	CB849227 MRA-0921
	526	28	0.7	908	13	BQ678480	BQ678480 AGENCOURT
	527	28	0.7	950	13	BQ641701	BQ641701 AGENCOURT
c	528	28	0.7	1047	29	CNS015TC	AL105882 Drosophil
	529	28	0.7	1091	12	BM557591	BM557591 AGENCOURT
	530	28	0.7	1201	13	BX420026	BX420026 BX420026
c	531	27	0.7	180	9	AI936867	AI936867 wp70d06.x
c	532	27	0.7	183	9	AI497974	AI497974 tm97g11.x
c	533	27	0.7	198	9	AI499045	AI499045 tn02d05.x
c	534	27	0.7	207	10	AW139025	AW139025 UI-H-BI1-
c	535	27	0.7	240	10	BF512823	BF512823 UI-H-BW1-
c	536	27	0.7	240	10	AW205815	AW205815 UI-H-BI1-
	537	27	0.7	294	14	CB702202	CB702202 AMGNNUC:C
	538	27	0.7	361	14	CB968119	CB968119 EtESTef65
c	539	27	0.7	375	14	CD658371	CD658371 EtESTef20
	540	27	0.7	392	14	CB774996	CB774996 AMGNNUC:M
	541	27	0.7	400	10	BE853884	BE853884 ux22h07.y
	542	27	0.7	406	14	CD664952	CD664952 EtESTeg50
c	543	27	0.7	414	12	BG909688	BG909688 TaLr1107E
	544	27	0.7	462	14	CB736553	CB736553 AMGNNUC:M
	545	27	0.7	484	9	AV632518	AV632518 AV632518
	546	27	0.7	485	12	BI895845	BI895845 EtESTed54
c	547	27	0.7	487	12	BG929784	BG929784 etsHEST02
	548	27	0.7	488	9	AA391431	AA391431 LD09869.5
	549	27	0.7	495	13	BU645005	BU645005 mgns017xD
	550	27	0.7	498	12	BI895846	BI895846 EtESTed54
	551	27	0.7	501	9	AI676586	AI676586 etmEST035
	552	27	0.7	503	9	AV632519	AV632519 AV632519
	553	27	0.7	511	14	CF103385	CF103385 EtESTeg70
	554	27	0.7	520	12	BI895346	BI895346 EtESTea32
	555	27	0.7	521	14	CD346767	CD346767 EtESTee97
	556	27	0.7	524	12	BM951289	BM951289 UI-M-EH0-
c	557	27	0.7	524	14	CD912324	CD912324 G550.113P
	558	27	0.7	526	9	AV703009	AV703009 AV703009
c	559	27	0.7	540	10	BF073650	BF073650 220587 MA
	560	27	0.7	556	12	BM951300	BM951300 UI-M-EH0-
	561	27	0.7	556	14	CD346698	CD346698 EtESTee96
c	562	27	0.7	566	12	BM305527	BM305527 EtESTee32
	563	27	0.7	566	14	CD347334	CD347334 EtESTee68
c	564	27	0.7	567	13	BQ599899	BQ599899 MI-P-E6-a
	565	27	0.7	575	13	BX509225	BX509225 DKFZp686M
	566	27	0.7	579	14	CD912323	CD912323 G550.113P
c	567	27	0.7	596	14	CF103512	CF103512 EtESTeg72
c	568	27	0.7	599	10	AW940549	AW940549 GH14459.3
	569	27	0.7	601	14	CD661453	CD661453 EtESTeg47
c	570	27	0.7	615	12	BJ215173	BJ215173 BJ215173
	571	27	0.7	628	28	BZ906589	BZ906589 CH240_29L
	572	27	0.7	632	14	CD579845	CD579845 EST_PSF00
c	573	27	0.7	641	28	AZ627945	AZ627945 1M0469C20
	574	27	0.7	659	10	BE627807	BE627807 uu54f01.y
c	575	27	0.7	699	14	CF871938	CF871938 tric029xe
	576	27	0.7	728	14	CB520243	CB520243 UI-M-GI0-
	577	27	0.7	728	29	CE097335	CE097335 tigr-gss-
c	578	27	0.7	730	29	CE539637	CE539637 tigr-gss-
	579	27	0.7	741	14	CF540685	CF540685 UI-M-GV0-
c	580	27	0.7	748	14	CF877379	CF877379 tric075xn
	581	27	0.7	754	14	Z78344	Z78344 HSZ78344 Hu
c	582	27	0.7	755	14	CB902165	CB902165 tric029xe
	583	27	0.7	779	13	BU055071	BU055071 UI-M-FO0-
	584	27	0.7	780	13	BU706387	BU706387 UI-M-FO0-
	585	27	0.7	794	29	CC476806	CC476806 CH240_302
	586	27	0.7	795	9	AV704315	AV704315 AV704315
c	587	27	0.7	805	14	CB905720	CB905720 tric075xn
	588	27	0.7	808	28	BH083677	BH083677 RPCI-24-3
	589	27	0.7	812	12	BG921179	BG921179 602823079
	590	27	0.7	815	9	AU118352	AU118352 AU118352
	591	27	0.7	815	9	AU137741	AU137741 AU137741
c	592	27	0.7	815	14	CB909566	CB909566 tric088xj
c	593	27	0.7	815	14	CF883425	CF883425 tric088xj
	594	27	0.7	817	14	CA317642	CA317642 UI-M-FW0-
c	595	27	0.7	823	9	AU205370	AU205370 AU205370
c	596	27	0.7	824	14	CK146312	CK146312 AGENCOURT
	597	27	0.7	829	9	AU139258	AU139258 AU139258
	598	27	0.7	851	14	CA789259	CA789259 AGENCOURT
	599	27	0.7	855	9	AU130348	AU130348 AU130348
c	600	27	0.7	859	29	CC532797	CC532797 CH240_410
c	601	27	0.7	877	12	BI689167	BI689167 603315977
c	602	27	0.7	889	14	CA475321	CA475321 AGENCOURT
	603	27	0.7	907	14	CB988790	CB988790 AGENCOURT
c	604	27	0.7	944	14	CA477795	CA477795 AGENCOURT
	605	27	0.7	947	13	BU505117	BU505117 AGENCOURT
	606	27	0.7	1026	13	BQ934612	BQ934612 AGENCOURT
	607	27	0.7	1128	29	CNS06RD1	AL411803 T7 end of
	608	27	0.7	4796	11	AK086146	AK086146 Mus muscu
	609	26	0.7	147	13	BY000062	BY000062 BY000062
	610	26	0.7	160	10	BF193150	BF193150 244630 MA
	611	26	0.7	172	10	AW629635	AW629635 hh67h08.y
	612	26	0.7	174	14	CD342201	CD342201 EtESTee49
c	613	26	0.7	179	9	AI843475	AI843475 UI-M-AQ1-
	614	26	0.7	185	10	AW214850	AW214850 up02d05.y
	615	26	0.7	187	10	BB562132	BB562132 BB562132
	616	26	0.7	195	28	AQ848999	AQ848999 LMAJFV1_1
c	617	26	0.7	200	10	AW919595	AW919595 EST350899
	618	26	0.7	202	9	AV753500	AV753500 AV753500
	619	26	0.7	202	13	BY000064	BY000064 BY000064
	620	26	0.7	202	14	CD729710	CD729710 4037103 1
	621	26	0.7	202	14	H33534	H33534 EST109643 R
	622	26	0.7	204	28	AZ397053	AZ397053 1M0161B23
	623	26	0.7	210	13	BY358698	BY358698 BY358698
	624	26	0.7	213	12	BG929698	BG929698 etsHEST01
	625	26	0.7	218	13	BY354960	BY354960 BY354960
	626	26	0.7	237	9	AA376262	AA376262 EST88910
	627	26	0.7	237	12	BM076910	BM076910 TrEST-A31
	628	26	0.7	257	12	BI895396	BI895396 EtESTea36
	629	26	0.7	268	14	CD553601	CD553601 B0362B09-
	630	26	0.7	270	10	BF088622	BF088622 RC0-HT088
	631	26	0.7	270	10	BF088700	BF088700 RC0-HT088
	632	26	0.7	279	14	CD659108	CD659108 EtESTef46
	633	26	0.7	279	14	CD666374	CD666374 EtESTef22
	634	26	0.7	280	13	BY522026	BY522026 BY522026
	635	26	0.7	281	9	AA361962	AA361962 EST71301
	636	26	0.7	282	10	BB562759	BB562759 BB562759
	637	26	0.7	282	10	BB580982	BB580982 BB580982
	638	26	0.7	282	14	CD666558	CD666558 EtESTef26
c	639	26	0.7	286	12	BG276186	BG276186 uv01d01.y
	640	26	0.7	289	10	BF040037	BF040037 BP250004B
	641	26	0.7	292	12	BI895497	BI895497 EtESTea58
	642	26	0.7	293	10	BB561999	BB561999 BB561999
	643	26	0.7	295	9	AV167233	AV167233 AV167233
	644	26	0.7	296	13	BY355017	BY355017 BY355017
c	645	26	0.7	297	29	CG465730	CG465730 KRIBB_2D_
	646	26	0.7	304	14	CD665473	CD665473 EtESTeg44
	647	26	0.7	305	9	AA300819	AA300819 EST13767
	648	26	0.7	310	14	CF545342	CF545342 lae77h02.
c	649	26	0.7	312	10	AW178929	AW178929 MR0-ST003
c	650	26	0.7	312	12	BI020956	BI020956 IL2-MT017
	651	26	0.7	312	13	BY185424	BY185424 BY185424
	652	26	0.7	313	9	AI944477	AI944477 bs01h04.y
c	653	26	0.7	317	12	BG929750	BG929750 etsHEST01
	654	26	0.7	319	12	BG953065	BG953065 MR4-CT053
	655	26	0.7	324	14	CD660221	CD660221 EtESTef56
c	656	26	0.7	325	10	AW371805	AW371805 CM2-BT030
	657	26	0.7	326	13	BU411790	BU411790 603152487
	658	26	0.7	326	29	CG288718	CG288718 OGWJS90TH
	659	26	0.7	328	12	BI895457	BI895457 EtESTea46
	660	26	0.7	328	14	CD600372	CD600372 RK123A3B0
	661	26	0.7	330	12	BI895509	BI895509 EtESTea63

	662	26	0.7	331	13	BY220998	BY220998 BY220998
c	663	26	0.7	332	13	BY778378	BY778378 BY778378
	664	26	0.7	332	29	CE800275	CE800275 tigr-gss-
	665	26	0.7	333	14	T08930	T08930 EST06822 In
	666	26	0.7	334	13	BY187135	BY187135 BY187135
	667	26	0.7	336	13	BY181564	BY181564 BY181564
	668	26	0.7	337	13	BY188050	BY188050 BY188050
c	669	26	0.7	337	28	AZ852656	AZ852656 2M0155K15
c	670	26	0.7	338	28	AZ780299	AZ780299 2M0017H02
	671	26	0.7	339	10	AW861888	AW861888 CM3-CT034
	672	26	0.7	340	13	BY098244	BY098244 BY098244
	673	26	0.7	340	13	BY186754	BY186754 BY186754
	674	26	0.7	341	13	BY136849	BY136849 BY136849
c	675	26	0.7	342	13	BY109162	BY109162 BY109162
	676	26	0.7	342	13	BY176442	BY176442 BY176442
	677	26	0.7	343	9	AI944453	AI944453 bs01f01.y
	678	26	0.7	343	13	BY188076	BY188076 BY188076
	679	26	0.7	344	10	AW464785	AW464785 BP230016B
	680	26	0.7	344	13	BY190822	BY190822 BY190822
	681	26	0.7	345	13	BY181165	BY181165 BY181165
	682	26	0.7	345	13	BY184180	BY184180 BY184180
	683	26	0.7	346	13	BY186564	BY186564 BY186564
	684	26	0.7	346	13	BY192552	BY192552 BY192552
	685	26	0.7	346	13	BY349322	BY349322 BY349322
	686	26	0.7	347	13	BY208762	BY208762 BY208762
	687	26	0.7	348	13	BY186480	BY186480 BY186480
	688	26	0.7	348	13	BY186884	BY186884 BY186884
	689	26	0.7	348	13	BY191302	BY191302 BY191302
c	690	26	0.7	349	13	BQ169410	BQ169410 WHE1755-1
	691	26	0.7	349	13	BY186927	BY186927 BY186927
	692	26	0.7	349	13	BY187211	BY187211 BY187211
	693	26	0.7	349	13	BY187368	BY187368 BY187368
c	694	26	0.7	350	10	BF041599	BF041599 BP250007A
	695	26	0.7	350	14	CF133709	CF133709 WHE4362_D
	696	26	0.7	351	13	BY180247	BY180247 BY180247
	697	26	0.7	352	10	BE839212	BE839212 RC0-FN014
	698	26	0.7	352	13	BY175643	BY175643 BY175643
	699	26	0.7	352	13	BY181335	BY181335 BY181335
c	700	26	0.7	353	12	BG986317	BG986317 CM1-HT114
	701	26	0.7	353	13	BY180349	BY180349 BY180349
	702	26	0.7	353	13	BY199405	BY199405 BY199405
	703	26	0.7	353	13	BY200143	BY200143 BY200143
	704	26	0.7	354	13	BY024500	BY024500 BY024500
	705	26	0.7	354	13	BY177868	BY177868 BY177868
	706	26	0.7	355	13	BY177097	BY177097 BY177097
	707	26	0.7	355	13	BY205243	BY205243 BY205243
	708	26	0.7	356	9	AV708885	AV708885 AV708885
	709	26	0.7	356	13	BY177769	BY177769 BY177769
c	710	26	0.7	357	9	AA065280	AA065280 e01500t T
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	712	26	0.7	358	13	BY177927	BY177927 BY177927
	713	26	0.7	358	13	BY178455	BY178455 BY178455
	714	26	0.7	358	13	BY187851	BY187851 BY187851
	715	26	0.7	359	13	BY200470	BY200470 BY200470
	716	26	0.7	359	13	BY203122	BY203122 BY203122
c	717	26	0.7	360	9	AI678308	AI678308 tu80e01.x
	718	26	0.7	360	12	BG274363	BG274363 WHE2227_G
	719	26	0.7	360	13	BY178712	BY178712 BY178712
	720	26	0.7	361	12	BI895742	BI895742 EtESTed37
	721	26	0.7	361	13	BY192038	BY192038 BY192038
	722	26	0.7	361	13	BY207151	BY207151 BY207151
	723	26	0.7	362	9	AJ006262	AJ006262 AJ006262
	724	26	0.7	362	10	BE292206	BE292206 601085056
c	725	26	0.7	364	13	BY785372	BY785372 BY785372
	726	26	0.7	365	9	AV170224	AV170224 AV170224
	727	26	0.7	365	13	BY187581	BY187581 BY187581
	728	26	0.7	365	13	BY192993	BY192993 BY192993
	729	26	0.7	365	14	CF849803	CF849803 psMA011xP
	730	26	0.7	366	9	AI756441	AI756441 EtESTea15
	731	26	0.7	366	13	BY188610	BY188610 BY188610
	732	26	0.7	366	13	BY202577	BY202577 BY202577
	733	26	0.7	367	13	BY020339	BY020339 BY020339
	734	26	0.7	369	13	BY021124	BY021124 BY021124
	735	26	0.7	370	13	BY174398	BY174398 BY174398
c	736	26	0.7	372	9	AA899172	AA899172 UI-R-E0-c
c	737	26	0.7	374	10	BF286766	BF286766 EST451357
	738	26	0.7	374	12	BI895484	BI895484 EtESTea55
	739	26	0.7	374	13	BY175970	BY175970 BY175970
c	740	26	0.7	375	10	BF548841	BF548841 UI-R-A0-a
	741	26	0.7	375	12	BI895759	BI895759 EtESTed41
	742	26	0.7	375	13	BY005428	BY005428 BY005428
	743	26	0.7	375	13	BY198412	BY198412 BY198412
	744	26	0.7	376	13	BY205060	BY205060 BY205060
	745	26	0.7	378	12	BG561070	BG561070 EtESTed91
	746	26	0.7	378	12	BI895438	BI895438 EtESTea42
	747	26	0.7	378	13	BY028081	BY028081 BY028081
c	748	26	0.7	378	13	BY133117	BY133117 BY133117
	749	26	0.7	380	14	CD345291	CD345291 EtESTef87
c	750	26	0.7	384	12	BG516259	BG516259 EtESTed56
	751	26	0.7	384	12	BI895013	BI895013 EtESTea02
	752	26	0.7	386	14	CB806753	CB806753 AMGNNUC:N
	753	26	0.7	388	13	BY174542	BY174542 BY174542
	754	26	0.7	388	13	BY174823	BY174823 BY174823
	755	26	0.7	389	12	BI895518	BI895518 EtESTea64
	756	26	0.7	397	9	AL709633	AL709633 DKFZp686N
c	757	26	0.7	398	13	BY018675	BY018675 BY018675
c	758	26	0.7	399	14	CB706256	CB706256 AMGNNUC:T
	759	26	0.7	401	14	CB548085	CB548085 AMGNNUC:M
	760	26	0.7	401	14	U80749	U80749 U80749 Huma
	761	26	0.7	405	9	AA065271	AA065271 f08502r T
c	762	26	0.7	405	9	AA065279	AA065279 e10500r T
c	763	26	0.7	405	9	AA065308	AA065308 c09501m T
	764	26	0.7	406	9	AA088367	AA088367 zl82c06.r
	765	26	0.7	407	9	AI482508	AI482508 vg48b04.x
c	766	26	0.7	407	12	BG560846	BG560846 EtESTed93
	767	26	0.7	409	28	AZ297519	AZ297519 RPCI-23-1
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	769	26	0.7	410	13	BY180983	BY180983 BY180983
	770	26	0.7	411	9	AV708830	AV708830 AV708830
	771	26	0.7	412	9	AI945592	AI945592 bs14e12.y
	772	26	0.7	412	9	AA575330	AA575330 vl86a04.r
	773	26	0.7	412	10	BF225249	BF225249 uz44e09.y
	774	26	0.7	412	12	BI895448	BI895448 EtESTea43
	775	26	0.7	415	12	BI895861	BI895861 EtESTed57
	776	26	0.7	415	28	AZ839702	AZ839702 2M0135N24
	777	26	0.7	415	29	CNS03JLV	AL247036 Tetraodon
	778	26	0.7	416	9	AA549687	AA549687 vk87g03.s
c	779	26	0.7	416	14	CB767989	CB767989 AMGNNUC:N
	780	26	0.7	417	12	BG516192	BG516192 EtESTed54
	781	26	0.7	417	13	BY189188	BY189188 BY189188
c	782	26	0.7	418	9	AI551096	AI551096 vx37a04.x
c	783	26	0.7	419	10	BF988701	BF988701 QV0-GN014
	784	26	0.7	419	13	BY201555	BY201555 BY201555
	785	26	0.7	419	14	CB968111	CB968111 EtESTef65
	786	26	0.7	420	13	BX613333	BX613333 BX613333
	787	26	0.7	420	14	CD346976	CD346976 EtESTee99
	788	26	0.7	421	13	BQ106149	BQ106149 fc0204.e
	789	26	0.7	422	9	AI756062	AI756062 EtESTea09
	790	26	0.7	423	9	AA246589	AA246589 LD05402.5
	791	26	0.7	423	13	BY208684	BY208684 BY208684
	792	26	0.7	424	13	BY636659	BY636659 BY636659
	793	26	0.7	425	28	AZ622153	AZ622153 1M0455C16
	794	26	0.7	427	14	CB795492	CB795492 AMGNNUC:N
	795	26	0.7	429	14	W53105	W53105 md14d02.r1
	796	26	0.7	430	9	AA224211	AA224211 zr14g02.r
	797	26	0.7	430	10	BB828537	BB828537 BB828537
c	798	26	0.7	430	14	CK330467	CK330467 H8219F04-
c	799	26	0.7	431	9	AJ285639	AJ285639 4A3B-AAV-
	800	26	0.7	432	12	BI895491	BI895491 EtESTea56
c	801	26	0.7	433	9	AI101450	AI101450 EST210739
	802	26	0.7	433	10	AW651728	AW651728 ba62f12.y
	803	26	0.7	433	12	BG235713	BG235713 EtESTed11
	804	26	0.7	434	9	AA416901	AA416901 zu13f07.s
	805	26	0.7	434	12	BG515995	BG515995 EtESTed47
	806	26	0.7	436	10	AW231111	AW231111 uo39f08.y
	807	26	0.7	436	10	BE028747	BE028747 EtESTea83

	808	26	0.7	436	12	BI895203	BI895203 EtESTea20
	809	26	0.7	437	10	BF451048	BF451048 uz73f05.y
	810	26	0.7	437	12	BI895266	BI895266 EtESTea24
c	811	26	0.7	437	12	BM305821	BM305821 EtESTee40
	812	26	0.7	438	12	BM630767	BM630767 170006875
	813	26	0.7	440	9	AW001869	AW001869 wt81c06.x
	814	26	0.7	440	10	BF189638	BF189638 235286 MA
	815	26	0.7	440	14	CD344312	CD344312 EtESTef79
	816	26	0.7	443	12	BM305480	BM305480 EtESTee31
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	818	26	0.7	445	10	AW502847	AW502847 UI-HF-BN0
	819	26	0.7	445	10	BF151730	BF151730 uz19g02.y
	820	26	0.7	445	13	BQ323226	BQ323226 IL2-CS004
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	822	26	0.7	448	14	N89616	N89616 zb10a07.s1
	823	26	0.7	449	10	BE381402	BE381402 601271288
	824	26	0.7	449	12	BI895042	BI895042 EtESTea06
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	826	26	0.7	450	9	AJ250795	AJ250795 AJ250795
	827	26	0.7	450	12	BI895253	BI895253 EtESTea23
	828	26	0.7	450	12	BI895387	BI895387 EtESTea35
	829	26	0.7	452	14	CD344183	CD344183 EtESTef77
	830	26	0.7	453	12	BI895590	BI895590 EtESTea84
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	832	26	0.7	454	12	BI895609	BI895609 EtESTea86
	833	26	0.7	456	10	AW376113	AW376113 RC0-CT020
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	836	26	0.7	459	12	BG247308	BG247308 602360011
	837	26	0.7	459	12	BM306808	BM306808 EtESTee36
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	839	26	0.7	460	12	BI895534	BI895534 EtESTea76
	840	26	0.7	460	14	CD449274	CD449274 Hd_mx17_0
	841	26	0.7	460	28	AZ629458	AZ629458 1M0482O21
	842	26	0.7	462	12	BI895602	BI895602 EtESTea86
	843	26	0.7	463	9	AA313553	AA313553 EST185432
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	845	26	0.7	465	9	AI893925	AI893925 md14d02.y
	846	26	0.7	466	12	BI895977	BI895977 EtESTed84
	847	26	0.7	467	9	AV627043	AV627043 AV627043
	848	26	0.7	467	14	CD342806	CD342806 EtESTee57
	849	26	0.7	469	14	CF138857	CF138857 UI-HF-BN0
	850	26	0.7	470	12	BG561523	BG561523 EtESTed78
	851	26	0.7	470	12	BI895944	BI895944 EtESTed78
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	853	26	0.7	471	14	CD658410	CD658410 EtESTeg22
	854	26	0.7	472	10	BF819805	BF819805 MR1-RT002
	855	26	0.7	472	12	BI232237	BI232237 RE28269.5
	856	26	0.7	473	12	BI896076	BI896076 EtESTee05
	857	26	0.7	473	14	CD344279	CD344279 EtESTef79
	858	26	0.7	474	12	BI895981	BI895981 EtESTed84
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	860	26	0.7	475	10	BB853548	BB853548 BB853548
	861	26	0.7	476	12	BG516213	BG516213 EtESTed55
	862	26	0.7	476	12	BI895773	BI895773 EtESTed42
	863	26	0.7	477	9	AU084762	AU084762 AU084762
	864	26	0.7	477	14	CD343511	CD343511 EtESTee71
	865	26	0.7	478	9	AI759180	AI759180 EtESTea15
	866	26	0.7	479	12	BI727921	BI727921 1031095F0
	867	26	0.7	479	12	BI895005	BI895005 EtESTea01
	868	26	0.7	479	12	BM306650	BM306650 EtESTee34
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	870	26	0.7	481	12	BG639466	BG639466 LP12447.5
	871	26	0.7	481	14	CB968298	CB968298 EtESTef67
	872	26	0.7	482	9	AL039573	AL039573 DKFZp434D
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	874	26	0.7	483	12	BG639468	BG639468 LP12491.5
	875	26	0.7	485	10	BF441154	BF441154 257319 MA
	876	26	0.7	485	10	BE305706	BE305706 601101469
	877	26	0.7	485	12	BM305489	BM305489 EtESTee31
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	879	26	0.7	486	14	CD345333	CD345333 EtESTef88
	880	26	0.7	487	9	AL599526	AL599526 DKFZp313D
	881	26	0.7	487	12	BM306307	BM306307 EtESTee28
	882	26	0.7	489	10	BF287438	BF287438 EST452029
	883	26	0.7	489	12	BG929616	BG929616 etsHEST00
	884	26	0.7	489	28	AZ600577	AZ600577 1M0418P23
	885	26	0.7	490	10	AW250335	AW250335 2822213.5
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	887	26	0.7	490	14	CF103520	CF103520 EtESTeg72
	888	26	0.7	491	12	BG929606	BG929606 etsHEST00
c	889	26	0.7	492	9	AL044264	AL044264 DKFZp434J
	890	26	0.7	492	13	BX281796	BX281796 BX281796
	891	26	0.7	492	14	CD658515	CD658515 EtESTef34
	892	26	0.7	493	13	BQ267093	BQ267093 NISC_ff16
	893	26	0.7	494	12	BI895962	BI895962 EtESTed81
	894	26	0.7	494	14	CD241486	CD241486 AGENCOURT
c	895	26	0.7	495	28	AZ474794	AZ474794 1M0292J10
	896	26	0.7	497	9	AA546433	AA546433 vk64f10.r
c	897	26	0.7	497	12	BI895902	BI895902 EtESTed65
	898	26	0.7	498	12	BM853089	BM853089 K-EST0134
	899	26	0.7	499	12	BI895131	BI895131 EtESTea14
	900	26	0.7	499	12	BI895990	BI895990 EtESTed86
	901	26	0.7	499	12	BM305561	BM305561 EtESTee37
	902	26	0.7	499	13	BY467533	BY467533 BY467533
	903	26	0.7	500	12	BI547486	BI547486 603191091
	904	26	0.7	500	14	CD580850	CD580850 RK011A1A0
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	906	26	0.7	501	12	BI895231	BI895231 EtESTea22
	907	26	0.7	501	12	BI895848	BI895848 EtESTed55
	908	26	0.7	503	13	BU970712	BU970712 HB15H07r
	909	26	0.7	503	14	CF864960	CF864960 psZS013xI
	910	26	0.7	505	10	BF116701	BF116701 uz01d12.y
	911	26	0.7	505	12	BI633683	BI633683 SD27830.5
	912	26	0.7	506	9	AU241443	AU241443 AU241443
	913	26	0.7	506	13	BX525122	BX525122 BX525122
	914	26	0.7	506	14	CB287664	CB287664 CMD64_E03
	915	26	0.7	506	28	AZ257283	AZ257283 RPCI-23-1
c	916	26	0.7	507	9	AA393263	AA393263 zt70b12.r
	917	26	0.7	507	10	BF829819	BF829819 MR3-HN006
c	918	26	0.7	507	12	BM247524	BM247524 K0803C08-
	919	26	0.7	508	12	BG635517	BG635517 SD12953.5
	920	26	0.7	509	12	BI895791	BI895791 EtESTed45
	921	26	0.7	509	13	BY475124	BY475124 BY475124
	922	26	0.7	510	12	BM889192	BM889192 kb06h06.y
	923	26	0.7	511	9	AU187439	AU187439 AU187439
	924	26	0.7	511	9	AA537406	AA537406 vj98c04.r
	925	26	0.7	511	10	AW762900	AW762900 ur59d07.y
	926	26	0.7	511	10	BE278686	BE278686 601158169
	927	26	0.7	511	12	BM305557	BM305557 EtESTee37
	928	26	0.7	511	14	CD343409	CD343409 EtESTee70
	929	26	0.7	512	10	BE101529	BE101529 UI-R-BO1-
	930	26	0.7	512	12	BM306609	BM306609 EtESTee33
	931	26	0.7	512	14	CB286895	CB286895 CMD48_E02
	932	26	0.7	513	28	AZ065784	AZ065784 RPCI-23-4
	933	26	0.7	514	10	BF868805	BF868805 IL3-ET011
	934	26	0.7	515	12	BI895463	BI895463 EtESTea47
	935	26	0.7	519	10	BE282191	BE282191 601100803
	936	26	0.7	519	12	BM003546	BM003546 1031111C0
	937	26	0.7	521	28	AZ642216	AZ642216 1M0505G07
	938	26	0.7	521	28	AZ928206	AZ928206 479.dif05
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	942	26	0.7	524	12	BM018466	BM018466 603646181
	943	26	0.7	524	14	CD344472	CD344472 EtESTef04
	944	26	0.7	525	10	BE027990	BE027990 EtESTea64
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c	946	26	0.7	525	14	CD554325	CD554325 B0374E02-
	947	26	0.7	525	29	CE330099	CE330099 tigr-gss-
	948	26	0.7	527	9	AA264019	AA264019 LD07443.5
	949	26	0.7	527	9	AA266914	AA266914 mz96f02.r
c	950	26	0.7	528	13	BX524444	BX524444 BX524444
	951	26	0.7	529	12	BM744523	BM744523 K-EST0018
	952	26	0.7	530	9	AV433675	AV433675 AV433675
	953	26	0.7	530	13	BQ550344	BQ550344 H4002G10-

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955	26	0.7	531	10	BF418570	BF418570 UI-R-BJ2-
956	26	0.7	531	14	CD550551	CD550551 B0314G10-
957	26	0.7	532	10	BE027846	BE027846 EtESTea88
958	26	0.7	532	10	BF022341	BF022341 uy56b03.y
959	26	0.7	532	13	BX514428	BX514428 BX514428
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961	26	0.7	533	14	CD347015	CD347015 EtESTef09
962	26	0.7	534	14	CD665231	CD665231 EtESTeg40
963	26	0.7	535	9	AL921244	AL921244 AL921244
964	26	0.7	535	13	BU698806	BU698806 LL2in1022
965	26	0.7	536	9	AI516567	AI516567 LD42469.5
966	26	0.7	537	10	BF454517	BF454517 maa06a01.
967	26	0.7	539	9	AL913586	AL913586 AL913586
c 968	26	0.7	539	14	CA886899	CA886899 B0133A08-
969	26	0.7	539	29	CE291482	CE291482 tigr-gss-
c 970	26	0.7	540	12	BG929829	BG929829 etsHEST02
c 971	26	0.7	540	14	CA896395	CA896395 B0198G11-
972	26	0.7	540	14	CD569565	CD569565 EtESTeg06
c 973	26	0.7	540	28	AQ765853	AQ765853 HS_5373_B
974	26	0.7	542	9	AI755960	AI755960 EtESTea21
975	26	0.7	542	12	BI895343	BI895343 EtESTea31
976	26	0.7	543	12	BI636199	BI636199 SD17809.5
c 977	26	0.7	543	14	CF103557	CF103557 EtESTeg73
978	26	0.7	544	28	AZ580599	AZ580599 1M0368K24
979	26	0.7	545	9	AA939801	AA939801 vz92h11.r
980	26	0.7	545	13	BY571246	BY571246 BY571246
981	26	0.7	545	14	CD569667	CD569667 EtESTeg03
982	26	0.7	545	14	CD665420	CD665420 EtESTeg43
983	26	0.7	546	13	BU053848	BU053848 UI-M-FD0-
984	26	0.7	546	14	CD665470	CD665470 EtESTeg44
985	26	0.7	547	12	BI228127	BI228127 RE25571.5
986	26	0.7	548	12	BM306232	BM306232 EtESTee27
987	26	0.7	548	14	CD345538	CD345538 EtESTef95
988	26	0.7	549	13	BX515407	BX515407 BX515407
989	26	0.7	549	14	CD343832	CD343832 EtESTee88
990	26	0.7	550	10	BE232078	BE232078 137005 MA
991	26	0.7	550	12	BM303486	BM303486 SnEST4a59
c 992	26	0.7	551	14	CA601243	CA601243 wl1.pk001
993	26	0.7	553	14	CD569553	CD569553 EtESTeg06
994	26	0.7	554	10	BE807600	BE807600 ss28a06.y
995	26	0.7	554	14	CD665561	CD665561 EtESTeg45
996	26	0.7	555	9	AI533089	AI533089 SD04787.5
c 997	26	0.7	555	14	CA888587	CA888587 B0147B11-
998	26	0.7	555	14	CD343065	CD343065 EtESTee61
999	26	0.7	555	14	CD570342	CD570342 EtESTef97
c1000	26	0.7	556	10	BE235417	BE235417 142887 MA

ALIGNMENTS

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RESULT 1
BQ684810
LOCUS       BQ684810                 907 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8346064 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250774
            5', mRNA sequence.
ACCESSION   BQ684810
VERSION     BQ684810.1  GI:21810126
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 907)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2394  row: f  column: 23
            High quality sequence stop: 665.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6250774"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_110"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of  California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             19.9%;  Score 786;  DB 13;  Length 907;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  786;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3137 ATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGG 3196
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Db          1 ATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGG 60

Qy       3197 TGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGA 3256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGA 120

Qy       3257 AGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAAT 3316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAAT 180

Qy       3317 ACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGG 3376
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Db        181 ACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGG 240

Qy       3377 CCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCC 3436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCC 300

Qy       3437 CTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCA 3496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCA 360

Qy       3497 GTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTG 3556
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Db        361 GTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTG 420

Qy       3557 TGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCA 3616
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Db        421 TGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCA 480

Qy       3617 TGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCA 3676
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Db        481 TGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCA 540

Qy       3677 TTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCA 3736
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Db        541 TTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCA 600

Qy       3737 ACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACC 3796
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Db        601 ACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACC 660
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Qy       3797 TCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATG 3856
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Db        661 TCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATG 720

Qy       3857 ACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTTACTTCATGACTC 3916
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGCAGCAGCCAAGTTTACTTCATGACTC 780

Qy       3917 TGAACC 3922
              ||||||
Db        781 TGAACC 786


RESULT 2
BU542554
LOCUS       BU542554                 908 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10322513 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6574439
            5', mRNA sequence.
ACCESSION   BU542554
VERSION     BU542554.1  GI:22853037
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2769  row: l  column: 23
            High quality sequence stop: 686.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6574439"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_40"
                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California,  Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life  Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            19.7%;  Score 779;  DB 13;  Length 908;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  779;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2679 CGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAA 2738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAA 60

Qy       2739 GGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTT 2798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTT 120

Qy       2799 CACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCAT 2858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCAT 180

Qy       2859 CACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAA 2918
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Db        181 CACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAA 240

Qy       2919 GGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGAT 2978
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Db        241 GGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGAT 300

Qy       2979 CCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAA 3038
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Db        301 CCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAA 360

Qy       3039 CCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGT 3098
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Db        361 CCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGT 420

Qy       3099 GTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCT 3158
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Db        421 GTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCT 480

Qy       3159 GCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCG 3218
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Db        481 GCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCG 540

Qy       3219 GAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGG 3278
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Db        541 GAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGG 600

Qy       3279 GGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGT 3338
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Db        601 GGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGT 660

Qy       3339 CATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATT 3398
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Db        661 CATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATT 720

Qy       3399 CATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAG 3457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAG 779


RESULT 3
BU838349
LOCUS       BU838349                 969 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_8123283 Lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6176926 5', mRNA sequence.
ACCESSION   BU838349
VERSION     BU838349.1  GI:24022744
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13554  row: a  column: 23
            High quality sequence stop: 626.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6176926"
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                     /dev_stage="adult, 36 yr"
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                     /clone_lib="Lupski_dorsal_root_ganglion"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match             19.2%;  Score 757;  DB 13;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  757;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1553 AACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTC 1612
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Db          9 AACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATGAACAAGCAGCAGAACTCTC 68

Qy       1613 CCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCATCCCCCAGGCCTCCC 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 CCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCATCCCCCAGGCCTCCC 128

Qy       1673 CAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGG 1732
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Db        129 CAGGGCCCCCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGG 188

Qy       1733 AGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCT 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 AGGGACCGCACAAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCT 248

Qy       1793 CCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTG 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CCCATGACCCCGACCCTGCCATCCCCGCACCCACTGCCACGCCCAGTGCCCGAGGAGCTG 308

Qy       1853 TCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAG 1912
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Db        309 TCATCCGCCAGAATTCAGACCCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAG 368

Qy       1913 CCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCG 1972
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Db        369 CCTGGGTCCGCCCAGATAACGAGGCCCCACCCAAGGTGCCTCAGAGGACCTCATCTATCG 428

Qy       1973 CCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCA 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CCACTGCCCTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCCAGGCAGTCCGTGCCA 488

Qy       2033 GACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCC 548

Qy       2093 CAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCG 2152
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Db        549 CAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCCTCTAGTAACCCCG 608

Qy       2153 ACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACG 2212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACG 668

Qy       2213 GGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGG 2272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGG 728

Qy       2273 ACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAA 2309
              |||||||||||||||||||||||||||||||||||||
Db        729 ACAGCTCCCCTGTGCTCTCCCCTGGGAATAAAGCCAA 765


RESULT 4
AL551911
LOCUS       AL551911                1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL551911 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI060YH23 5-PRIME, mRNA sequence.
ACCESSION   AL551911
VERSION     AL551911.2  GI:31273727
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12890305.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8486.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI060CD12QP1&cluster=8486.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI060CD12QP1.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone="CS0DI060YH23"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             18.6%;  Score 735;  DB 9;  Length 1201;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  735;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 317

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 377

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 437

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 497

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 557

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
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Db          558 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 617

Qy          367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Qy          427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          678 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 737

Qy          487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          738 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 797

Qy          547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          798 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 857

Qy          607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          858 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 917

Qy          667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 726
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          918 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCCATGCGA 977

Qy          727 GCCCTCTTCCTCATT 741
                |||||||||||||||
Db          978 GCCCTCTTCCTCATT 992

RESULT 5
BU542006
LOCUS       BU542006                 881 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10252775 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6573796
            5', mRNA sequence.
ACCESSION   BU542006
VERSION     BU542006.1  GI:22852489
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2768  row: b  column: 04
            High quality sequence stop: 680.
FEATURES             Location/Qualifiers
     source          1..881
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6573796"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_40"
                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California,  Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life  Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             18.5%;  Score 730;  DB 13;  Length 881;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  780;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         2679 CGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAA 2738
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 CGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAA 60

Qy         2739 GGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTT 2798
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 GGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTT 120

Qy         2799 CACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCAT 2858
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 CACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCAT 180

Qy         2859 CACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAA 2918
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 CACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAA 240

Qy         2919 GGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGAT 2978
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 GGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGAT 300

Qy         2979 CCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAA 3038
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 CCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAA 360

Qy         3039 CCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGT 3098
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 CCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGT 420

Qy         3099 GTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCT 3158
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Db          421 GTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCT 480

Qy         3159 GCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCG 3218
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 GCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCCTGGCTCCG 540

Qy         3219 GAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGG 3278
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Db          541 GAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGG 600

Qy         3279 GGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGT 3338
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Db          601 GGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGT 660

Qy         3339 CATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATT 3398
                |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db          661 CATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCCAACCCTACCACAAATT 720

Qy         3399 CATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGT 3458
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 CATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGT 780

Qy         3459 A 3459
                |
Db          781 A 781

RESULT 6
CD557991
LOCUS       CD557991                 910 bp    mRNA    linear   EST 11-JUN-2003
DEFINITION  AGENCOURT_14423308 NIH_MGC_180 Homo sapiens cDNA clone
            IMAGE:30387142 5', mRNA sequence.
ACCESSION   CD557991
VERSION     CD557991.1  GI:31584059
KEYWORDS    EST.
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM456  row: o  column: 23
            High quality sequence stop: 637.
FEATURES             Location/Qualifiers
     source          1. .910
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30387142"
                     /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_180"
                     /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site_1: NotI;
                     Site_2: EcoRV (destroyed); Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.68 kb. Library was
                     constructed by (Invitrogen). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             18.4%;  Score 727;  DB 14;  Length 910;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  727;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2952 CCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGAT 3011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGAT 60

Qy       3012 CCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTT 3071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTT 120

Qy       3072 GCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCA 3131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCA 180

Qy       3132 GATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACT 3191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACT 240

Qy       3192 GCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGA 3251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCGGGTGTATTACCTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGA 300

Qy       3252 GAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGT 3311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGT 360

Qy       3312 GAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGC 3371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGC 420

Qy       3372 CTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCA 3431
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Db        421 CTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCA 480

Qy       3432 CCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGG 3491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGG 540

Qy       3492 CTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACAT 3551
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Db        541 CTCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACAT 600

Qy       3552 CCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGA 3611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGA 660

Qy       3612 CGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCG 3671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCG 720

Qy       3672 CATCATT 3678
              |||||||
Db        721 CATCATT 727


RESULT 7
BC028888
LOCUS       BC028888                1515 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION  Homo sapiens misshapen/NIK-related kinase, mRNA (cDNA clone
            IMAGE:4751958), with apparent retained intron.
ACCESSION   BC028888
VERSION     BC028888.1  GI:20809392
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1515)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1515)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
```

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                Center code: BCM-HGSC
                Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                Contact: amg@bcm.tmc.edu
                Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
                Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                A.N., Gibbs, R.A.

                Clone distribution: MGC clone distribution information can be found
                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                Series: IRAK Plate: 29 Row: k Column: 19
                This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4751958"
                     /tissue_type="Skin, squamous cell carcinoma"
                     /clone_lib="NCI_CGAP_Skn4"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6.1"
ORIGIN

  Query Match             18.3%;  Score 724;  DB 11;  Length 1515;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  724;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3222 CAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGCTGGACCACCGTGGGGA 3281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGCTGGACCACCGTGGGGA 60

Qy       3282 CATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCAT 3341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAGTTCCTGGTCAT 120

Qy       3342 CGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCAT 3401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCAT 180

Qy       3402 GGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGA 3461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGA 240

Qy       3462 GGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGT 3521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGT 300

Qy       3522 CGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCC 3581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCC 360

Qy       3582 CCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGA 3641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGA 420

Qy       3642 CGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGG 3701
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGATGTGGTGCTGCAGTGGGG 480

Qy       3702 GGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAA 3761
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAA 540

Qy       3762 AGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACG 3821
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Db        541 AGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACG 600

Qy       3822 AGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCG 3881
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCCTCAGTCCG 660

Qy       3882 CTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTG 3941
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTG 720

Qy       3942 GTGA 3945
              ||||
Db        721 GTGA 724


RESULT 8
BM541693
LOCUS       BM541693                1026 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6448280 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531587
            5', mRNA sequence.
ACCESSION   BM541693
VERSION     BM541693.1  GI:18770559
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12213  row: h  column: 20
            High quality sequence stop: 681.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5531587"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_71"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb.  "
ORIGIN

  Query Match             18.2%;  Score 720;  DB 12;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  720;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2372 CTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGG 2431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 CTCTGGACGAGGCCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCCAGCGAGG 72

Qy       2432 AGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCA 2491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 AGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCA 132

Qy       2492 GAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCC 2551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 GAGATACCCCTGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCC 192

Qy       2552 ACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCC 2611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 ACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCC 252

Qy       2612 AGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACC 2671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 AGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACC 312

Qy       2672 TGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCAC 2731
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 TGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCAC 372

Qy       2732 CCTCGAAGGATGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGA 2791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CCTCGAAGGATGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGA 432

Qy       2792 GCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCA 2851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCA 492

Qy       2852 TCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACG 2911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 TCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACG 552

Qy       2912 TGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCC 2971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 TGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCC 612

Qy       2972 CTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGG 3031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 CTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGG 672

Qy       3032 GGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGG 3091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 GGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGG 732
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RESULT 9
BQ073811

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LOCUS       BQ073811                1022 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_7046407 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:5806711
            5', mRNA sequence.
ACCESSION   BQ073811
VERSION     BQ073811.1  GI:19902857
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1022)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2047  row: p  column: 08
            High quality sequence stop: 594.
FEATURES             Location/Qualifiers
     source          1..1022
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5806711"
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_101"
                     /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
                     XhoI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
```

```
  Query Match             18.1%;  Score 714;  DB 13;  Length 1022;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  714;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 97

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 157

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 217

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 277

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 337

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 397

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 457

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 517

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 577

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 637

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 697

Qy        667 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 ATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCCTCTGTGTGACATGCACCCC 751
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RESULT 10
BM451246

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LOCUS       BM451246                 936 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6392707 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5495254
            5', mRNA sequence.
ACCESSION   BM451246
VERSION     BM451246.1  GI:18500286
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 936)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
```

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             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12121  row: n  column: 23
            High quality sequence stop: 686.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5495254"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_67"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             17.6%;  Score 697;  DB 12;  Length 936;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-310;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2442 CAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCC 2501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCC 60

Qy       2502 TGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGA 2561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGGGGCCGCAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGA 120

Qy       2562 GGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCC 2621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCC 180

Qy       2622 TGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGT 2681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGT 240

Qy       2682 GGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGA 2741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGA 300

Qy       2742 TGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCAC 2801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCCTGGCAAGAGCTCGTTCAC 360

Qy       2802 GATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCAC 2861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCAC 420

Qy       2862 AGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGG 2921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGG 480

Qy       2922 TTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCG 2981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCG 540

Qy       2982 GAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCT 3041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCT 600

Qy       3042 GCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTA 3101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTA 660

Qy       3102 TGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGAT 3138
              |||||||||||||||||||||||||||||||||||||
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Db        661 TGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGAT 697


RESULT 11
BQ706178
LOCUS       BQ706178                 951 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353101 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278193
            5', mRNA sequence.
ACCESSION   BQ706178
VERSION     BQ706178.1  GI:21845077
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2465  row: m  column: 10
            High quality sequence start: 12
            High quality sequence stop: 710.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278193"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             17.5%;  Score 693;  DB 13;  Length 951;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-308;
  Matches  693;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2541 CATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCAC 2600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 CATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCAC 83

Qy       2601 CATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGG 2660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGG 143

Qy       2661 GTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGG 2720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGG 203

Qy       2721 CCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGC 2780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 CCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGC 263

Qy       2781 CCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAG 2840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAG 323
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Qy       2841 TGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCT 2900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCT 383

Qy       2901 GCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCA 2960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 GCAGTACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCA 443

Qy       2961 CAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGC 3020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGC 503

Qy       3021 AGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCG 3080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCG 563

Qy       3081 AAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGT 3140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGT 623

Qy       3141 GCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTA 3200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 GCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTA 683

Qy       3201 TTACCTGTCCTGGCTCCGGAACAAGATTCTGCA 3233
              |||||||||||||||||||||||||||||||||
Db        684 TTACCTGTCCTGGCTCCGGAACAAGATTCTGCA 716
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```
RESULT 12
BX359762
LOCUS       BX359762                1167 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX359762 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI061YG23 5-PRIME, mRNA sequence.
ACCESSION   BX359762
VERSION     BX359762.1  GI:30384366
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1167)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 8486.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI061AD12QP1&cluster=8486.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI061AD12QP1.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DI061YG23"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             16.1%;  Score 638;  DB 13;  Length 1167;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-282;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 GGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGT 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGT 376

Qy        123 GTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCAC 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCAC 436

Qy        183 GGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCA 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 GGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCA 496

Qy        243 CCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGA 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGA 556

Qy        303 CCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 CCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAA 616

Qy        363 CACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 CACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAG 676

Qy        423 GGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGT 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 GGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGT 736

Qy        483 GCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGA 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 GCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGA 796

Qy        543 CCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGT 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 CCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGT 856

Qy        603 CATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCT 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 CATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCT 916

Qy        663 AGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCC 700
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RESULT 13
BI000010
LOCUS       BI000010                 727 bp    mRNA    linear   EST 13-JUN-2001
DEFINITION  MR3-HN0063-040101-002-h01 HN0063 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI000010
VERSION     BI000010.1  GI:14404084
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 727)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
```

```
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-HN0063-
            040101-002-h01&t3=2001-01-04&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 714.
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                     /dev_stage="Adult"
                     /clone_lib="HN0063"
                     /note="Organ: head_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             16.0%;  Score 633;  DB 12;  Length 727;
  Best Local Similarity   100.0%;  Pred. No. 2e-280;
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Qy       3313 AAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCC 3372
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Db          1 AAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCC 60

Qy       3373 TGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCAC 3432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCAC 120

Qy       3433 CGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGC 3492
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Db        121 CGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGC 180

Qy       3493 TCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATC 3552
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Db        181 TCCAGTGCTGGCTTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATC 240

Qy       3553 CCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGAC 3612
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Db        241 CCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGAC 300

Qy       3613 GGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGC 3672
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Db        301 GGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGC 360

Qy       3673 ATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGC 3732
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Db        361 ATCATTAAGGATGTGGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGC 420

Qy       3733 TCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGC 3792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGC 480

Qy       3793 CACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGG 3852
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Db        481 CACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGG 540

Qy       3853 AATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATG 3912
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Db        541 AATGACAAGGTGTTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATG 600

Qy       3913 ACTCTGAACCGTAACTGCATCATGAACTGGTGA 3945
              |||||||||||||||||||||||||||||||||
Db        601 ACTCTGAACCGTAACTGCATCATGAACTGGTGA 633


RESULT 14
BM800664
LOCUS       BM800664                1037 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  AGENCOURT_6418992 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5535199
            5', mRNA sequence.
ACCESSION   BM800664
VERSION     BM800664.1  GI:19117487
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1037)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12222  row: o  column: 08
            High quality sequence stop: 658.
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ORIGIN

  Query Match             15.7%;  Score 621;  DB 12;  Length 1037;
  Best Local Similarity   99.9%;  Pred. No. 7.7e-275;
  Matches  671;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 66
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Db        140 ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTGCGGGAC 199

Qy         67 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 126
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Db        200 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAGGTGTAC 259

Qy        127 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAG 319

Qy        187 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 GACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCGC 379

Qy        247 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 AACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCCGGGAAACGATGACCAG 439

Qy        307 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAGAACACA 499

Qy        367 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 426
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Db        500 AAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTCAGGGGT 559

Qy        427 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 486
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Db        560 CTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTG 619

Qy        487 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTGGACCGC 546
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Db        620 CTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGNGGTGAGTGCTCAGCTGGACCGC 679

Qy        547 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 606
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Db        680 ACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAGGTCATC 739

Qy        607 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 666
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Db        740 GCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCTCTAGGA 799

Qy        667 ATCACAGCCATC 678
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RESULT 15
BI916276
LOCUS       BI916276                629 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603178186F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5242509 5',
            mRNA sequence.
ACCESSION   BI916276
VERSION     BI916276.1  GI:16180239
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 629)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11611  row: k  column: 22
            High quality sequence stop: 629.
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                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             15.6%;  Score 616;  DB 12;  Length 629;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-272;
  Matches  616;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3091 GGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGG 3150
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Db         14 GGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGG 73

Qy       3151 CTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCC 3210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 CTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAAACTGCGGGTGTATTACCTGTCC 133

Qy       3211 TGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACC 3270
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Db        134 TGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACC 193

Qy       3271 ACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAG 3330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 ACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGGATTAAG 253

Qy       3331 TTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTAC 3390
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Qy       3391 CACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGAC 3450
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Db        314 CACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCCACCGCCCTCTGCTGGTCGAC 373

Qy       3451 CTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCAT 3510
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Qy       3511 GCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGC 3570
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Db        434 GCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGC 493

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Search completed: March  3, 2004, 03:10:41
Job time : 6345 secs
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